

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met/Asp	SEQ ID NO: in USNN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, !=possible nucleotide insertion)
16223	46591	A	16318	219	1912	PHPTRRSAQSQVQYIEKDWP EGLEGGVLGQLVAFDSFTVSF HFVSAGNSPSPDESEERERDPKV LTFPEYITSLSDSGTKHMAAGV RMECHSKGRCPSSCPLCHVTSS PDTPAEPVLLEVTKAALLNTQS FPCSLMQLLQEATMSSLWCSTG GDVIEDWCRCDSTAAGGCVPVS CSFLSAHRLRLSTVHEPSTLVV LEWEHSEPPIGVQIVDYLRRQE KVTDRMDHSKVETGEHLLHG LVLIQGDKTKTKNAPLPHGFAP GPQYPRAMQEEQGEEEAVLLL QEAAVLLPLRVRDIRSCCRFRRH ELLFLMLFPFLLLWAETVLFSV DDIISGAKSPCAMPSSQVPDKQL TTIYFQPLIARFSFSSRKGLLRIM SSHCHGDCDVSSTLDSYTVSAN HALPLPARFTLWGVDTNTGRRS RPSDVIVYM*ITYFPFPSSIEAD KIVNLFNGYTSGKEQQTAYNTL LDLGSPTLHRVLYHYNQHYESF ASF*LKYLPLCLIHRKAGLILSQL GDLSSWCNGLLQEPKISLRSS LKYLCCRYSEIKPYGLDWAELS
16224	46592	A	16319	1	2031	
16225	46593	A	16320	1	739	MKRAGSSGGRGECDISAGRL GLEEAARLSCAVHTSPGGRRP GQAAGMSAKERPKGKVIKDSV TLLPCFYFVELPILASSVVSLYF LELTDVFKPVHSGFSCYDRSLS MPYIEPTQEAIPIFLMILSLAFAG PAITIMVGEGILYCCLSKRRNG VGLEPNINAGGCNFNSFLRRAV RFVGVHVFGLCSTALITDIIQLY TGHQAPYFLTVRTPNTSLNVS CT*NSYLAEDIRSRSDLTLTHSG

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16226	46594	A	16321	48	1359	GDKNQNPRNWP/GEKGKGNLGRKETGRSNSRSHSSRSKSR*QSSSRSRSRSHSRKKRHSSRSRSRTYSRSWSRDRMYSRDDRH*YEVIVDCSRHGREYKGREPRHGSGSLERPTEQETSQPKIRKEIVETKGTA RGNCCTTGLLRPKTMVVERSYGPQDRVAVGTWPHPGTERWAS SWDVSSSVRHQSEGVVQGWEHRCTHKSQQEVGACVNFRTPKVI LIYNLYLPVSHQFSKTFMSIVIVQKNLYLHNDFRALNVTHIYRLTIPNTTCFTATQDDEDKQIFHTAAQHRSHTSSYQYLSLTSRSHREI VFYTRGLGAPFPAGDGHGKFQRLGKPYSHSVHIVVIPQDKTQHISINTPHKNSETTKQHITCSFAYGLYYYQQKEDNPYAWPQVPAAAEMVSRLAQSRHSQQSILHFHSQSYHTDHISTV
16227	46595	A	16322	227	3020	SCIKP RRRKEMGRSNSRSHSSRSKSRSSRSRSHSSRSRSHSRKRYSSRSRSRTYSRSRSRDRMYSRDRYRRDYRNNRNGMRRPYGYRGRGRGV/YYQGGGGRYHRRGYRPVWNRRHSRSRPR/GRSRSRSRSPKR RSVSSQRSRSRSRSRSRSRSRSPRSSSRSSSPYSKSPVSKRRGSQE KQTKAEGEPQEEESPLKSQSIEPKDTFEDPSESIDEFNKSSATSGDIDWPGLSLAYDNSPRSPHSPSPIATPPSQSS
16228	46596	B	16323	258	3728	
16229	46597	B	16324	1	435	
16230	46598	A	16325	1120	1209	ASSDNPP*SEPRVSLTIEQQEIDFFLDTGTAFSVLSSCPGWLSRSRSTVTRGILGQPVTRYFSHLL
16231	46599	A	16326	1291	1582	IHQSAICI*LKVKCKHTNQQPVSSSGFVNAPIDTLYLATLVPGPWRTLCVHTLYL.VNL.VGMWRTFVSSSGIVNAPISALSQTTWLYQSA GCGWGQIRE

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16232	46600	A	16327	2	840	APAVATEVLPGAGLTAGVLLW SDPKEPSNPGSSHVRGASLDLN PAHPTILSYTMQKLEELDVVL FDRSGHRTKFTNVGRMLLERG RVLLQAADKLTTDAEALARGW ETHLTIVTEALVPTPAFFPLIDK LAAKANTQLAJIIT^VLAGAWER LEQGRADIVIAPDMHFRSSSEIN SRKLYTLNMVYVAAPDHPHQ EPEPLSEVTRVKYRGIAVADTA RERPVLTQQLDKQPLRTVSTIE DKRQALLAGLGVATMPYPMVE KDIAEGLRVVSPESTS
16233	46601	A	16328	3	923	RFLSDGIIISVDSAGKVQFWDS ATGTLVKSHLIAANADVQSIAVA DFFPGHESRATEALCWAEGQR LFSAGLNGEIMEYDLQALNIKY AMDAFGGPWMSMAASPGSQL LVGCEDGSVKLFQITPDKIQFER NFDRQKSRLSLSWHPSGTHIA AGSIDYISVFDVKSGSAVHKMI VDRQYMGVSKRKCIVWGVAFL SDGTIISVDSAGKVQFWDSATG TLVKSHLIAANADVQSIAVADQR RQFRGGHSRGNSLPSAGPCAS NSS*EAVGADKTVPASHS*RAH CGPTAQQR*YLGDTDHLVFRP
16234	46602	A	16329	2	1059	
16235	46603	A	16330	582	1540	
16236	46604	A	16331	1	720	
16237	46605	A	16332	1	477	
16238	46606	A	16333	1	540	
16239	46607	A	16334	1	261	
16240	46608	A	16335	964	1574	LRWCCGSQLFRGYWGGVTGR YLTVLPPHLAVGCMAPWGPFS VRIAAVVFIQIFAGEVFWCPVM CVRGLCTPVLTGVPGIIGNSHIP AIVFTCSLQLTVGGTRWWRC CAAGDVTKPPALVGVGGETPR PQLPIGVTTVILLQVQLVWKFGR NVSMSVWALRVPGLAFQSRH/ ASWKFCRHSFLHCNAYIPLHTQ ECRSSHISFLDQ
16241	46609	A	16336	3	87	
16242	46610	A	16337	1	1398	

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16243	46611	A	16338	1596	2205	LRWCCGSQFLFRGYWGGVTGR YLTVLPPHLAVGCMAPWGPFS VRIAAVVFIQIFAGEVFWCPVM CVRGLCTPVLTGVPGNGNSHIP AIVFTCSLQTLVGGTRRRWWRC CAAGDVAKFPALVGVGGETPR PQLPIGVTTVILLQVLVWKFGR NVSMSVWALRVPGQAFQSRH/ ASWKFCRHSLFLHCNAIYPLHTQ FCRSSHISFLDQ
16244	46612	B	16339	276	442	
16245	46613	A	16340	1	300	
16246	46614	B	16341	1	903	
16247	46615	A	16342	119	889	RQHILESHSRPLCTTWLPLLIQ DPRTLQSAAMLLTQSLEFGGIFT RTRMKFGAVTWIGGPPGLGDQS PSSCSSLREKDPPTTSGPQTHQ PKEHLTNFKSGVPRPRRDACLGP SPLAASP AFLKGQVQPQLISLC PDPLFPHPNLISLRPNPLCPHPD LVSLCPDPFPFAFLEAHKNFQTPE PQQPGIPPEPPPPGACYKCQKSD HQAKECLQPRIPPKPCPICAGPH WKSDCSTHLLAATPRAPGTLAE GSLTDSFSA
16248	46616	B	16343	1	498	
16249	46617	A	16344	3	903	
16250	46618	A	16345	1	684	
16251	46619	A	16346	2	1028	
16252	46620	A	16347	1	338	
16253	46621	A	16348	2	392	
16254	46622	A	16349	790	2184	
16255	46623	A	16350	773	890	
16256	46624	A	16351	467	606	
16257	46625	A	16352	1569	1841	
16258	46626	A	16353	430	980	LLTEDALDDLIPSFLLTGQQTPA FGRRVSGVIEADGSRRRKAAA LTESNYRVLVGEVDDEQMAAL SRLGNDYRPTSAVERGQRYASR LQNEFAGNISALADAENISRKII TRCINTAKLPKSVVALFSHPGE LSARSGDALQKAFTDKEELLKQ QASNLHEQKKAGVIFEAEEVIT LLTSVLLKTSASRSTSRRHOFQA PGATVLYKGDKMVVLNLDRSR* RGIT*AAGI*PS*AEKSWGDI* RSYHSFNCA

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16259	46627	A	16354	1	343	MKRAPVIPKHTLNTQPVEDTSL STPAAPMVDSLIARVGVMARG NAITLPVCGRDVKFTLEVISVGVI VLRRPLGYGQVMNVTRSCLLR THWMISLLFY*LVNRHRRSVE EYLVS
16260	46628	A	16355	1	584	MLRDLLKNVNDLKGFPEDVRI TKYSNSNSQSPWMEEQIRDA WGSMLVKNVRETDEVGKGQI RMRTVFEQAIIDQRSSTDNEGAP VIPKHTLNTQPVEDTSLSTPAAP MVDSLJARVGVMARGNAITLP VCGRDVKFTLEVISGVIVLRRPL GYGQVMNVTRSCLLRTHWMIS SLLFY*LVNRHRRSVEEYLVS
16261	46629	A	16356	62	350	SLPNLDNAACSSSSPRTTR*SL SVSAAALRRRLPSAISDHTREVF STLSPRSTSRVNFTSRPHTGKV MALPRAITPTRAINESTIGAGV DNEV
16262	46630	A	16357	291	502	RLFEVHHVHKHLLGDNRYP WIMQPSAHHP/RSPTTR*SLSV SAAALRRRLPSAISMPDTLRP NAGVC
16263	46631	A	16358	1	378	
16264	46632	A	16359	159	433	SYVKYFPHQPAQKYFQQIHS GLHNADHVHKHLLGDNRYP IMQPSAHHP/RSPTTR*SLSV AAALRRRLPSAISMPDTLRP AGVC
16265	46633	B	16360	1	624	
16266	46634	A	16361	3	299	
16267	46635	A	16362	163	699	
16268	46636	A	16363	795	980	
16269	46637	A	16364	663	734	
16270	46638	A	16365	391	1248	
16271	46639	A	16366	1	1143	
16272	46640	A	16367	1	271	
16273	46641	A	16368	1	493	MSKRRWLTGNGSDRENIRLD GFLVSDEEKRYKCEDCGKAFN RSSNLTTTHKKIHTGEKPYKCEE CGKAFKRSSILTTKRIHTGEK YKCEECGKVFKYKSSLSTHKIIH TGEKPYKCEECGKAFNWSSHL TTHKRIHMERNPTNVKNA LSTPLPLNNIK
16274	46642	A	16369	728	1428	
16275	46643	A	16370	3689	3864	NYKSFFKWS/SQMMSMTKIYRG PLDHPDSPCSNVNDIEGTPPEE STAQPLLHPRPAGSS

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16276	46644	A	16371	2	126	WPLLLLGCLSLTKEWGFQA*LE KHVKRVKFPShNLVPGRSI
16277	46645	A	16372	728	2207	
16278	46646	C	16373	1	873	
16279	46647	A	16374	1220	2097	
16280	46648	A	16375	73	1438	QDLRLFYLKDTMFSKLAHLQR FAVLSRGVHSSVASATSVATKK TVQQPPTSDDIFEREYKGGAHN YHPLPVALERGGKGILWLDVEG RKYDFPLSSYSAVNQGHCHPKI VNAL\KSQVGQN*PLTSRAFYN NVLGEYEEY\TKLFNYHKVLP MNTGVEAGETA\CKLA\RKWG L/YTVKGQKQYKVAIVFAAGNF WGRTLSAISSSSTDPTSVDGFGP MPGFDIIPYNDLPALERALQDP NVAAFMVEPIQGEAGVVVPDP GYLMGVRELCTR\QVLFIADEI QTGLARTGRWLA\DVYENVRD IVLLGKALSGGLY\VPVS\AVLCDD DIMLTIKPGEHGSTYGGNPLGC RVAIAAL\EV\LEEEENLAENADK LGIILRNELMKLPSDVVTAVRG KGLLNAIVIKETKDWD\AWKVC LRLRDNGLLAKPTHGDIIRFAPP LVIKEDELRESIE\INKTILSF
16281	46649	A	16376	600	806	

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16282	46650	A	16377	I	2255	EPDVCAKMAGRSMQAARCPD ELSLTNCSVVNEKDFQSGQHVI VRTSPNHRYTFTLKTIPSVPG SIAFSLPQRKWAGLSIGQEIES LYTFDKAKQCIGMTIEIDFLQK KSNDNSPYDTDKMAAEFIQQF NNQAYSVGQQLVFSNEKLFG LLVKDIESMDPSILKGEPATGK RQKIEVGLVVGNQVAFKEAKAE NSSLNLLIGKAKTKENRQSIINPD WNFEKMGIGGLDKGVFSDFIIRR AFASRVFPPQIVEQMGCKHVK GILLYGPGCGKTLARQIGKM LNAREPKVVNGPEILNKVVGES EANIRKLFADAEQQRLRGANS GLHIIIFDEIDAICKQRGSMAGS TGVHDTVVNQLLSKIDGVQL NNILVIGMTNRPDLIDEALLRG RLEVKMEIGLPDEKGRQLQILHH TARMRGHQQLSADVDIKEV ETKNFSGAELEGLVRAAQS MNRHIKASTKVEVDMKEA QVTRGDFLASFLENDIKPAFGTN QEDYASYIMNGIIKWC DDGELLVQQTKNSDRTPLV LLEGPHSGKTALA KIAK EESN FPFIKICSPDKMIGFSETAKCQA MKKIFDDAYKSQLSCVV VDDIE RLLDYVPIGPRFSNLV QALLV LLKKAPPQRKLL IIGTTSRKDV LQEMEMLNAFSTT IHPVNIATG EQLLEALELLGNLKDERTTIA
16283	46651	B	16378	I	2181	
16284	46652	A	16379	I	441	
16285	46653	B	16380	47	482	
16286	46654	A	16381	I	636	MRDPNTKRSRGFGFVTCATVE EVDAAMNARPCVKVGRV RAVSREDSQRPEDTEELHLDY FEQYKGKIEVIEIMTDQGSGKKR GFAFVTFDNHDSMDKTVI QK HTVNGHNC EARKALSKQEMAR ASSSQRGRSGSGNF GGGGGGGGGGGG GGG GGGGYGG/SGDG YNGNGF GGGSYND FVN YNN QSSH FPGM
16287	46655	A	16382	I	762	
16288	46656	B	16383	59	1042	
16289	46657	B	16384	76	848	
16290	46658	B	16385	179	400	

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16291	46659	A	16386	27	372	VGSLRRPGPPREETRRLRRRRS LEPWAFLLEAKAVG*QPSSLFQ WEGPMGLCSTPLVMNMGDSL ITKHLFQVPLTITSPGPRTRRPH S*YPSPLSATGVWAAVWCKQP HFPAK
16292	46660	B	16387	134	284	
16293	46661	A	16388	1	2013	
16294	46662	A	16389	313	770	IFGFVVAMHGAPGQAVALLELQ LTGDQSLGLSQRHMAALDALV HLLHGGGLAVLTAGAAPEHET RGIAGLREEQCRNPRCVKRGW AQEKQA*PGQRGGRKSSSPFWSF TL/DSASAGPRAAHLHLPDVLS LQTLHHGLHRLLHPELQLSHG
16295	46663	A	16390	1	2753	
16296	46664	A	16391	1	1363	
16297	46665	A	16392	26	181	
16298	46666	A	16393	1	867	
16299	46667	A	16394	1	1447	
16300	46668	A	16395	31	659	APALPGCEHMMAIRELKVC LLGDTVGVKSSIVCRVQPHDFDH NISPTIGASFMTKTVPCGNELH KFLIWDTAGQERFHSSLPLYLR GSAAAIVYDFTEAGFHFFHPLK KWV\KRLKELGPENIVMAIG NKCDLSDIREVPPEGMLKEYA ESIGAIVVETSAKNAINNIEELFQ GISRQIPPLDPHENGNNGQTIKVE KPTMQASRCC
16301	46669	A	16396	1	1182	
16302	46670	A	16397	1	513	
16303	46671	A	16398	146	429	TFYTCFSPLVIPFSFSIHTKPYPG HHQSFYMTNVSSNNPTISPLTT RPPFLSILPAGLSHAAPNPA**SP EKHRPFLSLHTTPQKFHRPNTSTL F
16304	46672	A	16399	1	435	
16305	46673	A	16400	56	477	ARAAGKGESCEGPGVGRGCFSS YRQTPCCQRLVNVPKTRRTF CKKICGKH\PRHKVTQYKKGD SFYA\QGRRRYDRKQSGYGGQT KPIFRKKAKTTK\MLAIKRCKHFE LGEPNCRSKR\MLAIKRCKHFE LGDKKKRGQVQF
16306	46674	A	16402	183	373	IHGSENPTPERETLFWHAENG SALASC*KSGGQAPKRKVRTTL ILKAEILILGMLVLRSHGM

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16307	46675	A	16403	1	881	MPFKCKKQHTFNKTSPEGAI FTHGCLCTSPFNSELSEHGLNL KLSSWEHLHHRSSQQTLSVRLH VPTPQPVEHEFIQLIYIHTGAKL QASKVIIATKDGKRRKSPWLQ KYPKLILREASSVSEELHKEVQ EAFLTLHKGHGLFRDLVRIQK DLITPVSRILIGNPCTKYLN RLFTVWPWPKGSNIKIITEA AACETFLKLNDYLQIETIQALEE LAKEKANEDAVPLCMSADFP RVMGMSYNGQDEVDIKSRAA YNVTLLNFMDPQKMPYLKEEP YFGMGKMAVSWHHIDENL IQLQLWDPVDGTTASSA AVPKQ GRDKRREVPTLSQPNSQEGLI SAFHSRCVHAFYKLT SLPDVPSDILLAEGLAASRAGQA LWRCDKSSLTLVRKINLQGK RDGGRSATNQQSOPHLDNTGL ERQLEQKVGRCRSPWRGLGHL EGNAQKGHLHHGVNKGNGQHL L*MPSSPLPGGQKGRLVGML WVLT*VYKIQH/GT/PAAVEG*D EAFLAVWLGEVGVDGFSPLVPSL LWHS*RGCCSIHGPIELELN QIFIM/SASSLPFSPCQNKVPLSG
16308	46676	A	16404	1	459	
16309	46677	A	16405	1	2025	
16310	46678	A	16406	1	816	
16311	46679	A	16407	1	217	
16312	46680	A	16408	3	135	
16313	46681	A	16409	21	218	
16314	46682	A	16410	392	3744	LNYKMLLKNLSPMSMLKAFS AIPMQPPAQTNLPTAKPNGFP LLSQYNACPPP*EAG/QVDL CSTIPLNLLPDSLPLTVPTGPLPQ GSVGLVLRGRASSAKGITHTGL INSDSVDEIKLITSAKVPVSIAG ESIAQLLLL.PNIILNKGDKTRGP GMGSRGEKAAYWIVNISKQRP TCTIHQGRKFEGLVDTGADVS VISSLWPSSWLKHPTNMGLVG VGKAEEVYVGSTFILPCTGLDGQ KGTIOPYIM
16315	46683	A	16411	1	783	
16316	46684	A	16412	1	1911	

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16317	46685	A	16413	3	1381	KTPFVGYQHQRPKVDKTTKMG RNQSRKAENSKNQSTSSPPKDR SSLPATEQSWTENDFDELTEVG FRRSAITNFSELKEHVLTRRKEA KNLEKRLDEWLTRINSVEKTLN DLMEKTMAQELRDArtsfns *FNQVEKRISVIEDQIDEIKQDD KAAETCNWRWVSESLRQLRAS VDAFHARASHYHNAGECLHOLA ALNSRLNCAQEMARRDSIGEV PVPWRTVVGGSIAGEAKLDHL RLVSLIGREVNKENSPPAATRWL FSFQAGALAGGQIVLQAAKPN AHGQPVVA TRNLLNPAGIVAV LKQRPLLVA AAQAFYLRDPID LRACR VFKTFLPETRIMTSYYAI EWSLWTLVDVLHAE NSESAHM SHNSYDPPSDVARHLTHLPMS IPDYIIA RFRYR HRSRVR LTARK LSPAFMRCSSIEQYSTMLERG FNGGYCRSTTVRVVTEATRML
16318	46686	A	16414	1	1191	
16319	46687	A	16415	1	1909	
16320	46688	B	16416	1	1791	
16321	46689	A	16417	1	1818	
16322	46690	A	16418	1	1044	
16323	46691	B	16419	1	1140	
16324	46692	A	16420	1	1062	
16325	46693	B	16421	1	972	

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16326	46694	A	16422	I	1758	MDTFLQAERKDYM <b>E</b> AYELIEQ EEQGVKELNRPLTAPSALHPRD EAHLMVDKLFDVLLSDVCQYF IEDFCIDVHHINSRWI/AVCQYFI EDFCIDVHHINSRWIKDLDNVRP KTIKTLEENLGN <b>T</b> QDIGM <b>K</b> D FLSKTPKAMATKAK <b>I</b> KWDL <b>I</b> K LNNFCTAKETTIRLPVPNPCGPV AETPLSRVFLV <b>R</b> EAKT <b>L</b> KPHQ STCLSKGRDN <b>S</b> IDS <b>W</b> W <b>K</b> TAAR <b>V</b> KTAISSTPT <b>I</b> PILK <b>D</b> Q <b>T</b> QEW <b>S</b> VS ATFTSD <b>G</b> KIRLFYTD <b>S</b> KGKH <b>G</b> KQS <b>L</b> TTAQVN <b>S</b> KS <b>D</b> DT <b>L</b> KING VED <b>H</b> K <b>T</b> IF <b>D</b> GD <b>G</b> KTY <b>Q</b> NV <b>Q</b> Q <b>F</b> DEGNYTSGDNH <b>T</b> LRD <b>P</b> HY <b>V</b> ED KGHKY <b>L</b> V <b>F</b> EA <b>N</b> T <b>G</b> ENG <b>Y</b> OG <b>E</b> ESLFN <b>K</b> A <b>Y</b> GGGT <b>N</b> FR <b>K</b> ES <b>Q</b> L <b>Q</b> QS <b>A</b> KK <b>R</b> DA <b>E</b> LA <b>N</b> GA <b>G</b> I <b>E</b> NND <b>T</b> TL <b>K</b> V <b>M</b> K <b>P</b> LT <b>S</b> NT <b>V</b> T <b>D</b> I <b>E</b> R <b>A</b> N <b>V</b> F <b>K</b> M <b>N</b> G <b>K</b> W <b>Y</b> L <b>G</b> EW R <b>R</b> EWS <b>S</b> SG <b>D</b> R <b>K</b> SL <b>A</b> RL <b>S</b> KT <b>G</b> T <b>L</b> L <b>A</b> ALTY <b>K</b> CTR <b>D</b> Q <b>W</b> T <b>V</b> Y <b>C</b> R <b>V</b> E <b>K</b> N <b>L</b> Q <b>D</b> MRW <b>Y</b> Q <b>R</b> C <b>Q</b> T <b>C</b> R <b>D</b> F <b>Y</b> AN <b>K</b> M <b>P</b> A <b>T</b> EL <b>V</b> TR <b>S</b> PK <b>G</b> R <b>S</b> K <b>L</b> R <b>L</b> R <b>Y</b> QL <b>V</b> FI <b>S</b> LK <b>G</b> K <b>P</b> AR <b>K</b> G <b>K</b> A <b>S</b> SG <b>S</b> KL <b>S</b> LL <b>S</b> SS <b>K</b> T <b>V</b> AL <b>A</b> GM <b>G</b> R <b>G</b> DEF <b>Q</b> ME <b>L</b> E <b>S</b> ED <b>L</b> T <b>S</b> ER <b>D</b> G <b>I</b> L <b>R</b> T <b>P</b> T <b>S</b> N <b>Q</b> KK <b>S</b> AY <b>G</b> SL <b>I</b> R <b>T</b>
16327	46695	A	16423	I	4449	
16328	46696	A	16424	3	3859	QFLPNLDSTVLGENYFDGTYQ MLYLLVKGT <b>I</b> PVEIHTATV <b>I</b> FVS FQLSVATE <b>DD</b> FYTSH <b>N</b> LV <b>K</b> N <b>L</b> L <b>F</b> FL <b>K</b> IPS <b>D</b> K <b>I</b> R <b>I</b> S <b>K</b> IR <b>G</b> K <b>S</b> L <b>R</b> K <b>R</b> SMGF <b>I</b> E <b>I</b> E <b>I</b> GD <b>P</b> PI <b>Q</b> FI <b>S</b> NG <b>T</b> T <b>G</b> M <b>Q</b> L <b>S</b> EL <b>Q</b> E <b>I</b> A <b>G</b> SL <b>G</b> QA <b>V</b> IL <b>G</b> N <b>I</b> S S <b>I</b> LG <b>F</b> N <b>I</b> SS <b>M</b> S <b>I</b> T <b>N</b> PL <b>P</b> SP <b>D</b> SG <b>W</b> IKV <b>T</b> A <b>Q</b> P <b>V</b> ERS <b>A</b> F <b>P</b> V <b>H</b> V <b>A</b> F <b>V</b> S <b>I</b> LL <b>V</b> IT <b>Q</b> P <b>V</b> AA <b>Q</b> P <b>G</b> OP <b>P</b> QQ <b>Q</b> PS <b>V</b> K <b>A</b> T <b>D</b> S <b>D</b> G <b>N</b> C <b>V</b> S <b>V</b> G <b>I</b> T <b>A</b> TL <b>R</b> L <b>K</b> D <b>S</b> NN <b>N</b> Q <b>V</b> N <b>G</b> LS <b>G</b> NT <b>T</b> IP <b>F</b> S <b>C</b> W <b>A</b> N

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16329	46697	A	16425	65	1905	RTSSRKTTNHCSEIKEDETNWK NIPCSWIGRINIVKMAKLPKPPL VIPRQTSGVGVLQQPTDHLRLR VLTVRRKTNKQKGPHHQNPIC SPSSKTKVLEVLARAFRQEKEI KGIVGVKEEVKLSLFADDMVY LENPIVSAQNLLKLIISNSFKVSG YKINVQKSQAFLYTNNRQTESQ IMTELPFTTAKSRIKYLGQLTR DVKDLFKENYKPLLNEIKEDETN KWKNIPCSWVGRINIVKMAILP KVIYRFNAIPIKLPMTFIELEKT TLKFIWNQKRARIAKSIISQKN KAGGITLPDFKLYYKATVTKTA WYWYQNRDIDQWNRTEPESEIM LHINYNYLIFDKPEKNQKQWGKDS LFNIWCWENWLAICRKLKLDPF LTPYTKINSRVIKDLNVRSKTIK TLEENLGNTIQDIGHMGKDFMSK TPKAMATKAKIDKWDLILKLKF CTAKETTISVNRQPTWEKIFAI YSSDKGLISRIYNELKQIYKK NNPIKKWVKDTNRHFSKEDIYA AKRHMTCSSSLAVREMFIKT TMRYHI.LTPVEEVRAVAGEMAKTR RCQNVKGASEEGIRAHCFVSH *PHCP/LWRATTLMETLKFKPIE VPCPKPLEKSVSLLL
16330	46698	B	16426	I	2348	
16331	46699	A	16427	1	660	MPNFFIDRPPIFAWVIAIIIMLAGG IAILKLPLVAQYPTIAPPVATISA SYPGADAKTVQDTVTQVIEQN MNGIDNLMYMSSNSDSTGTVQ ITLTFESGVQVQNKLQLAMP/LL PQEVSQQGVSVKESSSSFLMVV GVINTDGTMTQEDISDYVAAN MKDAISRTSGVGDVQLFGSQY AMRIWMNPNELNKVERNSRQQ DVGERDISSGSRKVNKESEDE EVT
16332	46700	A	16428	1	975	

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16333	46701	A	16429	1171	2007	AVDIVQGLVRGWGRQGWLLS GRGIPEGPLLLWGAATVGSWR LLPLTGVCGLPLGAAPVPLIS*LL GGAQVQLLREEEAAGHELVQQL VDGALVLLLDGLPLHVVADE RCCVLQDLPVLVHKDEVRLLR GGTAALRVVLLVLVVDALDLV EQALGAQGLGVVLLLEVHSLVV KGLEVRLLIILPPDLVEALLGLP PLLFLGLQSFDNGDSDGRVLL EALDDLRGLVVAIDAINGTALDH LRRASQGVVQPELLLVFRRHPR QLLLHTFOHTDCGQVRLQDIV
16334	46702	B	16430	1	768	
16335	46703	A	16431	1	2553	
16336	46704	A	16432	3	573	CEMHVSQKNEHDKTPEHSRK SRPSLLRPVSAAPAKKMKMLRG KDLSSIAAVGKYGTL/PGIFL*Q GPPGAEEPGGV*KLPPLHRTLQ PGAGVWL*APAARQPSIGVSS* LPRAP*GGSVPVNISIYLVFSYCF *AMIVLF*NPVY*LT*L*LLIPM HL*GAIHHLGTLQLVPLPVTSV VSILTRIQWVLE
16337	46705	A	16433	110	1347	LTATGMELSMGTTWTSLCK AENAACQQEKPHIWLCSISFL RLKRRRTTKNTGTKIATV VTIPPITPLPTAFCAPAPVLLT SGIPPRLNASENPOLLSS/SSSD STGTVQITLTFESEGTADIAQVQ VQNKLQLAMPLLPQEVEQQGV SVEKSSSFLMVGVINTDGT TQEDISDYVAANNMKDAISRTSG VGDVQLFGSQYAMRIWMNPNE LNKFQLTPTVDVITAIAQANAQV AAGQLGGTPPVKGQQLNASIIA QTRLTSEEFKGKILLVKNQDG RVLLRDVAKIELGGENYDIIAEF NGQPASGLGIKLATGANALDT AAAIRAEALAKMEPPFSGLKIG YPYDTTPVNVNISIHEVGKTLVE ANNLVFLAMNLVLOEFPADVIS TIAGPPSLRSSRVPGL
16338	46706	B	16434	1	2550	
16339	46707	B	16435	1	630	
16340	46708	A	16436	270	455	
16341	46709	A	16437	174	492	GALQPPPCTVGAPFWAGQGW PLPQLAGRCGGRTGRTGAAAC GACGPAGVPGGLGLGGPRTRSS RPALLAPNGGLSTRASCGCGC TESPSSGWPTSAALDFLPGP

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16342	46710	A	16438	3	413	
16343	46711	A	16439	31	507	
16344	46712	A	16440	1	537	
16345	46713	A	16441	152	247	
16346	46714	A	16442	44	208	EEMTSKMYKVIIRKTMKAVC TQVKHPAIASICKAVL*VGPWS GHFKYAGLPTL
16347	46715	A	16443	1	549	
16348	46716	B	16444	376	862	
16349	46717	A	16445	2	1603	TNVSTTIATVVLNALARATKLL PPGHRSPNPATAAASSPPPTLA HCSLSRHHQPLRGEQQPQAIRT TAGRCKALSSCPSPFFECGSRSG APPGACGGQFRVSNAKLEPQAR PSSPVGGPLDLMACRVAAST REMAMLIAQALQQTINYGRDDE NGHTHSACEVHHGGRVPELSV PSFSWRNRNPNPSFIMGSITPTDY TLSKCYLPREDVVLIIYCGVSTN EQPDEEVPRTRPPTVAVSIGFAV RQELEFGVVIYHCLEYRLYTGR GRGAFCNGQRLRVSGETASGM LPGIQQHIIHQQEQNQLQVGASTEL PCNLHHTTRIVASA PSSAPSA PEDGT ESKTCNFRV TSSKG YCVCLAL PRV PFPLTTGYK HLHK PPPTGTHSTY HSMCLLN QPG WLRT ISIIL FLNN KICW QKKG REIK JEDY FPEYA NYTV PEDGH LSA HYL ISL LCM WLQH SGQDS YL TDX YRR GEN SFVM VNS VAL NGD GCG CSE TE AELIEV SHRL NCS REV GEHLNA TGEL GEERA HGR QQA ACG FTIA
16350	46718	A	16446	1	648	

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16351	46719	A	16447	329	2497	GEGQAVLQGKMGGEKKPVGAGEEKQKEGKKNKE/GSGDG SRAELNPWPEYIYTRLEMVNILKAEHDSILAEKAEKDPSKIKVT LPDGKQVDAESWKTPVQIACGISQGLADNTVIAKVNNTWD LDRPLEEDCTLELLKFEDEEAQAVYWHSSAHIMGEGMERVYVG GCLCYGPPIENGFYDDMYLEEGGVSSNDSSLEALCKKIIKEKQA FERLEVKKETLLAMFKYNKFCKRILNEKVNTPTTVYRCGPLID LCRGPHVRHTGKIKALKIHKNSSTYWEBGKADMETLQRQYGISFP DPKMLKEWEKFQEEAKNRDHRKIGRDQELYFFHELSPGSCFFLP KGVYIYNALIEFIRSEYRKRGFQEVVTNPJFNSRLWMTSGHWQH YSENMFMSFEVEKELFALKPMNCPGHSLMFDHRPRSWREPLPLRA DFGGLHRNELSGALTGLTRVRVRFQQDDAHIFCAMEQIDEIKGC LDFLRTVYVSFGFSFKLNLSTRPEKFLGDIEVWDQAEKQLENSL NEFGEKWEI(NSGDGA)YGPKIDIQIKDAIGRYHQCATIQLDFQL PIRFNLTYVSHDGEDKKRPVIVHRAILGSVERMIAILTENYGGK LAPFWLSRQVMVVPVGPTCD EYAQNVRRQQFHDAKPMADIDL DPGCTLNKKIRNAQLAQYNFILVVGEKEKITGTVNIRTRDNKVKH
16352	46720	C	16449	189	456	
16353	46721	A	16450	3	1414	
16354	46722	A	16451	95	293	

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16355	46723	A	16452	1	1136	MKKRPGHSLFQFQLMFLRFSE ARQPLSEEDVASLWRPLHLPS ADWQRAALSLWTHRTRTREVLK EEDVHLTYQDWLHLEI <sup>Q</sup> PEA ^MLFQILNGRTSTSGRSMSTFL SPRLQGAVTETCRLRVPFLSTH* WISTKAQGVMTTQKILJLWSLVA AQEMRILFPDCRRW*LTWSCK TS^CLSATPLPRSTSSLRFSADG SRL*QAGGA <sup>W</sup> LPAPFRDRGSC^C TNGSSAACRLSSAAA <sup>S</sup> QRNS PSLPDASSSTWSTLR*ETSAPT EVP*HRTSLPTS <sup>Q</sup> GPPRLSAE QRPLPDGR/RSYWPSARRNA/RL ILT/FCSGVVAEPGACAA <sup>L</sup> PVEE TLPEPAAPGTAEATRRAVQCQR VRVGAIGFPFLLLDGA <sup>V</sup> VTS DLK
16356	46724	A	16453	3003	3482	HRPRTRPCPWRRNHHHLGRAP L*PQRARR*SPNPPEDGSEDEHL *QLC
16357	46725	A	16454	598	759	KVILGLWTEEAQVGGQQGLRAP TPRLLHHVLK*DIKR* AHRPDA VAHACNPNTLG
16358	46726	A	16455	1	1767	
16359	46727	A	16456	2	572	
16360	46728	A	16457	1	726	
16361	46729	A	16458	155	1334	HALGRRGGSQELSAAGAASP SGSERRAPGALPCAWAAALLV LGAPPASPRGGFAAGKTMLLK EYR^CMLTV^DEYK <sup>I</sup> QQLYM ISKHS <sup>H</sup> IEQSDRGEV <sup>V</sup> VQKE PFEDPHHGNGQFTEKRVYLN <sup>K</sup> LPSWARAVVPKI <sup>Y</sup> VTEKAWN YYPYTITEYTC <sup>S</sup> FLPKFSIHIET KYEDNKG <sup>S</sup> NDTIFDNEAKDVE REVCFIDIA <sup>C</sup> DEI <sup>P</sup> ERY <sup>Y</sup> KESED PKHF <sup>K</sup> SEKTGRGQLREGWRDS HQPI <sup>M</sup> CSYKL <sup>V</sup> TVKSEVWGLQ TRVEQFVHKVVRDILLI <sup>G</sup> HRQA FAWVDEWYDMTMDEVREFER ATQEATNKKI <sup>G</sup> IFPPAISISSIPLL PSSVR <sup>S</sup> AP <sup>S</sup> AP <sup>S</sup> PLSTDAPEFL SVPKDRPRKK <sup>S</sup> APETL <sup>T</sup> LDPDE KKATLNLPGM <sup>H</sup> SSDK <sup>C</sup> CRPKSE
16362	46730	A	16459	26	355	
16363	46731	A	16460	86	489	
16364	46732	B	16461	1	201	
16365	46733	A	16462	3	367	

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16366	46734	A	16463	58	553	VARSAPPDGAVCGAGPSRRTE MAEQSDEAVKYYTLEIQQKHN HSKSTWLILHHKGIVYDLTKFLE EHPGGEEVLREQAA\GGD\ATENF EDVGHSTDAREMSKTFIIG\ELH PDDRPLNKPPPEP*RRCFKETLI TTIDSSSSWWTNWV\PAISAVA VALMYRLYMAED
16367	46735	A	16464	185	489	
16368	46736	A	16465	134	345	
16369	46737	A	16466	572	1017	
16370	46738	A	16467	911	1013	
16371	46739	A	16468	1	157	FGGNQKGERTGQKGKGGERAK RKDFPGAVCISALGLLAKGCG* SWRPSSAN
16372	46740	A	16469	71	369	SCGLSLIKMTTSQKHDRVFAEP MGEKPGVGSAGLIGEVLG\KKLE ERGFDKAYVVLGQFLVLLKDE DLFREWLKDTCG/APNAKQSR DCF*CLREWCDAL
16373	46741	A	16470	1	831	
16374	46742	A	16471	368	679	SSQLNKPSSLNPVSEEFCLWL LLLQKELLTRITSLEKNTNDLV DLKNTA*ELHEAHTSINS*IDQV EERISECEDHLTEIRHSEKMKTA LLK*DMQTRREKKK
16375	46743	A	16472	536	717	
16376	46744	A	16473	1	1632	
16377	46745	A	16474	1	651	
16378	46746	A	16475	1	903	GGGGRMKLIDYGLSGYQEESA E\VKAMDFITSTAILPLLGCLG VFGLFRLLQWVVRGKAYLRNAV VVITGATSGLGECAKVFYAA GAKLVLCGRNNGGALEELIRELT ASHATKVQTHKPVLYTVDLTD GAIVAAAELQCFGYVVDILVN NAGISYRGTIMDTTVVDKRV METNYFGVALTKALLPSMIKR RQGHIVIASSIQGKMSIPFRSGI CQPSKHAQTQAFVFCLAVPEM\I QFEIEVTVISPGYIHTNLSVNAIT ADGSRCGVMDTTAQAEALW RWPRMFLLWGRRRKM
16379	46747	A	16476	359	1094	
16380	46748	A	16477	1	906	
16381	46749	A	16478	1	371	
16382	46750	A	16479	11	257	
16383	46751	A	16480	2	419	
16384	46752	A	16481	1	2514	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met cod	SEQ ID NO: in USN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=I, unknown, *=Stop codon, /=possible nucleotide deletion,  =possible nucleotide insertion)
16385	46753	A	16482	262	822	AGCTRKTRIJDVVYNASNNEVLRTKTLVKNCIVLIDSTPYRQWYESHYALALGRKKGAALKLVRVTSI*GLWGQQPDSSLLVMKTLSSSATEGREMRAF*AEEGQHWGVQGSRKLPGPFLP*AHIFVSPFQTPEEEELNKRSKKIQKKYDERKKNAKISSLLEEQFQQGKLLGEKADELEVGSRRD
16386	46754	A	16483	2	799	SQWLKLPSPLPHAGISRYINWDQAP*KTGGPRESPYHKKREVMKLGRPSCPN/NPKIGPPAGIQHSPVCRGG*QVNTRAPEVWTVGNF\SWGLICRCTP*NKDPSPIVVLLQC HLNNNGAWFRTQGPWVEFCIVASSDQQQPYRIQWVRSPLNLACPLGPAKKGEPKLDSLRLKEEIKFQKNDLKKLRLKEI*LKRKKNCQI PAVLPGRQFPARGKLSGRA/SRFQQGPQLWAEQDGFCAGEQKSLEFLSFRKNPRPRKGQIKFLVFVFHPC
16387	46755	A	16484	1	681	
16388	46756	A	16485	287	694	IISSRPAPASAPRRWGLSWSQRCWC**TPSPSPRPRPAEGICLRRGRGRGAGGGLPFRPHGSLVHS GAQPPHFPHLPGGARQTCGAPPGSWSCVL/CRAETGAAAAGSPAAAGSTRKRLGRAQGRGCRVAALRLSPTH
16389	46757	A	16486	189	381	QGAGSVGRGQQQLKPGPFLEKLLSLGCT/LSG*ALRARACCSPPCRPGAGCQPQAPVAQAGHP

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16390	46758	A	16487	1	2388	QGRLVAKPPRPARSTAADSSTPRDMLGLRPLLALVGILLSGCVLSQECTKFKVSSCRECIESPGCTWCQKLNFTGP GDPD SIRC DTRPQLLMRGCA ADDIMDPTSLAETQEDHNGGQKQLSPQKVTLYLRPGQAAAFNVTFRAKGYPIDLYYLMDL S YSM LDDL RNVKKLGG DLLRALNEITE SGRIGFGSFVDKTVLPFVNTHPDKLRNP C PNKEKECQPPFAFRHV LKL TNNSNQFQTEVGKQLISGNLDAPEGGLDA MMQVAACPEEIGWRNVTRLLVFATDDGFHFAGDGKL GAILTPN DGRCHILEDNL YKRSNEFDYPSVGQLA H KLAENNIQPIFAVTSRMVKTYEKLTEIIPKSAVGELSE DSSNVVHLIKA YNKLSSR VF L DHNALPDTLKVTYD SFC SNGVTHRQ@PRGDC\DG VQIN VPITFQVKV TATEC I QEQSFVIRALGFT DIVTVQVLPQCECCR DQS RDRSLCHGKG FLECGICRCDTGYIGKNCEC QTQGRSSQ ELEGS CRKDNN SII CSGL GDC VCG QCL CHTSDVPGKLIYGGYCECDTINCERYNGQVCGPGRGLFCGKCRCHPGFEGSACQCERTT EGC LNP RRVECSGRGRCRCNVCECHSGYQ LPLCQEC PGCPSPCGK YISCAECLKFEGKGPFGKNC SAA CPG LQLSNNPVKGRTCKERDSEG C W VAY
16391	46759	A	16488	353	1205	
16392	46760	A	16489	11	440	FRALTEGDTQLNW NIVSF PVAEELSHI HENL VSF LETV NQPH HQN VSVPSNNVHAPYSSDKEHMCTVVYFD DCMSIHQCKIS CESMGSHPNIRWVSLMACCECIGPECIDYGS KTVKCMNCMF* RQMQTKAT**NNRYKKLKK

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16393	46761	A	16490	515	1808	KRKQTGEFGFNSFE/WCDSDLCEMNAGMPKGNLNEQDPKHCPESEKCLLSIEDEESQQSILSSLNHSQQSTQPEMHKYGQLVKVELEENAEDDKTENQIPQRMTRNKA NTMANQSKQILASCT'LLSEKDS ESSSPRGRIRRLTEDDDPQIHHPKRKVSRVPQPVQVSPSLLQAKE KTQQLSAAIVDSLKLDEIQPYSS ERANPYFEYLHIRKKIEEKRKLL CSVIPQAPQYDDEYVTFNGSYLDGNGPLSKICIPITTPPPSLSDPL KELFRQQEVVRVMKRLRQHSIER EKLIVSNEQEVLRVHYRARTL ANQTLPFSACTVLLDAAEVYNVP LDSQDDSKTSVRDRFNRAROF MSWLQDVDDKFDKLKTCLLM RQQHEAAALNAVQRLWEWQLK LQELDPATYKSISIYEI^QEFYVPL VDVNDDFELTP
16394	46762	A	16491	1	699	
16395	46763	B	16492	6	5954	
16396	46764	A	16493	22	585	
16397	46765	A	16494	1	837	
16398	46766	A	16495	1	1422	
16399	46767	A	16496	13	189	
16400	46768	A	16497	193	366	GRPGIFKSFCRW*^C*FHMEFI WKSSA*/WSGVWHAGNICLSSINPEDLRAQSFCSSG
16401	46769	A	16498	1	888	
16402	46770	A	16499	3	531	DAWADAWADAWADAWALQS RRRRRTQLTLSSPHDCYRGLQSLLLILCKMATLKEKLIAPIVAAE ^EA^TVPPNN^RITVLDGDQVGMA CAISILGKSLA^DEALDVLED KLKGNDGSFQHG^S^LFL^QTPK ^IVGRIKDYS^G^TAQF^RIVVGN WQGVRSARRGKVRSNLVQRNVNVFK
16403	46771	A	16500	2	406	
16404	46772	A	16501	2	394	
16405	46773	A	16502	1	399	
16406	46774	A	16503	74	464	FAFNMPPEPAKSAPAPKKGSKK AVTAKQKKDGKKRKRKSRSRKESSVYVKVLKVQVHPDTGISSKA MGIMNSFVNDFERIAGAEASRL AHYNKRSTITSRE^QTAVRLLLP G^ELAKHAVSEGETK^AVTKYHQ
16407	46775	B	16504	84	832	
16408	46776	B	16505	201	829	
16409	46777	A	16506	1	804	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met/	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, ^=possible nucleotide insertion)
16410	46778	A	16507	3	615	PECIIIGIDILSSGQNPHIGSLTR VRAIMVGKAKRKPLELPLRKI LNQKQYRIAGGIEISATIKDLK DAGVVIPTTSLFDSPIWVQKTT DGSWRMTVDYRQINQVATPIA AAIPDVASLLQINTSPDTW/PI RPPISNGD*GVSGR*ACCLEPLA GPHR*ITSEASRILEQGPAIFCR* LLSF*ETALGLLLGFGGN*TFDY
16411	46779	C	16508	25	153	
16412	46780	A	16509	1	1317	
16413	46781	A	16510	1	1557	QVPGCIIGIDILSSWQNPHIGSLT GRVRAIMVGKAKWKPLELPLP RKIVNQKQYHILGGTVISETIK DLKDTEAVTPTTSPFNNSPIWPV QKTDGSWRMTVDYCKLNQVV TPIAAVPDV/VSLEQINTSPG TWFEWSPKIKALQQVQAQVA ALPFGPYDPADPMVLEVSVAD RDAIWSLWNAAIGESQRRLGF WSKALLSSADNYSPFERQLLAS YWALVETERLTVGHQVTLRPE LPIIMNWVLSDPSSHVKVSGAQQ HWKCAVHT/IIKWKWWYIRDWA QAGLEGTS*LYWPRASRYQQG HQDLFILRSRDLPSQVFI RDKLME RRNRTGRTKARIWEVTDRT VRTWIGEAVAAAADGVTFSV PVTPTHFRHSYAMHMLYAGIPL KVLQSLMGHKSISSTEVYTKVF ALDVAARHRVQFAMPESDAVA MLKQLS
16414	46782	A	16511	41	428	
16415	46783	A	16512	1	1026	

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16416	46784	A	16513	648	1886	LDPEVAWAKWQHSTVKGPQK QFAFWSQGQQYTFTGLPQGYIN SLSLCYNNLPRDLDRFSLPQDIT LVHYIDDIMLTGSSEQELAYTL DLLVRRRLCAKGWEINLTEIQA STSVKFLRVQWCGACQDIPSK MKDKLLHLFPPTTKKKASLFGF RRQCIPHLECGPEQEKAHQQAQ AAVQAAVPLERYDPADPMVL/ V/ELTWLWPLLSAQFASSGDQH *ALHMAPFLGVVSQLPGKKLIL DIFHHGKGRVLFSL*TLTPDM GLPILHIMLLPRLPSVNSQNALS TVMPGFTGPGIKGWKHWHSPS PLVIH*QNFCCFLFP*HYVLLA R S*FORKEPCHQET*O*FH*TGS* GCQLDTLGSCYF*VNKLRRELQ CWLG*LTQTIKMKSVYYISITEN CWMKRSVPVKRKILEEEA
16417	46785	A	16514	I	402	
16418	46786	A	16515	I	396	PTRPGERSVHVEIPRRVGSAG HAQWAGPVRVARPQLNAQLE GWLSQVQSTKRPARAIIAPHAG YTYCGSCAAHAYKQVDPITSITQ RFRYSSYYDESGEIVRSIEHLDK MGMSSIIEQLDPVSFSNYLKKYH
16419	46787	A	16516	2	358	
16420	46788	A	16517	2	769	
16421	46789	A	16518	I	1017	
16422	46790	C	16519	54	294	
16423	46791	A	16520	I59	245	GISVSCSMYL*PDRSAGYYGLF KDRKEK
16424	46792	A	16521	I	1227	
16425	46793	A	16522	I	2697	
16426	46794	A	16523	200	696	YGIVTGPSLCAGDKQPKKQEK NPVLVSPEFVDEALCACCEEYLS NLAHMDID/IGPGGPAVPQPPRA GPSSSSVTPSGPVSPLQLGLWA VGRCLGIDPFCLVQPLLPQASR SFTPLFCSGTLEDSHCLRDRVW ATFLGSWHSIVTKSMDCATKW TAHYPKCVLCGC
16427	46795	B	16524	I	960	
16428	46796	B	16525	I	2183	
16429	46797	A	16526	306	1844	
16430	46798	A	16527	59	189	YNSGCLYGSQCSVCRCL*GVRN QVRSQQQAMMAMAILVNKG G
16431	46799	A	16528	I	2034	
16432	46800	B	16529	I	855	
16433	46801	A	16530	I	834	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met/	SEQ ID NO: in USN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, ^=possible nucleotide insertion)
16434	46802	A	16531	65	172	
16435	46803	A	16532	321	429	
16436	46804	A	16533	460	647	
16437	46805	C	16534	529	804	
16438	46806	A	16535	3	433	
16439	46807	A	16536	1	484	
16440	46808	A	16537	511	681	QQGYTPFQGSGRESFLASSFWWL/PGLPWLA^AA*LQALTPSSH <sup>S</sup> LLSYLCSLLFCHP
16441	46809	A	16538	51	634	PVPTFGLPARHTGAEKRRKNSGGEQLSKNNLYIRGLPPGGTDQDLIKLCQPYGKIVS/TRAFLDKTTIRCKGYGFVDFDSPAAQKAVASLKANGVQAQMAKLQERDPA^GLSVSLLL'SMYEQELENMLKPFGHVISTRILRDANGVSRGVGFARMESTEKCEVVIQHFNGKYLKTPPGIPAPSEPLLCKIADG
16442	46810	A	16539	1	759	
16443	46811	A	16540	74	352	
16444	46812	A	16541	1	747	GSAVYLCYKKSVAKTNTVSYKAGLICRYPQEDYESFSLPESVPLFCLPMGATIECWPSNSKYPLPVFSTFVLTGASAEKVYGAIIQFYEPYSEENLTEKQRLLLGLTSADGKSDSSKTIHTNKCICLLSHWPFDVAFRKFLTFLYR^YISIGAHVLPIEKHSHFMHKVPFPSPQRPRILVQLSPHDNLILSQPVSSPLPSG GKFSILLQNLGPENAVTLLVFAVTEHKILIHSLRPSVLTSVTEAL
16445	46813	A	16542	319	969	
16446	46814	A	16543	131	342	NSDMGLNLGSALTG*PWVAIEFCCFGFFQIIVFSCLLGWL*VAPHPNLPSSPAEYMDFREAQEGTDVIY
16447	46815	A	16544	1	1086	
16448	46816	A	16545	469	759	
16449	46817	A	16546	3	598	
16450	46818	A	16547	227	604	
16451	46819	A	16548	416	1814	
16452	46820	A	16549	763	867	
16453	46821	A	16550	1	1419	

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16454	46822	A	16551	915	3125	SLAGMRLTGTVGSGGEVRL/TAK AGARVGPPELVGRPLEGECWY FSGVSRRTQAQQQLLLSPNEPG A FLIRPSESSLGGYSLSVRAQAKV CHYRVMSMAADGSLYLQKGRLF PGLEELLTYYKANWKLIQNP LL QPCM P QKA PRQDVW ERPHSEF ALGRKLGEGYFGEVW EGLWL GSLPV AIVKVIKSANM KLT DIAK EI QTLKGLR H ERLI RLH A VCSG GEPVYIVT ELMRKG NQLA F L GT PEGRALRLPPLLGFACQVAEGM SYLEE QRVV H RDLA ARNVLVD DGLACKVADFGLARLLKDDIY SPSSSSKIPVKWTAPEA ANYRV FSQKSDVWSFGVLLHEVFTY Q C P YEGMTN HETLQQIMRGWF FGCISRSEA VRRLQAE G N ATGA FLIRVSEKPSADYVLSV RDTQ A VRHYKI WRRAGGR LHLNEAVS FLSLPELVN YHRAQSLSHGLRL AAPCRKHEPEPLPHW DDDW E R P REEFTLCRKLGSGYFGEV FEGL WKDRVQ AIVKVI S RDNLLHQ Q MLQSEI QAMKKL RHKHIL A LY AVVSVGDPV YI IT ELMMA KGSLL ELLRDSDEKVL PVS ELL DIAW Q VAE GM C YLES QNYI H RDLA AR NILV GENTL C KVGDFGLARLIK EDVYLSHDH NIPYKWT APEAL S RGHYSTKSDVWSFGILLHEMFS RGQV PYPGMSNHEAFL RDAG
16455	46823	A	16552	1	990	
16456	46824	A	16553	1	2847	MTAREHS PRH GARAR AMQRAS TIDVAADM LG LSLAGEPHRACT GLQTTGYPGLDP PSG*TRK*GRG MSALFL*TASAGA*LH*FSSLVA GAPP G*CGNVQVF/WLAHAQA MGTNNPFLSSIAFFQDSLINQM TQVKLSVYDV KDRS QGTVKSA ESDR VGNITVIGWQMEEKS DQ RPPV TRS VDTVN GRLHPP APTV MHSLSHRHS KNSN FRAL ALM VLPV DESLTEALGIRSKYASLR KDTLLKSVFGGAICR
16457	46825	A	16554	1	327	
16458	46826	A	16555	259	3109	
16459	46827	A	16556	262	3159	
16460	46828	A	16557	1	1398	
16461	46829	A	16558	123	393	
16462	46830	A	16559	245	424	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, ==possible nucleotide insertion)
16463	46831	A	16560	1	531	
16464	46832	A	16561	2348	2775	
16465	46833	A	16562	373	555	LRIQVTFDDVAVEFTPEEWALL DTTQKYLRYRDVML\ENYMLA SVGKSNITLLGMVACTCS
16466	46834	A	16563	165	457	
16467	46835	A	16564	310	349	K*TMK*EMGKFK*FY/YLEQED YANANALLSPAPALPKEKRTDS NGR VYFVNHNTRITQWEDPR QGQLNEKPLPEGWEMRFTVD IPYFVDHNRRRTTYIDPWSTRP
16468	46836	A	16565	1	2217	
16469	46837	A	16566	1402	1860	
16470	46838	A	16567	461	696	KRMCFCTSLSARSSGSMYMSC RICCSMMPFSSVFRSISRYSR AAFWAWTETRLCWQAAMPRQ QPPGLLHQWTTSP
16471	46839	A	16568	1	601	
16472	46840	A	16569	468	1213	
16473	46841	A	16570	2	365	EGCFQKIKLHDHILSPPMPFWK CSNPDVAFPGPKSLKVKRQLS* DGRQLRRGSLGGALTGRYLLP NPVAGQAWPASAETSNLVGMR SQALGQSAPSLTASLPCVSKCW ENIPPWMNCPPIK
16474	46842	C	16571	220	408	
16475	46843	A	16572	840	1091	QSLQHDVTL*VPVLLSYPEPAPS GHGLLRGSAQIAL*TIPADPAGT YLKTREPTLGCQTVPLPAPHLS VDTVCRLCLSSVWPQ
16476	46844	A	16573	1	1356	
16477	46845	B	16574	1	1084	
16478	46846	A	16575	2	526	QPRGKKFSKNKPRKQNFPTPKH MRVVLPPF/PPLKFFIFPKGLKFL EGGCPNISPPQKKGSLPKIPR*V LIRPPIRKKLFPCTARVKLGPQ GSFKTAAPSSSSP*SADPVYLAG K/PRQSSPGGTGGLNPPRRLQ PQPHPGPSWHSSSSRGPGGHPR RESAERSRCASGNPGQQ
16479	46847	A	16576	36	167	RQLFENTQSDETKQEQNQNK K*STATESRKVPQTGKSKSYWP
16480	46848	A	16577	171	527	
16481	46849	B	16578	1	471	
16482	46850	A	16579	1	294	
16483	46851	A	16580	185	299	GLQYLGKSGLKVKRGKVV*S ACCKKKGAALGTVASPL
16484	46852	A	16581	3	414	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met cod	SEQ ID NO: in USNN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, ^=possible nucleotide insertion)
16485	46853	A	16582	462	928	WGVPGLPGRHLLPLPSQPPPSW LSILYVSWAALTCTFLNSGESTA AKFFCPNLSAISY^HTEAIPPTWQ GVHLSWAFGNGAPDIFSGPGGL L^P/A/PQP/DLALGALFGAGVLV TTVVAAGGITTLLFIQHHTTQEI H^QIVQWIKTTL^ILATVSYVIG
16486	46854	A	16583	1	654	
16487	46855	A	16584	66	323	RVSLEIHVIQKRRPHHLSLLSFW TRMKTFRRRK/WGEAEESATDT TSETNKVGTGVFVLSLWVPVL VRNLAGPGVVLGNICKHFPVC
16488	46856	A	16585	1	1530	
16489	46857	A	16586	615	873	FVFLWSLMMVMYRWGFGVAV LSVC*FSF*QSGPSAAGLLEFAG GPFQTPFAWVSVVEAAEQRIML NSKRCCIVPLVVSSQRGTRP
16490	46858	A	16587	286	626	PCKLFPCCNTCY^S^RV^DFFRVA GKRSLLNNYTSWVNTSMLVPR VAFAAGGFLQQAAVLCVHLLG SPILGAADSSVTPFCWMANAH ICGLQLQNTLSFAEPIYLGQEHA QLS
16491	46859	A	16588	226	489	PYLSVIFFFDYGINEEQCQRPQ GDGQNFHRHNGWIKINPSCISF AIFFPFGAEKNMWSTPVEAFN LLST^AF^LFGYKCTLVISS
16492	46860	A	16589	1	1344	
16493	46861	A	16590	1	257	
16494	46862	A	16591	73	374	ESETEHKRPKGKJHSPKRSCNMCG QWAFAHASLTVSYCLLTCNET CSGDGCEGGMRID^DPPVSQTR FFITLL^LCFPAGGPQPAYFCTQ TQCHVETPRVSQ
16495	46863	A	16592	1	666	
16496	46864	A	16593	95	1840	
16497	46865	A	16594	1740	2026	
16498	46866	A	16595	39	487	SRLLDPRVRLLFRQFCETRPGLEC YIQFLDSVAEYEVTPDEKLGEK GKEIMTKYLTPKSPVFAQVGQ DLVSQTEEKLLQKPCKEFLSAC AQSVHEYLGEFPHEYLDMSFF DRFLQWKWLE/RVCAQCVRAT GKMYACSRLEKKR1QKRK
16499	46867	A	16596	1	591	

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16500	46868	A	16597	71	1994	EQEQRGRQQGLLAPPAPAAAA AARAAAAAAAAPQALTAPPAG SVADRRLSMELENIVANTVLLK AREGGGGKRKGKSKKWKEILK FPHISQCESLRRTIDRDYCRVC DKQPIGRLLFRQFCETR PGLEC YIQFLDSVAEYEVTPDEKLGEK GKEIMTKYLTPKSPVfIAQVGQ DLVSQTEKLLQPKCKELFSAC AQSVHEYLRGEPFHEYLDMSMF DRFLQWKWLERQPVTKNTFRQ YRVLGKGGFGEVCAQCVRATG KMYACKRLEKKRKKGESM ALNEKQILEKVNSQFVVNLAY AYETKDALCLVLTIMNGDLK FHIYNMGPNPFEERALFYAAE ILCGLEDLHRENTVYRDLKPEN ILLDYGHIRISDLGLAVKPIEG DLIRGRVGTVGYMAPEVLNNQ RYGLSPDVWGLGLIYEMIEGQ SPFRGRKEKVKREEVDRVRLET EEVYSHKFSEEAKSICKMLLTK DAKQLRGQEEGAEEVKRHPF FRNMNFKRLEAGMLDPPFVPD PRAVYCKDVLDIEQFSTVKGVN LDHTDDDFYSKFKSTGVSIPWQ NEMIETCFKELNVFGPNGLTP PDLNRNHPPEPKKGLLQLRKF RQHQNNSKSSPKTSFNHHINS
16501	46869	A	16598	1	963	
16502	46870	A	16599	192	609	RPKGARELRLHPGPRYGRTPQ NCPWARPGCLHEAL*G WKICL HCKCPQEEHMVTVMPELEMECT ISKLMDFQRNSTSDDSGCAL EEYAWVPPGLKPEQVHQQYSC LPPEEKVVPVNSPGEKLRIKQLL HQLPPHDNEV
16503	46871	A	16600	1	915	
16504	46872	B	16601	30	820	
16505	46873	A	16602	99	248	RLEKHINCSRVI*SWAASPGITA AAVRYVTLNPPGTFLEGVAKG QYTFT
16506	46874	A	16603	1	717	
16507	46875	A	16604	271	556	TAACLQSHHFKSSGQLSFERKW PKVGTITRSIASLLSGPVFGLIHH LAFSAHVPREGPTTPWNYFPRV AAP/RRWTPGEHARTTGLGAA PCVLLWA
16508	46876	C	16605	135	341	
16509	46877	A	16606	125	226	
16510	46878	A	16607	194	547	

SEQ ID NO: NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, /=possible nucleotide insertion)
16511	46879	A	16608	2073	2338	
16512	46880	A	16609	1127	1282	
16513	46881	C	16610	1	2094	
16514	46882	A	16611	523	706	QHPLPNPCCHQPFHLCLRR*TL HCLRQQ*WPPLRQLPKIMLIL LRSHPQHPCLLQLD
16515	46883	B	16612	190	805	
16516	46884	B	16613	90	2812	
16517	46885	A	16614	44	216	RCRRRLIPHPRRLSPVVIRRIQVP Q/VQPGAGPSRPGHTRDPGAA AAHCPGPDGSAH
16518	46886	A	16615	1	1107	MTEEPLQALVLSAVLVLQEAY VRRSLTALGLDTFANFAHFSSEM QPLSDAPCGLVTVGTVTRPLVAYS VEVGGFTIICGLSLASGNISGWC QLYLLLTQCRRAATLWDSGM GGGRQSSRQTSVPRWTLDKCI PGPKLTTTRPQMDFKALGQQA HVEHQTHEDIRPQVDTQAPGG HKALGEQQDPVGHQASVGYS QVPQDSLQALAGQATPEIPLG LQLHITVLVQEIQELIEAQTRAP GPCAEVRALPAPAAEPEPAWEE APPERALELEGAPAKDQTNEEL PEITA/PYC/EPLALTLELKAWLE RKVGGGRGIDQHSPSQLPCCP*S WARWQTCRQRAGHLAWPPV RCREASLIH*NHSPAAAGPFILL
16519	46887	A	16616	1	792	
16520	46888	A	16617	1	963	
16521	46889	A	16618	1	378	
16522	46890	A	16619	1	494	MKPRTLAVSVTVLKGGVSRV SFWCSDVFRVSSFWWVRLAD SGVKLRTFAVSVTPLKAARLEL FVPPGGFVVSLASGVKLQFVEV SVTAHKGSVDPKSEKQQDLLQ RGKEQSHTGEHPSRLP/PAG SGSLLLFSYLAAPTSC*LVQPSG LF*QGADWCIYNP
16523	46891	A	16620	137	262	

SEQ ID NO: NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion,  =possible nucleotide insertion)
16524	46892	A	16621	1	2786	EVSLREATQRKLRRFSELRGKL VARGEFWDIVAITAADEKQELA YNQQLSEKLLKRKELPLGVQYH VFVDPAGAKIGNGGSTLCAQC LEKLYGDWNSFTILLHSDEW KKKVSESYVITIERLEDDLPIKE KELTELRNIFGSDEAFSKVNLN YRTENGSLLHLCCICGGKKSH IRTLMLKG\LRPSRLTRNGFTAL HLAVYKDNAELITSLLHSGADI QQVGVGGTALHIAIAGHLEA ADVLLQHGANVN
16525	46893	A	16622	174	722	
16526	46894	A	16623	1	1554	
16527	46895	A	16624	1	843	
16528	46896	A	16625	2	745	ECWDGEHDIETPYGLLHVIRG SPKGNRPALITYHDVGLNHLKC FNTFFNFEDDMQEITKHVFVCHV DAPGQQVGAQSFPQGYQFPSM EQLAAMLPSPVQHFGFK\YVIGI GVGAGAYVLAKFALIFPDLVEG LVLVNIDPNKGKWDWAATKL SGLTSTLPDTVLSHLFSQEELVN NTELVQSYRQQIGNVNQANL QLFWNMNYSRDLIDINRPGTV PNAKTLRCPVMLVVGDNAPAE DGVVECNK
16529	46897	A	16626	3	949	
16530	46898	A	16627	1	633	
16531	46899	A	16628	2	1324	
16532	46900	A	16631	1	591	
16533	46901	A	16632	138	832	
16534	46902	A	16633	55	586	IFVHPTAASTMPSKFDPEKIV VYLRCTGGEVGATSLAPKIGP LGLSPKKVGDDIAKATGDWKG LRITVLTIQNRQAQIEVSPAS ALIIKALKVEPPRDRKKQKNIKH SGNITFDEIVNIARQMRHRSLAR ELSGTIKEILGTAQSGVGCNVDG RHPHDIDDDINSGAVECPAS
16535	46903	A	16634	1	735	
16536	46904	A	16636	3	346	
16537	46905	A	16637	57	649	GPRRAYGGRMAGGGGDLSTR LNECISPVANEMNHLPAAHSHDL QRMFTEQGVDDRLLYDIFVK HFQRWKVEISNAKKTFPFLEG LRDRDLITNKMFDSDSCRNL VPVQRVVYNVLESELEKTFNLPV LEALFSDVNMQEYPDJLHJYKG FENVIHDKLPLQESEEKEREERS GLQLSLEQGTGENSFRSLTWPP

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met/Asp	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, ^=possible nucleotide insertion)
16538	46906	A	16638	1	1665	
16539	46907	A	16639	348	1534	
16540	46908	A	16640	1	627	
16541	46909	A	16641	1	1343	
16542	46910	A	16642	76	479	IRAVSRSRERPGSRSRVLQAC^GGGAFPGP*SAEISRLVRSHNLGGYSC/TEGGGGCRKGSCCLQHSCLLWHSCLLPASKNTVCSKDLGGCSCCTQESRAPACSWSPRTQGGSASSHDLGSCRNAWETPSRQLGRSW
16543	46911	A	16643	130	675	
16544	46912	C	16644	118	420	
16545	46913	A	16645	1	987	
16546	46914	A	16646	1	494	
16547	46915	A	16647	360	1510	
16548	46916	A	16648	375	2187	VTAAAAATAMAESGESGGPPGSQDSAGAEGAGAPAAAASAEPKIMKVTVKTPKEEFAVPENSSVQOFKEEISKRFKSHTDQLVLIFAIKGILKDQDTLSQHGIHDGLTVHLVLIKTQNRPQDHSAQQNTAGSNVTTTSSTPNSNSTSGSATSNPFGGLGLGLAGLSSLGLNTTNFSELQSQMQRQLLSNPEMMVQIMENPFPVQSMSLNPDLMRQLIMANPQMQLIQRNPESIHMNLNPDIRQTLERLARNPAMMQUEMRNQDORALSNLESIPGGYNALR RMYTDIQEPMLSAAQEFGGNPFASLVNTNTSSGEQSQPSRTENRDPLPNPWAPQTSQSSSASSGTA STVGGTTGSTAAGTSGQSTTAPNLVPGVGASMFTNTPGMQSSLQQTENPQLMQNMLSAPYMRSMQOSLSQNPDLAAQMMLNPNPLFAGNPOLQEQMRRQLPTFLQQM QNPDTLSAMSNPRAQMALLQIQQGLQTLATEAPGLIPGFTPGGLALGSTGGSSGTNGSNATPSEN TSPTAGTTEPGHQQFIQQLMLQALAGVNPLQNPEVRFQQQLEQLSAMGFLNREANLQALIATGGDINAAIERLLGSQHISIISIVS
16549	46917	A	16649	269	440	
16550	46918	A	16650	469	746	RLNLPGPLCAGTSILFAVLMEAI GVSCIRQAGGGHVASHIY^GLM/PALAL^DTEPRNPSALPETCLCGSGPQSQMGHQTSHLLSSPGTLSF
16551	46919	A	16651	1	1026	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met cod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=-possible nucleotide deletion, !=possible nucleotide insertion)
16552	46920	A	16652	719	906	
16553	46921	B	16653	1	1971	
16554	46922	A	16654	200	239	
16555	46923	A	16655	109	177	
16556	46924	A	16656	1	1542	
16557	46925	A	16657	1	453	
16558	46926	A	16658	2	487	
16559	46927	A	16659	1	1260	MEDAEGTVTLLAVTLLVARDLN CIOPQTGPGG!PEESIVIGDVSS MHVIAPEDLPVGQDVVEDSDI DDPPDPVRALPLQIHACGRVGF AHDDWSEGGDPAADTLIDPSQ DARYLKCEGMQAPHNSNPVAQ KTEISYHIWIA!P!REPKSGKVTG TLC DLLKDLTVIHS!LPIKQGCS GLGVLVQGTQ!PQNTDTCTC QVSAVEGKGEGLMQLASLSRR VTIWAYGDSQERDLK!TQLEKIT AIKDMKEMQKEYRIMEKAHS RQRKQH!HKGP!PERKEQAAIFAV LQPPLVITRQ!TGSGVDPQKTPA DLQKRCRTVRRKTSQKAVAS TLTKRITTQKLNNAKD!HNSPTR EQNCTENEFDELTEVGFRRWVI TNSELKEHVL!TQCKEAKNFDK RLEELLIQITSLEKNIS!LMLMEL* S FALSFCV!VILFVN!DATAFCWL VFLLTVRHLFCRSAGVFWGSTP DPVCLVITSGGCRTAKIAACSF SGPLWCCFLCLEWAFS!ILYFS CISFMSLIAVFSNWVLRSLS
16560	46928	A	16660	1	799	
16561	46929	A	16661	1	969	MHVIAPEDLPVGQDVVEDNDI DDPGQAKKTMEEQWT!LVSLLS TSQQQGPVPGGSTASSATDKLS RWELTLLYSTT!FLAREAFRRA CLSGGTQRDWSQ!TLLNLWLT PLGVFW!SFLGW!WLQLLEVPD PNVVPHYATGVVLFGL!SAVVE LLGEFPWVLAQAHMFV!KLKV AESLSV!LKS!VTAFLV!WLPH WGLY!FSLAQLFYTTV!LGLCYV IYFTKLLGSPESTKLQLTPVSRIT DLLPN!TRNGAFINWEAKLAW GFFKQFFLKQ!LTEGG!RYVG HFLNVLNFGDQGVYDIMNN!G SLVARLIFQPIEESFIYS
16562	46930	A	16662	1	1665	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met/Asp	SEQ ID NO: in USN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /'=possible nucleotide deletion, /+=possible nucleotide insertion)
16563	46931	A	16663	I	1521	MDVSSPPCVDGVSVILPPLLIQPRQ TGSGVQLQQNPTDQLQLRVLTV KRKTKNQKGPHQNSICTSPSS KTKEYTFFSVQHHTYSKIDHIV GSKAVLSQLRKRTIEITNCLPDHS AIKLELRKKLTLQNHKTTWKQN NLLNDYWVHNKMKAEIKMFF ETNKNKDTTYKNLWDTVKAV CRGKFIALNAHKRKQERSKIDT LTSQLKELEKQEQTHSKASRRQ EITKIRAELEKIEETQKTVQKIHES RWSWFEKINKIDRPLAGLIKKKR EKSQKDAIKNDKLDITTDPTET QTTIRDYHKKHLYAIKLENLEEM DKFLDTYTLPLRNQESLNRPITG SEIEAISNLSPTKKYRTRRIHSR II.SEVQGGAVLEVLAIRAQEK EIKCIOLGKEEVKLSLFAADDMIV YLENPTVSAQNLLKLISNFSKVS RYKINVQKSQAFLYTNRRQTES QIMSELPTIASKRIKYLGQLTR DVKDLFKENYKPLLNEIKED/N KWKSIKPCPRGRINIM
16564	46932	A	16664	2	2315	
16565	46933	A	16665	I	912	
16566	46934	A	16666	I	912	
16567	46935	B	16667	199	619	
16568	46936	B	16668	64	1815	
16569	46937	A	16669	I	239	
16570	46938	A	16670	1	242	FREDGKTAGCIGHEPSPVLLGLRL GLQPWG*GWGCSHAGASAPDL VAGSAHSCGLWLPGSLHHHPA QCLPALLCGHLCLSVQDQQNG LLGR
16571	46939	A	16671	58	505	ASSRTRPSCTLARGRRWFPQPL SGRQRQRGRRGSRVG/YGTA QNSTTLTSPAASASEATVSGHW PSTAPCCV\PAGAG\SATMWRSP A*AACGSAAWTSTWSRRSPGP GAAAGYGGVRTFCQ\PA\GLTR/L ANRSTAGLCGWGLTLSCRETEL
16572	46940	A	16672	242	2952	
16573	46941	B	16673	474	2690	
16574	46942	A	16674	97	451	
16575	46943	A	16675	667	893	

SEQ ID NO: NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, v=possible nucleotide insertion)
16576	46944	A	16676	3	639	RIRVHPTPAAFMPPKFDPEIK VGYLRCGEGVGTASALAPKIG PLGLSPKVVGDDIAKATGDWK GLRITVKLTIHNRQAQIEVAPSA SALIIKALKPEPPRDRKKLKLKLN SGNITFDENGNCSTDMR/HRS SRELSGTTKEILGTAQSVGCNV DGRIPHDIIDDDINSENDKQPRKS KMRTSFSPQIPGHEHFHFLLLL QHVHQLALTL
16577	46945	A	16677	350	984	VYLEVAPGGESRPLSALGPQR IGPPGSCLPKKSQVNDICQROP GIDWKGP*GLQVKLTHSRTGQ APDCTRVP/VLPSCP*FIQSPSRE PPKRPEKKPEKTFKHQLGIFTFL NEICSTLLRQMRHRSLSPEKLS GTPLKEIPGGLPQSSWAGNV*W AAIPHDNIDDIQOWVLWKPAPV SDIFIVTVGVKGPPSVFTEISW EVLEMVTGGVG
16578	46946	A	16678	252	964	
16579	46947	A	16679	1	182	
16580	46948	A	16680	275	639	
16581	46949	A	16681	376	418	
16582	46950	A	16682	1135	1591	
16583	46951	A	16683	3	420	AAKEIEVGGGRKATKSFQKIQV RLVRELEKKFSGKHVVFIQARR ILPKPTRKSRTKNQKQPRRSRTL TAVHDAILEDLVFPSEIVGKIR VKLDGSRLIKVHLDKAQQNNV EHKVETFSGVYKKLTGKDVF EFPEFQL
16584	46952	A	16684	1	879	
16585	46953	A	16685	2	691	HEEKAMFSSSAKIVKPNQEGK DEFESGHPLGLFLELEMNSDIL KASAQGT*IIATAS*RKLKVGGCS ESLFH*SFVPRSLKLKTFPKNP KVRA*LRRIGKKVPGVKAMS VLYPPSEGEFLPLSPTSEKARTK K*AKSRPPGARTLDDKLVHDAH PLRDFGFPSPGNFWAKRIPRSNL DGQPGS1KVFPWTKAQAQNQCW NTRVETFFLVSYK\KLTGQGC*F LEFPRVFN

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
16586	46954	A	16686	1	452	TLLVIPRKMRS A VELQQTSDL QLRLDLTVRKKTNKRKA TASTS QKGHLHQNPICRSPSTKPLKEV G FRRSVITNFSELKEVDRVTYHKE AKNLENRLDEWLTRINSVEKTL NDLKELKTMARDLHDACTSF NRRFDQVEERVTVTEDQIN*QTE SNSINFTKRSSTPKPHL\RSPTSK TKEVGFRRSVITNFSELKEDVR TYHKEAKNLENRLDEWLTRINS VEKTLNDLKELKT MARDLHD A CTSFNRRFDQVEERVTVTEDQI
16587	46955	A	16687	1	618	
16588	46956	A	16688	280	353	SCNSIFARSVRACCS*VASSSFC C
16589	46957	A	16689	1	459	IKYSSPMKSTFVDPVDPVAVAV IYCLAA GLVII RIPFFQLVPLKEE KMVLLNMDYIYE MASLNLVTH RNEAPFGSRVRSSLPATEQSWM ENDFDKLTEVGFRRSVITNFSEL KEHVLTHHKEAKNLEKRLDKW* QTRINSVEKTLNDLMELKTM A* EEKMVLLNMDYIYE MASLNLVTH RNEAPFGSRVRSSLPATEQSWM MENDFDKLTEVGFRRSVITNFSEL KEHVLTHHKEAKNLEKRLDKW QTRINSVEKTLNDLMELKMT
16590	46958	A	16690	2	403	LALSGEMT LVLFM LLLAGGWWT HDKPEMPM PRA TS GGT RKGK T KAALKDLIATWKEV C VSSPATE QSWMENDFDELTEVGFRRSVIT NFFKLKEYV LTHHKEAKNLEK MLDEWLTRINSVEKTLNDLME LKNM A*ELTEVGFRRSVITNFF KLKEYV LTHHKEAKNLEKMLD EWLTRINSVEKTLNDLMELKNT
16591	46959	A	16691	1	676	
16592	46960	A	16692	1	1965	
16593	46961	C	16693	1	3075	
16594	46962	A	16694	78	152	CAAGFGLPVFY*GFLHRC SLSLGV
16595	46963	B	16695	1	904	

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16596	46964	A	16696	1	2026	EQEASYGRDAFAKAIYERLFC WIVTRINDIIEVKNYDTTIHGKN TVIGVLDIYGFIEFDNNNSFEQFCI NYCNEKLQQQLFIQLVLIKQEQEE YQREGIPWKHIDYFNNQIIVVDL VEQQHQKGIIAILDACMVNGK VTDEMFLAEALNSKLGLKHAHFSS RKLCAASDKILEFDRDFRIRHYA GDVVYVSIGFIDKNDKDTLFQDF KRLMYNNSNPVLKNMWPEGKL SITEVTKRPLTAATLFKNSMIAL VDNLASKEPYYYVRCIKPNDKKS PQIFDDERCRHQVEYLGLLENV RVRRAGFAFRQTYEKFLHRYK MISEFTWPNHDLPDSKAEVKKL IERCGFQDDVAYGKTKIFIRTPR TLFTLEELRAQMLIRIVLFLQKV WRGTLARMYKRTKAALTIIIR YYRRYKVKSYIHEVARRFHOV KTMRDYGHVWKWPSPPKVLRR FEEALQTIFNRWRASQLIKSIPA SDLPQVRRAKVAAVEMLKGORA DLGLQRAWEGNYLASKPDTPQ TSGTFVPVANEKLRKDKYMNV LFSCHVVRKVNRFSKVVEDRAIFV TDRHLYKMDPTKQYKVMKTIP LLQLTCLN\WSNGKDQLVVFHT KDNKDILVCLFSKQPTHESRIGE LVGVVLVNHFKSEKRHLQVNVN TNPVQCSLHG\KKCTVSVETRL NQPQPDFTKNRSGFILSVPGN
16597	46965	A	16697	1	1665	
16598	46966	A	16698	1727	1908	FLFFYIC*RELYFQLCGQFWNK CNVLLRRMYILLIWGGGEFCRYQ LGLLGAEINSVPGYHC
16599	46967	A	16699	1	384	
16600	46968	A	16700	1	636	
16601	46969	A	16701	1744	2283	
16602	46970	A	16702	194	368	
16603	46971	C	16703	62	205	
16604	46972	B	16704	1	1257	
16605	46973	A	16705	1	1077	

SEQ ID NO: NO:	SEQ ID NO: of peptide sequence	Met hed	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion,  =possible nucleotide insertion)
16606	46974	A	16706	I213	1228	AQN*QTQRTSTPKPHLSSPSTK TKENDFDELREEGFRRSVITNFS KLKEDVRTHRKEAKNLEKRILD EWLTRINSVEKTLNDLMEALKT MAQELRDTYTSFSSRFDVQEER VSVIEDQMNDMKREEKFREL/K RVQRNEQSLQEIWWDYVKRTNL RLIGVPEKIQTTIREYKKHYAN KLENLEEMDKFLDTYTCPRLN QEEVESLNRPVTGSEIEAIIINSPL TKKVQDQADSQPNSTRVFKTV CISSLGHTTASADTQDVCQLPV TSLLEQGLSSKSAGFLDYAVQR LWLLGTEPL
16607	46975	A	16707	33	263	
16608	46976	A	16708	204	1756	
16609	46977	A	16709	760	821	TMRTHGHRKGNI*QR/R**PEST KNSNKFTRKKNQTPSKREWMK LETHLSKLSQGQKSKHMFSLI SGN*TMRTHGHRKGNIHWGL LWG
16610	46978	A	16710	1	879	
16611	46979	A	16711	311	514	KNAHHIQWPSKKCKSKLQ*DTIS HQLEWQSLKSQETTGTRMKME TITLSKLSQGQKSKHCMFSLIGG N
16612	46980	A	16712	24	1268	AGLCAARARMRLFRWLLKQPV PKQIERYSRFPSPPLSIKQFLDFG RDNACEKTSYMFRLKELPVRL ANTMREVNLLPDNLLNRPNSVG LVQSWDMQSFEELL*YENKSP DPQVLDNFQVLVIKVRDRHND VVPTMAQGVIEYKEKFGDFP STNIQYFLDRFYTNRJSFRMLIN QHTLLFGGDTNPVHPKHIGSIDP TCNVADVVVKDAYETAKMLCE QYYLVAPELEVEEFNAKAPDKP IQVYVVPSPHLFHMLFELFKNSM RATVELYEDRKEGYPAVKTLV TLGKEDLSIKISDLGGVPLRKI DRLFNMYSTAPRPSLEPTRAA PLAGFGYGLPISRLYARYFQGD LKLYSMEGVGVTDAVIYLKALSS ESFERLPVNPKSAWRHYKTTPE ADDWSNPSSPRDASKYKAKQ
16613	46981	A	16713	175	465	
16614	46982	A	16714	240	381	FFLSFPPLCQSS*NQNLLPW/ICA KVCSTPVEVSKTTNPLEGRNSG HI
16615	46983	A	16715	268	1524	
16616	46984	A	16716	1	378	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method in USN 09/540,217	SEQ ID NO: location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion,  =possible nucleotide insertion)
16617	46985	A	16717	708	987
					IQLPGHRSQQAGASHTDARQ QDPGNSHSDFVRISHSLPCLER QDRRSAGHNGSATVPGTEACG RAYKAPAGHYZHSGAGQSLPAA SHRSFSSP
16618	46986	A	16718	I	2052
16619	46987	B	16719	I	606
16620	46988	A	16720	I	541
					QHQRKQKRQLRAQQNLSWEI AKEYQNEEDSLGGSRVVVCDI NKEMLKVGKQKALAQQYRAG LAWVLDAAEELPFDDDKFDIYT IAFGIRNVTHIDQALQEAEHRLV KPGGRFLCLEFSQVNPNPLISRLY DLYSFPRVIVPLGEVAGDWKSY QYLVEISIRRFPSEQEKFKDIME DAGFVHKVTVYESTLTSGIVAIHSG FKL*FLCLEFSQVNPNPLISRLYD LYSFQGHPCPGRGRHRWRLEVL VPCREVSEGFLRLKEFKDHDRR CRLSTR
16621	46989	A	16721	526	933
16622	46990	A	16722	191	468
16623	46991	A	16723	2	677
					GKVHVLLERRGFHRTEMHLQKI LLLPVLSSSSSDP/STLSVSLV RMFSSADE*SVSEASSEPESSFS RRSSCSFGSEPSAFSSFPVLDL ASLSVVFLLFRAFS/SSHVM*WL PSSS*VGS/STSARAQLPSYVPSF SVKTKSGLKSALRFFPKAFCRL PSTMGPSSSSPESDALSALHRHLV ILDVWVLQIKPRVRKPCRRSHF RKRAQPAVRPLTFRSLLVLR
16624	46992	A	16724	31	187
16625	46993	A	16725	215	947
16626	46994	A	16726	I	378
16627	46995	A	16727	2	7567
					GGGGARRQRGDAGGGAETAP SEILSPAAEERSGRSETLRRGT AAGRMATVVVEATEVPEPGSI ANPAASTSPSLSHRFLDSKFYLL VVVGGEIVTEEHLRRAIGSIELGI RSWDTNLIECNL DQEELKFVSR HSARSPSEVPG QKIL HHRSERF *ETV VLIQ PFLMEGSSGTEVRL MITDAARHKLVLTGQCFENT GELIQLSGGSFSFQNIEFTDQEIG ELLSTTHPANKASLTLCFCEE
16628	46996	A	16728	101	365
					VITGQPNTNPNLQATPDIQGTL ARLGPA/LHPRGIIPFIGHQSA/R PHAPAPANPNKRTLFRPPPLSPP SPEPPGSGQQGAGLGARALP

SEQ ID NO: NO:	SEQ ID NO: of peptide sequence	Met no	SEQ ID NO: in USN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion,  =possible nucleotide insertion)
16629	46997	A	16729	1170	2847	VASC*ENACKQNQRQKPCDYL NRCRKGLWQNSTTLHAKNSQ* TVLYKTIKFQLEKTTLKFIVWNQ KRAHIAKSILSQKNAVGITLPD FKLYYYKATVTKTAWYVYQNR DIDQWNRTEPSEIMPHIYNHLIF DKPDKNKKWKGKDSLNFNKWCW QNWLAIACRKLKLDPFLPTYTKI NSRWIKLDLHVRPKTIKTLEENL GNTIQDITGKDFMSKTPKAM ATKDIDKWDLJKLKSFCTAKE TTIRVNQRPTKWEKIFTT
16630	46998	A	16730	79	536	
16631	46999	A	16731	232	771	
16632	47000	A	16732	3	339	
16633	47001	A	16733	279	416	
16634	47002	A	16734	1	1760	
16635	47003	A	16735	309	1718	
16636	47004	A	16736	10	417	IAIMNDTVAIRTRKFMTNRLLE RKQMVIDVLHPGKATVPKTEIL EKLAQMYKTPDPVIFVFGFRTH CGGGKTTGFGMIYDSLADYAEK NEPKHRLARHGLYEKKKTS* QRQERTNRMKKVVRTAKANV VAG*KPNE
16637	47005	A	16737	96	609	EKFMTNRLTSGETKWWI*CPFT PGRRTV*AQKIR/EKLAQNVQ RPHPDVIFVFGFRTHFGGGKTT GFGMIYDSLADYAKEKMNPKH RLAIRHGPMEEGKRPSSKGKGN GKERKNN*RKVQGGLAKGP LLGAGQKEEMKCLGSLEIIGSQ PKELKVLPMMLAVATVDFSQE
16638	47006	B	16738	1	1041	
16639	47007	A	16739	3	447	VSVPFIFIWLTCKSFLKFDLKS TNVLQSL/GKFQSEVSKRQKLA TVFSSFTSTGLCQGSVAFISRCP PLASGSDSVWRGGSVVFFSFRP* RLMISLLGSCVSHQFPKELEF** KKMPYKIPTAHHQQQDDQQRG HEHKQSQPDAVPHLG
16640	47008	A	16740	1	2385	
16641	47009	A	16741	1	639	
16642	47010	A	16742	1	993	
16643	47011	A	16743	127	426	CTDKITLVFGV*MLTPKPKD/CD DSAV*ELLWLTNQLSACVVP GLYHLHVRSLWIPYRCLFLSTMC GVCQCTVAMQLDCLADSFNA VFKLTEAGHMAR

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16644	47012	A	16744	3	374	SLRLQFYYKISFQTQDQANKLS DSDASHLHPLAPCSEPTRTNVH TKLPRERPQSQIASPYPLPPCPE RLKKQTNKKKNW*EPSPHILPP RNAAAHGTGSRASKSLPAPPPT VSPRPRPGAPGT
16645	47013	A	16745	16	253	
16646	47014	A	16746	163	588	TFHAVLHIENAGYFNSNIPFFRIL NHNPPLTTVEDPYLFKLPLALKYL *VL*YSHESRDDLYSF*IFHQRL SILHIG*NVIRKF*LSY*KKVIGE EKN*EDV*WSRQPAGEEQC*R THIDLE/PCRHMEEYYLTKKAK GKRCSSL
16647	47015	A	16747	2	363	GTSQTLRLRSLASACIFQPKVRL L SREEIPLNLNY*SVSPNSNPNL YSRHTILTAMLTLQLGTCVLLPI GLLVPVYPNCPSPTGLQVTPFLPS PCGSGWPAASFTYSSNRFRTNLL FCVFIL
16648	47016	A	16748	1028	1621	
16649	47017	A	16750	1	112	LGNTWG*QPCPKRLKIWLSLEFT KINVIRHMWKKFKRL
16650	47018	A	16751	91	597	LKNRRRSRSPSIRQSIGSTSRSW LTSLFYLDHTADVQVV*REFIP LKPRQ*ED*MFQSWLHAWGDT LEEAAFEQCAMAMFGYMTDTGT VEPLQTVETQGDDLQSLLFH FLDEWLYKFSADEFFP/GWGEES FSLSKHPOGTEVKAITYSAMQV YNEENPEVFVIIIDI
16651	47019	A	16752	226	668	IYFFRLHAWGDTLEEAQECA MA\MFQGYMTDTGTVPELQTSRS \KTQGDDLQSLLFHFLDEWLYK FSADEFFP/REVKVLSIDQRNFK LRFN\GWGEEFSLSKHPOGTEV KAITYSAMQVYNEENPGSFCD HWTFKTTQKIKRLPTGKK
16652	47020	A	16753	3	942	
16653	47021	A	16754	3	419	SLYHNSSQKRHWTFSSSEEQLAR LRADANRKFRCKAVANGKVLP NDPVFVLEPHEEMTLCKYYEKRL LEFCSVFKPAMPYRSV\LTCAFL ACKVDEFNVSNPQFVGNLRESP LGQEKALEQILEYELLIQQLNF HLIVHN
16654	47022	A	16755	312	537	
16655	47023	B	16756	209	1381	
16656	47024	A	16757	1	927	
16657	47025	A	16758	1	3987	
16658	47026	A	16759	2	175	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met/	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion,  =possible nucleotide insertion)
16659	47027	A	16760	2395	2700	
16660	47028	A	16761	2	1118	
16661	47029	A	16762	26	1205	
16662	47030	A	16763	1	1594	
16663	47031	A	16764	1	595	
16664	47032	A	16765	1	1029	
16665	47033	A	16766	1172	1364	
16666	47034	A	16767	253	389	
16667	47035	A	16768	489	855	
16668	47036	A	16769	2	401	
16669	47037	A	16770	415	694	EAKLHLNLCDMSWLCCPTKGK RKQALEVLNLGPFLAPFWIAK SYFFTSPKTQVSSL*FLRYKRIK LQCRPKTCTNPSRTRSCALPGR FIPPF
16670	47038	A	16771	1	765	
16671	47039	B	16772	1	1095	
16672	47040	A	16773	82	311	KANSDVPGFGGVNLEHLMEAC NS/GTNLLNSKRLNNDCICLASH TDVSIIARKCCLVVSCLLRLGL SILRSKESH
16673	47041	A	16774	2	683	
16674	47042	A	16775	1	2703	
16675	47043	A	16776	1	555	DHNSSPAREQ/SSMENKFHELT EVGFRKITSLEKNINIDLMELK TARELREAYTSIKSRIDQAKESI SEIEDQNLNEIKCEDKVREKRMK SNKQNFQEIWVDYVKRPNLRLT GVPESDRENGTKLENTLQEIIQE NFPNLARQANIQIQEIQRTAQR QSSSRATPIIIIVRFAKFEIKEKM LRAAREK
16676	47044	A	16777	1	839	
16677	47045	A	16778	1	504	
16678	47046	A	16779	1	2367	
16679	47047	A	16780	1	1566	
16680	47048	A	16781	146	464	VTGWTNYEGNGRWRRERSRQLC GCCSRKSSSSWG1SLMKGSGAP LRPGRRMMWSGFRKCSDTQVM YS*R*LLETMTLASIMR*THTK* NALRKCSALKDCFLGKALTL
16681	47049	A	16782	1	1782	
16682	47050	B	16783	221	1075	
16683	47051	A	16784	1	627	
16684	47052	A	16785	1	1539	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met ind	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion,  =possible nucleotide insertion)
16685	47053	A	16786	1	1318	LSPVLSLSPDMSFTTRSTFSTN YRSLGSVQAPSYGARPVSSAAS VYAGAGGLATGIAAGGLAGMG GIQNEKETMQSLNDRALASYLDR VRSLETEENRRLESKIREHLEKK GPQVRDWSHYFKIIJEDLRAQIF ANTVDNARIVLQIDNAIRLAAD DFRVKYETELAMRQSVENDIH GLRKVIIIDDTNITRLQLETEIEAL KEELLFMCKKNHEEVVKGLQA QIASSVGLTVEVIDAPK/FQDLRQ DSWADIRQAQYDELARKEPRG A*TKYWFSDLRRESTTVVTIQ FAEVVGAA*DDASQSWRTYSPS SLGDPTWGFPWRKS*RASLLEN SLREG*RPAYALT/QMEQASTG LACTFESELGTDPGAEQGQRQAQ EYEALLNNIKVKLEAEI*ATYRRL LEDGEDFNLGDA LDSSNSMQT IQTITTRIVDGKVVSETNDTK
16686	47054	A	16787	1	253	RVRTLKTSTSTCLYWENKDS/ DHPERSSP*YMSPSHRYGSLVK ASITKPAFLKTSGRFLTCSSQFC PLISKISDGFSHLPPFST
16687	47055	A	16788	1	276	AAAAGPPGPLVMFTYRERVG LRSVHILRASHTDARLQRQEPT ERLQFHSSGLLIRFSRETEPIGV YIKD*EEWAYKMMVFAKSHD LPFAN
16688	47056	A	16789	1	203	LLHTSTKNEWLQ*GKRDPLIVF YTQYLF*EKTRK*NQRQAGSL ALGPKPGLRLPGLNPVVENQFI
16689	47057	A	16790	8	361	RGLDGQGGGRDGSSSSGGGGRR RRRCCLLLAPAPAVIRASGRGP R*DCWRAGCA*AWRPC/RLAR RMWTLRSPLTRSLYVNMTSGP GGPAAAAGGRKENHQVARKR LNVCVFTRSVSETA
16690	47058	A	16791	674	1076	VQLFRSAGSRDHHRFLGRGRN KQTKTLYPTPIPSCSLVYORKQN GSLLWTSRMPSSVFPCTLTPSFS LPLRISQTTHPNLRGPSCPKGLG IALISLVRHWLKI*ATSQVQAL WSFSMWMIYFWLPVQKPHASR
16691	47059	B	16792	296	1470	
16692	47060	A	16793	1	334	
16693	47061	A	16794	718	2541	
16694	47062	A	16795	2	406	
16695	47063	A	16796	74	464	
16696	47064	A	16797	159	610	
16697	47065	A	16798	1	273	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met cod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion,  =possible nucleotide insertion)
16698	47066	A	16799	1	543	
16699	47067	B	16800	1	873	
16700	47068	A	16801	1	558	
16701	47069	A	16802	27	136	
16702	47070	A	16803	89	363	
16703	47071	A	16804	579	994	
16704	47072	A	16805	129	362	PKIIQPRRATTRFTSIHGWRICPS IPCFPEATINRRRCVKVDSVTCH LLTQR*YKSSKVQERC*SCRIQG QKISDCY
16705	47073	A	16806	878	1811	
16706	47074	A	16807	1	843	
16707	47075	C	16808	19	231	
16708	47076	A	16809	1	1650	
16709	47077	A	16810	3	404	
16710	47078	A	16811	279	428	
16711	47079	A	16812	3	507	
16712	47080	A	16813	1	1128	
16713	47081	B	16814	1	567	
16714	47082	A	16815	3	1206	GSEGQQAGPGGAATAAAAME DEMPKTLVVGNLNSRDVTEALIL QLFSQIGPCKNCKMIMDTAGN DPYCFVEFHEHRHAAAALAM NGRKIMGKEVKVNWATTSSQ KKDTSNHFHVFGDLSQPITTE DIKAAFAPFGRISDARVVKDMA TGKSKGYGFVSFNFNKWDAENA IQQMGGQWLGGRQIRTNWATR KPPAPKSTYESNTKQLSYDEVV NQSSPSNCTVYCGGTSGLTEQ LMRQTFSPFGQIMIEIRVFPDKG Y SFVRFNS/HMESGRHMAIVSV NGTTIEGHVVVKCYWKGKTLID MINPVNQQQNQIGYQPQYQGQWG QI WYGNAQQQIGYQMPNGWQV PIAYGMYGQAWE/SSQGFNSDT VFLAPWDGDPNFGSCNRLQGQ NGISLLPNRPSGYRVAGYETQ
16715	47083	A	16816	1425	1564	
16716	47084	C	16817	151	339	
16717	47085	A	16818	67	373	FCDCHHFLMFKSPHIWPVGIFS SWLCCFFWACLHHSSLIALLSC TKRYSGLILYFLCSSFEITVSSKS SVSF*RRMVFRNQVQLGSRACC C*GVAAPRPF

SEQ ID NO: NO:	SEQ ID NO: of peptide sequence	Met bod	SEQ ID NO: in USNN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, ^=possible nucleotide insertion)
16718	47086	A	16819	1	799	MGPHWLWLHLALVLLPPSALL LPSCEKGVLRVRFYHEKWIVY HKESTKERHGYCTLGEAFNRL DFSSAIQDIRRFNYYVVKPLLPRY KFQLRNAITKDRQRSSGVQLP HAGQPQGADPTQDERRQVAGD TPGDPRALAGGGVVDRTYPGS YEASGRPGLQLALAIEDLLRDS AIGCTCFCDRCPVGAQRLLAHS LALAAPGAEKREVVKLLLVAY VRRRPGKNLTTQNCQPAAGYI PPGHQ*AAASHARSWKNQQPP PRVLIGSA
16719	47087	B	16820	28	438	
16720	47088	A	16821	366	793	AWVEQSJKVLIKEGGIQLLLTIV DTPGFGDAVDNSNCWQPGINIV DSKFEDYLNAESQVNRCQMPG NRVHCCLYFIAPSGHGPGLHN*R LPPSGRIG*YMFVTTWHCLLLR LKPLDIEFTKHLHEKVNIPIJAK ADTLMPEEC
16721	47089	C	16822	228	374	
16722	47090	A	16823	291	604	AWELEKSHLRRGLDPSPHNINIR VEPKF*SKYGGVQLLITIVDTP RFGDAVDNSNCWQPVINYIDIK FEDYLNAESRVNRCQMPGNRV Q**LYFIAPSGHGPGLHN
16723	47091	A	16824	148	498	
16724	47092	A	16825	1	595	DRPRITGGGKSGTEYPNLPTL KATIENKNSVLNTATIKMKDVQ TSTPAEQDLEMA^SEGEQKRLE EYENNQPQVKN^QIHSRDDLD I^QSSQTVEDGDI^SLCCNCKNV LLIDQHEMCKDCVHLLKIKNT FCLWKRLLKLDNHCEQLRVKI RKLKNKASVLQKRISKEEIKS QLKHEILELEKELCSLRFAIQQE
16725	47093	A	16826	1	828	
16726	47094	A	16827	1	540	
16727	47095	A	16828	295	460	
16728	47096	A	16829	2	1355	
16729	47097	A	16830	650	1184	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met	SEQ ID NO: in USNN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, ^=possible nucleotide insertion)
16730	47098	A	16831	725	2368	AVDIIKEIKHPQKHKKKLPAFQLR PFPLREETIPCGNGVSFPRCEPPCL AEVYMCNLNEMLKDEKKGCMN KSGAGENPQERTAQKRKFPSPP HSSNGHSPQDTSTSPKPKKKKP GLLNSNNKEQVVKQPLECIEQTQS KAMTMLTIEQLSYLLKFAIQKM KQPGVRRKLKPVPLEQHPDYA EYIFHPMMDLCTLEVKGLRQMY GCTEAFLADAKWILHNCIIYNG GEWLRTQIAKVVKICHEVCV SQVCPECYLAACQKRDNWFCE PCVSWIYDISACQPV*WKLVIQ MFLPM/WKADIL/RGEEG*YTSE LIGWL*SLSCDCSAGTSISHPSD SD*RWLTHEGRRVSWP\VNVC YLMSKEIPFSVKKTSIFNSAM QEMEVYVVENIRRKFGVFNYSF RTPYTPNSQYQMLLDPTNPSAG TAKIDKQEKVKLNFDMTASP1 LMSKPVLSSGTGRRISLSDMPR SPMSTNSVVHTGSDVEQDAEK KATSSHFSASEESMDFLDKSTG QLRAGERGGGLDTGVSHGCT I.GGPKVQSVIKQQASVLQDTMN
16731	47099	A	16832	2	164	PSTLRAEAWPP*NGSPVPLASS QASSSSRGPTSCIPRYVAPSE RRLPLTAA
16732	47100	A	16833	51	498	
16733	47101	A	16834	1	531	
16734	47102	C	16835	257	358	
16735	47103	A	16836	63	193	SGRLAPHTSRRTSANCSDDAKS SDSCSPSRKT*WSGRNTNRIH
16736	47104	A	16837	1	834	
16737	47105	A	16838	258	545	CQNPQILASPSTKDLMLGGRNT NKDTLKACLRVVKRSECSQ KPAS*MCTERNPTSMREVHDLE RKYAVLYQPLFD*AVLKLMMQ FMNLRKEGM
16738	47106	A	16839	66	476	
16739	47107	A	16840	1	1362	
16740	47108	A	16841	1	747	
16741	47109	A	16842	522	687	
16742	47110	A	16843	112	861	
16743	47111	A	16844	87	472	TVTFSQCRFGKMLPLEKAFASP QELPSAGSAHAGVSSRSSRK NPRPSLRGPLLTLEFSRLRFREF VY\PEAAGPFIHTLARLDELCREQ WLMPEARSKEQMLELLVLEQF L/SILPDKVRPWVVAQYPES
16744	47112	A	16845	1	393	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met cod	SEQ ID NO: in USN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, ^=possible nucleotide insertion)
16745	47113	A	16846	621	1099	
16746	47114	A	16847	1	453	
16747	47115	A	16848	209	1175	
16748	47116	A	16849	1	546	
16749	47117	A	16850	187	421	LGESSQ*GSP\PPPTGGCGPATG Q*PLGQSFQRKELAAIFAVSQY SLVVPGPGMGETEATGIWSRPPA NGNSPTVEWHIK
16750	47118	A	16851	3	1654	
16751	47119	A	16852	166	465	
16752	47120	A	16853	1	558	
16753	47121	A	16854	51	380	RNNNNLLTHHFVLIQFLIPRKET KYYLVITPYSLISIVLSNFFYYS PESLNNDNTCYHHEEADTPWR*F LAIFEGLFNIAHQMQNMPFLL WKQVPETLVQQQLPRIN
16754	47122	A	16855	3	550	
16755	47123	A	16856	1	462	
16756	47124	B	16857	1	2811	
16757	47125	A	16858	3	514	ASGTAPEIQRAPTRPRRKRRK LLPL/TKAEAKAKALKAKAVL KGVIHSKKKKKIRTSPTRRPKT LRLRQPKYPRKSAPRRNKLDH YAIIKPLTTESAMKKIEDNNTL VFIVDVVKANKHQIKQAVKKLY DIDVAKVNTLIRPDGEKKAYVR LAPDYDALDVANKIGII
16758	47126	A	16859	73	396	FFQFSPPKNCVWWNCVAEVLL KYKTGETNDFELLKNQLLDPDI KRLPWLNRSQTVVEEYLAFLG NLVSAQTVFLRPCLSMIAHFV PPRVIIKEGDVDVSDSSDDEDD
16759	47127	A	16860	132	357	YVSKFAGRLSSSSSESETSTSPS LMITRGGTWKGSNHAETRSEE NSLC*YKITKKSQILFHYCDFY STKAISI
16760	47128	A	16861	380	597	
16761	47129	A	16862	179	280	QRDIKSCVQILQWEGSTRPFTN E**YMANVRNS
16762	47130	A	16863	2	175	
16763	47131	A	16864	178	374	
16764	47132	A	16865	386	2120	
16765	47133	A	16866	887	1104	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion,  =possible nucleotide insertion)
16766	47134	A	16867	1	708	MEVAALEHLDHRLREKVKQQN ALRHQVVLRQRRLEELQLQHS LRLLEMAEAQNQRHTEVAKTMR NLENLEKAQMKAQAEAHITS VYLQLKAYLMDESLNLENRLD SMEAEVVVRTKHELEALHVVNQ EALNARDIAKKNQYLEETLVR ERKKRERYISECKKRAEKKLE NE/LHGAQADPGSDLNPRADPP RAPAATVRRHHPGQPACQGGG AAAALEHVVPDGGDLWQGQR HWH
16767	47135	A	16868	1	1327	
16768	47136	A	16869	1	1776	
16769	47137	A	16870	1	397	
16770	47138	A	16871	1	1974	
16771	47139	A	16872	1	336	
16772	47140	A	16873	3	661	GRGGHNFAPNLTARSAVTSGL GGPPAAVMVGSLNCIVAVSQN MGIGKNGDLPWPPLRNEFRYF QRMTTTSVEGKQNLVIMG\KK TW\FSIPE/RRNRPFKG*EFNLVL SRELQGNLPQGAHFLRSRLDDA LKLTEQPELANKVGMVWIVG GSSN\YKESMNHSSSLKLFVTRII QDFESDTFFPEIDLEKYKFLPEY PGVFFDVQEEKGIKYKFEVHEK
16773	47141	A	16874	38	755	ALKTCVNPDAKDNIAGSSGH LRTLSPVVSRSCLKEEERRRR RMKRRQRSSRRRSRRRMRRR RRSR\RRRMKRRKRRRMRK RSSFILM\FFMLLLSGIPLL\YME VIMGQWLHVDNIRVWKQLVP WLCSMSY/SSQSVCASVSLYNS TIISWNF\YFAHPLPWHDCHPLV KNISVTDWAHQYFLYHTTLHA SDHSEEAAEALVNRSLGCLLG RDHRDLDKFPEIRRAHTGGAR
16774	47142	A	16875	1	1830	
16775	47143	A	16876	2	1142	
16776	47144	A	16877	1	435	
16777	47145	A	16878	1	963	
16778	47146	B	16879	247	1092	
16779	47147	A	16880	1	1653	
16780	47148	A	16881	1	2268	
16781	47149	A	16882	301	555	
16782	47150	A	16883	1	630	
16783	47151	A	16884	731	834	
16784	47152	A	16885	1	2277	
16785	47153	A	16886	45	2446	
16786	47154	B	16887	625	696	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met/Asp	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion,  =possible nucleotide insertion)
16787	47155	A	16888	193	315	WPGGGYSLLCFWCPLSFGAA G/W*PPPGHH*PYSPKQEHYRT NSDTLIFLSSRTLVLQGS*GIKV AGSEGPKYNE*PRNPVPLSCL HLFGC
16788	47156	A	16889	1	588	
16789	47157	A	16890	2	229	
16790	47158	A	16891	1	502	
16791	47159	A	16892	516	576	
16792	47160	A	16893	144	435	
16793	47161	C	16894	1	996	
16794	47162	A	16895	424	632	
16795	47163	B	16896	446	1944	
16796	47164	C	16897	207	470	
16797	47165	A	16898	1	396	
16798	47166	A	16902	1	585	
16799	47167	A	16903	141	906	
16800	47168	B	16904	99	276	
16801	47169	A	16905	1	756	
16802	47170	A	16906	1	383	
16803	47171	A	16907	1	582	
16804	47172	A	16908	3	615	PECIIGIDILSSGQNPHIGSLTR VRAIMVGKAKRKPLEPLPLPKI LNQKQYRIAGGIEEISATIKDLK DAGVVIPITSLFDSPWVWPVQKT DGSWRMTVDYRQINQVATPIA AAIPDVASLLKQINTSPDTW/PI RPPISNGD*GVSGR*ACCLEPLA GPHR*ITSEASRILEQGPAIFCR* LLSF*ETALLLLLFGGGN*TFDY
16805	47173	A	16909	3	415	PVK/VGA*GGQVINGVLAQV* TVGPVGPRTHPVVIFPVPECRIG RDILSSWQNPHHTGSLTGRVRAF MVKGAKWKP*ELPLPRKTVNQ KQYRIPGGIAEIS/A/TIKNLRRG VVIPTTSRFNSPIWPVQKTDGS W*TAADY
16806	47174	A	16910	232	633	
16807	47175	A	16911	1	1677	
16808	47176	A	16912	328	381	LLKLQH*MQSPYLVGPSEQ
16809	47177	A	16913	3	811	
16810	47178	A	16914	1	1125	
16811	47179	A	16915	1	1191	
16812	47180	A	16916	113	485	
16813	47181	A	16917	1	357	
16814	47182	A	16918	12	398	
16815	47183	A	16919	498	595	TEMASTTTCT/RFHDEYQLFEEL *KGAFSVNGT
16816	47184	A	16920	5	367	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met/hed	SEQ ID NO: in USNN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, -=possible nucleotide deletion, +=possible nucleotide insertion)
16817	47185	A	16921	190	2005	VLYPLHLGTTGKGGAGGASSG EEGSEARRRRRIGGLWGRPHATL SGHLPSPAPAHPTPSRASYFR TRKVRAALGDSAAGPVPGLAA RLLASGSPRSQPGHSPGPEMAS TTTCTRFTDEYQLFEELGRGAF SVVRRCMKIPTQGYAAKIJNT KKLSARDHQKLEREARICRLLK HPNIVRLHDSIISEGFHVLVFDL VTGGEFLFEDIVAREYYSEADAS HClQQILESVNHNCHLNGIVHLD LKPENLLLASKSKGAAVKLADFG GLAIEVQGDQQAWFGFAGTPG YLSPEVLRKDPYGKPVDMWAC GVILYILLVGYPFFWDEDQHRL YQQIKAGAYDFPSPEWDTVTPE AKDLINKMLTINPAKRITASEAL KHPWICQRSTVASMMHRQETV DCLKKFNARRKLKGAIITML ATRNFSAAKSLLKKPDGVKEST ESSNTTIEDEDVARKKQEEIKVT EQLIEAINNGDFEAYTKICDGPL TAFEPPEALGNLVEGMDIIRFYF ENALSKSNKPNIHTJJLNPHVHLV GDDAACIAYIRLTQYMDGSGM PKTMQSEETRVWHRDGKQW NVHFHRSGSPTVPIKPCIPNGK ENFSGGTSLWQNI
16818	47186	A	16922	1	288	
16819	47187	A	16923	318	458	
16820	47188	A	16924	1	578	
16821	47189	A	16925	803	1068	
16822	47190	A	16926	1	660	
16823	47191	A	16927	2	325	TSSENNNGPKR*IHSTESLYLLQ GSVVAHDHYIGLPEIPIGAYQA NILVEDATIGIVDNELLTSSKDR ELLEYRNTKISPLIIDDHSSLEKQ TFSLLDSSNQVLEYLS
16824	47192	A	16928	156	573	
16825	47193	A	16929	405	599	GLEPPQKPGLVTSILQANPVLP CGNSQSR*TSTRCWYEHLCQTQ SHLQMQQYHEAYQSACALA
16826	47194	B	16930	1	1676	
16827	47195	A	16931	1	1125	
16828	47196	A	16932	27	818	
16829	47197	A	16933	1	4986	
16830	47198	A	16934	1	4401	
16831	47199	A	16935	153	370	SVLETCMSTAFPVSCHSFKTA VLRISLS*ISAQGGPIDLFSQCHP SSSTGVSSINHRGSWDTPGQSL VVICL

SEQ ID NO: NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion,  =possible nucleotide insertion)
16832	47200	B	16936	47	501	
16833	47201	A	16937	49	1714	
16834	47202	A	16938	1	999	
16835	47203	A	16939	140	2029	FAARAGPGGSRRARRGNKWAR MPYEIKKVFASLPQVERGVSKII GGDPKGNNFLYTNGKCVILRNI DNPALADIYTHEAHQVVVAKY APSGFYIASGDVSGKLRIWDTT QKEHLLKYEYQPFAGKIKDIAW TEDSKRIA VVGEGREKFGAVFL WDSGSSVGEITGHNKVINSVDI KQSRPYRLATGSDDNCNAFFEG PPFKFKFTIGDHSRFVNCVRFSP DGNRFATASADGQIYIYDGKTG EKVCALGGSKAHDGGIYAIWS PDSTHILLASGDKTSKIDVDSV NSVVSTFPMGSTVLDQQLGCL WQKDHLSSVSLSGYINVYLDRN NPSKPLHVIKGHSKSIQCLTVH KNGGKSYIYSGSHDGHINYWD SETGENDSFAGKGHTNQVSRM TVDESGQLISCSMDDTVRYTSL MLRDYSGQGVVKLDVQPKC\  VAVGPGGYAVVVCIGQIVLLK DQRKCFSDNPGYEPEVVAH PGG\DTVAIGGVGDGNVALYSIL GTTL\KDEGKLLAEKGPVTDVA YSHUDGAFLAVCDASKVVTVFS VADGYSENNVFYGHIAKIVCL AWSPDNEHFASGGMDMMVVY WTLSDPETRVKIQDAHRLHHVS SLAWLDEHTLVTTSHDASVE
16836	47204	A	16940	31	449	
16837	47205	A	16941	1	53	
16838	47206	A	16942	1	389	GMPTSTIASCSQDGRVFIWTC DASSNTWSPKLLHKFDNDVWH VWSWSITANILAVSGGDNKVTEG QQNEQ*QDRWGLAPHPPAPGL PLPGPTNTTGKSPQLQQDYFP RRSYRCSSHRLIICLNVIGNAL
16839	47207	A	16943	1	438	
16840	47208	B	16944	1	1267	
16841	47209	A	16945	635	808	

SEQ ID NO: NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, ~ =possible nucleotide insertion)
16842	47210	A	16946	37	1319	QGEGHGRGLHGFLGRPESQIPS WSRSAPLIRLEIWGALAPSLAD HSEGSPE*SVINTVDTSHHEYMI Y\DAQMDYYGHPPGQPASSDRS VKIF*CAQWEGRSLFADLQGS WRGPVWQVGWGFTPLLRATS WAFVASLLTGKFYISWERGKT GTLGRRATSNAGTRLKLNFGC CWAPIGLTVLHSWACWVVS RGPSLLDFTPGEGQWEVKIN NAHTIGCNAVITWAPACCTWK PHRRPHRGOKPNYIKRFASSGC NDNLINKLWKEEEDGQWKEEQK LEGHSDWVRDVAWAPSIGPA HQHHRPAAPRMGRVSIWTCD ASSNTWSP*IVDKFNDVVWHV SWSITANILAVL\CGDNK\VPL WKESS*WAKWVVPSSDVKORG PGLPYQPSSDQEGLPARNEQVNK DQGGALAPPPAQLPGPAPSPGP
16843	47211	A	16947	1	1021	MSGEFIDHSIARIJYPGIFGTDA GSCIDQRGITGKLQQPPEDRRL GEGKLNTKDIHTKTPSVRH QRPKVDKTTKIGKKQSRKTGNS KNQSAPPKECSSSPAMEQSW TENDFDELREEGFRRSNYSELK EEFRTHGKEVKNLEKRLDEWL TRITNAEKLKDLMELKTKARG LQRVSVMEDEMNEMKQEEKFR EKRIKRNKQSLQEWIDVYVKRPN LRLIGVPESDGENTKLENTLQ DIIQESFPNLARQANIQIQEIQR MPQRDSLRRATPRHIIVRFKTV EMKEKMLRAAREKA/HALIPK LTT*LEVKLSSANVKEQKL*QT VFQTTVQSN
16844	47212	A	16948	1	393	
16845	47213	A	16949	1	2631	
16846	47214	A	16950	1	1155	
16847	47215	A	16951	1	1185	
16848	47216	A	16952	1	942	
16849	47217	A	16953	1	615	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
16850	47218	A	16954	474	2678	IKPQRWGKKQSRKGTGNSKNQS ASPPPKERSSPAMEQSWTEND FDELREDSFRRLVITVNSYELKKE VRTNGKEVKNLEKKLDEWLTR ITNAEKLKDLMEKLTMAQELP DQCTSLSRCDQLEERVSVMED EMNEMKCEEKFREKIRKRNEQ SLOEWHYVVKRPNLRUJGVPE DGENGTKLNTLQDIQENFPN LARQANIQIQEIQRMPQRYSSR RATPRHIVRFTKVEMEKMLR VAREKGQVTHKGKPIVRLTADL LAETLQARREWGVPIFNILKEKN FQPRISYPAKLSFIDKSTRQKV KDTQELNSALHQADLIDYRTL HPKSTEYTFSAHPTYSKIDHI VGSKALLSKCKRTEIITNCLSDH SAIKLELRKKLTRNHSTTWKL NNLLNDYVWHNEMKAIEKM FFETENKDKTYQNLWDTFKT VCRGKFIANAHKRQKERSKID TLSQLKGLEKQEQTTHSKASRR QEITKIRAEELKERVGRWRIGEA ADLVGVSSQAIRDAAEKAAGRPH PDMEIRGRVEQRVGYTIEQINH MRDVFVGTLLRRAEDVFPVIGV AAHKGGVYKTSVSVHQAQDLA LKGLRVLLVEGNDPQGTASMY HGWPVDPLH HAEDTLLPFYLG KDDVTTYAKPTCWPLDIIPSCL ALHRIETLMGFDEGKLPDP HMLRLAIETVADHDYDVIVDS
16851	47219	A	16955	1	675	
16852	47220	A	16956	1	1032	
16853	47221	A	16957	3	978	HEAKHQMADDAGGSSGGPKA LVPGPGIG\NPVAFRRGPGIVIR GPGSRPGGRGRGR\GRGARGSK \AEDKDWM\MPVTKLG\RALVKD H*RSKFPWKEIYLFLSPH*RNQR IIDF\FLGGILLSKDEGF*LCPVQ EQDPCPASRTQASRPFVAIGGL QMAHVGLG\*VLPRKVATGHP VGAIILAKLS\IPVPRR\GYLGNK VLAKP\HTVP\CKV\ITGRGCGSVL VRL\PA\PRGLGMVSAPVA\KKL LMMAGI\DDCYTSARG\CTATL GQIWP\PRATL*LPFLRTYKLP*PP DLWKGR\LYLPS\PIKEFT\DHLV KDHP\ESSVQDSELQLVATT
16854	47222	B	16958	124	274	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met/hod	SEQ ID NO: in USNN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion,  =possible nucleotide insertion)
16855	47223	A	16959	202	2264	KWPKNPQQQRMAAIGTDKE LSDLLDFSAMFSPPVNNSGKTRP TTLGSSQFSGSGIDER/GTTSW GTSGQPSPSYDSSRGFTDSPHY SDHLNDSRLGAHEGLSPTPFMN SNLMGKTSERGSFSLYSRDTGL PGCOSSLLRQDGLGSGPAQLSS SGKPGTAYYSFSATSSRRPLH DSAALDPLQAKKVRKVVPGLPS SVYAPSPNSDDFNRESPSPSPK PPTSMFASTFFMQDGTHNNSSDL WSSSNNGMSQPGFGGILGTSTSH MSQSSSYGNLHSHDRLSYPPHS VSPTDINTSLPPMSSFHRGSTSS SPYVAASHTPPINGSDSILGTRG NAAGSSQTGDALGKALASIYSP DHTSSSFPSPNTPVGPSPSLTG TSQWPRPGGQAPSSPSPYENSLH SLQSRMEDRLLDRLLDAIHVLRN HAVGPSTSLPAGHSDIHSSLGPS HNAPIGSLNSNYGGSSLVASSR SASMVGTHREDSVSLNGNHSV LSSTVTTSTDLNHKTQENYRG GLQSQSGTVVITEIKTENKEKD ENLHEPPSSDDMKSDDESSQKD IKVSSRGRTSSTNEDEDLNPEQ KIEREKERRMANNERERLVRV DINEAFKELGRMCQLHLKSEKP QTKLILHQAVAVILSLEQQVR ERNLNPKAACLKRREEEKVSA VSAEPTTLPGTHPGLSETTNP
16856	47224	A	16960	1190	1327	
16857	47225	A	16961	386	554	ATISFRYSQCK*AEQGCDSELG LFTKIRKSGYWGV*ATISFRYSQ CKALEIHLTAPVVPSPALRIWGF QIPGFNQLSFHPSPESKGSFLPC
16858	47226	B	16962	499	915	
16859	47227	A	16963	1	1785	
16860	47228	A	16964	1	3036	
16861	47229	A	16965	2	710	
16862	47230	A	16966	349	493	SS*VRWVSGR*HPQ*STLSAPLG ETSGCHQGLHDLK1VVL
16863	47231	A	16967	1	1335	
16864	47232	A	16968	83	426	
16865	47233	A	16969	93	345	APALCLQILLDCKSVRNRTSRF RPREGVIQYKKGGGAAGKGG TGNAPGFLLF SKDS*KDPTPLPP PLLL*GQRDH*IQLHQE
16866	47234	A	16970	1	1302	
16867	47235	A	16971	1	1174	
16868	47236	A	16972	274	1428	

SEQ ID NO: NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
16869	47237	A	16973	411	629	HCLSHFQNTGPRGDVDFQQEL\ FPVLMADIRKEERSHLCRSSRR TWTLILDKS*IQGSRLSSKEQGW GWGTSRK
16870	47238	A	16974	618	1552	
16871	47239	A	16975	1	558	
16872	47240	A	16976	1	765	
16873	47241	A	16977	2	418	
16874	47242	A	16978	130	1965	
16875	47243	A	16979	1	1062	
16876	47244	A	16980	1	558	
16877	47245	A	16981	37	676	
16878	47246	A	16982	1	1014	
16879	47247	A	16983	1	2964	
16880	47248	B	16984	259	1751	
16881	47249	A	16985	1	987	
16882	47250	A	16986	1	1047	
16883	47251	A	16987	3	1413	GLHAARGPWVVQAWISITM\ER KEVCYGQLGCFSDEKPWAGTL QRPVKLLPWSPEDIDTRFLYT NENPNNFQLITGTEPDTEASNF QLDRKTRFIIHGFLDKAEDSWP SDMCKKMFEVEKVNClCVDWR HGSRAMYTQAVQNIRVVGAET AFLIQALSVKPCLGPVLVWVGVR EGQQDAARGTALE.DEVHVIAHS LGAHT/AEAGRSWGRPRGRITD DLGTA*YKVDGMG*ERRGVRF SI*P*GGGV*AGFGERR*RKN VGKSTAGWRM\GLDPAGPCFQ DEPEEVRLDPSDAVFVDVHHTD SSPIVPSLGFQGMSQKVGHLDFFP NGGKEMPGCKKVNVLSTTIDG IWEIGGGFVSCNHLRSFEYYSSS VLNPDGFGLGYPASYDEFQESK CFPCPAEGCPKMGHYADQFKG KTSAVEEQTFFLNTGESGNFTSW RYKVSVTSLSGKEKVNGYIRIAL YGSNENSKQYEIFK
16884	47252	B	16988	95	315	
16885	47253	C	16989	1	780	

SEQ ID NO: NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USNN 09/540.217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, !=possible nucleotide insertion)
16886	47254	A	16990	2	1426	SGTLDRMLIFWTTLFLGAAK GKEVCYEDLGCFSDTEPWGGT AIRPLKLWPSPEKIGTRFLLYT NENPNNFQILLSDPSTIEASNF QMDRKTRFIIHGFIDKGDES WV TDMCKKLFEVVEEVNCIFVWDW K KGSQATYTTQANNVRVVGQA VAQMLDILLTEYSYPPSKVHLI GHSLGAHVAEGASKTPGLSK/ RLQGLDPVEASFESTPEEVRLUD PSDADFVVDIHTDAAPLIPFLGF GTNQQMGHLDFFPNNGESMPG CKKNALSQIVLDLGWAGTRDF VACNHLRSYKYYLESILNPDGF AAAYPCTS YKSFESDKCFCPCPDQ GCPQMGHYADKFAGRSTSEQQQ KFFLNTGEASNFARWRYGVSI LSGRATATGQIKVALFGNKGNT QYSIFRGILKPGSTHSEYEDAKL DVGTIKVKFLWNNNVNP TLP KVGATKITVQKGEEKTVYNFC EDTVREDTLLTLP C
16887	47255	A	16991	1	1407	
16888	47256	A	16992	954	1663	EPSPDPAHAPS VALLHTGNQSK VLPWPRNPCM KRW* K*KMLKI SWVHEWVTSN WISTA VRSLRV FAPKNV FQ** ALGP SGWLVYC
16889	47257	A	16993	3	242	
16890	47258	A	16994	1	1815	
16891	47259	A	16995	1	375	
16892	47260	A	16996	3	2005	
16893	47261	A	16997	1	651	
16894	47262	A	16998	114	275	
16895	47263	A	16999	1	270	
16896	47264	A	17000	140	876	PPALVVGRRQKSWRMF EQMRA NVGKLLKGIDR VNPENLATLE R\YVETQAKENAYDLEPNLAVP ESCTKFNPAFFQTNGSTAQDSC *KALTNLPH TDFTL\CKC\ MIRP GHIQ EVERIPTD F CYLGGPGWE TWPFSRAFWESPGMKTVDLLW KV*LG FEDSVRK FICHVVGUT YQHIDR\WLLAEMLGDLFGQAS *RCWMSKYGWSADESGQI FIC SPRREH LTPRNIV EKIDFDSVSS MASSQ

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met/ codon	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, ^=possible nucleotide insertion)
16897	47265	A	17001	1	777	MSGENVTKVSTFILVGLPTAPGLQYLLFLFLTYLFVLFVENLAIILIVVWSSTSLLHRPMYYFLSSMSFLEIWYVSDITPKMLEGFLLQQKRISFVGCMQTQLYFFSSLVCTECVLLASMGYDRYVAICHPLRY\N LACTDFSTAELV/SFILAFLVVFPLLATLISYWHITLAVLIRIPSATG CWRASFSTCASHLTWVTVFYTA LLFMYVRPQAIDSQSSNKLISA VYT VTPPIUNPLIYCLRNKEFKD ALKKALGLGQTSH
16898	47266	A	17002	2	876	
16899	47267	A	17003	1	894	
16900	47268	A	17004	377	501	
16901	47269	A	17005	3	823	
16902	47270	A	17006	1	874	
16903	47271	C	17007	156	287	
16904	47272	A	17008	1	1140	
16905	47273	A	17009	1299	3135	ISGSVCILLWLQLLPAYNLIIHTWEHRHSPPGT/RMSRLAKRNAWEADR/YAEAKLAARRQGPSSLMSSREGGWGEGSQSRNSSHGALKEAQFIIITNAEKS LKDLME LKTMAQELRDECTSLSRQFDQLEEKVSVMEDEINEMKQEEKVREKRIKRNEQSLQEIWWDYVVKRPNLHLIGVPESDRENGTKLENTLQDIIQENFPN LARQANQI OQEIQRM PQRYSRRATPRHIIIVRFTK VEMKEKMRRAKEREKIQTTIREYYKHL YTNKLENLEEMDKFLDTYSLPRLNQEEVESLKRPTGSEIGAIINSLPTKKSPGPDGFTAEFYQRYKKELVPFLKLKFQSTEKERILPN SFYEASILIPKPGRDTTKENFRPISLMNINAKILNKILANQIQQHQI EKLIIHHDQVGFIPGMQGWFNIRKSINVQHINRTNEKNHMIISIDA EKA FDKIQQPFFMLKTLNKLGIID GTYLKIVRAIYDKLTANII LNGQKLEAFPLKTGTTRQGCPLSPLLFNIVLEVLRALARQEKIKGQLGKEQVKLSSLFADDMIVYQVLENPIVSAQNLKLISNFSKVSGYKINVQKSQAFLYTNNRQTESQIMSELPTIASKRIK
16906	47274	C	17010	189	457	
16907	47275	A	17011	2	2600	
16908	47276	A	17012	107	1493	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met/hd	SEQ ID NO: in USNN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion,  =possible nucleotide insertion)
16909	47277	A	17013	3	2209	IHTKTPSVCHHHQRPVKVDKTTK MGKKQSRNTQNSKNQSTSPPP KECSA PAMEQSWMENDFDEL REEGFRRSNFSELTEEVTHR K EAKNLEKKIRQMVTRITNV EK SLNDL MELKNMARELRDKCTS FSSRFDQLEERVSIEQDMNEM KQEEKFREKRVKURNEQSLOEIR DYVKRPNLRLIGIPESDEENGT KLENLTQDIIQENFPNLARQAN IQIKEIQRMPQRYSSRATPRQIIV IVRTEVEMREK\MLRAAREKG RVTHKGKTIIRLTVDLSAETIQA RRESTRQVKVNKDQELNSAQHQ ADLTDNYRTLHPKSTETYTLFSA PHHTYSKIDHIVGSKALLSKCK RTEIITNCLSDHSAIKLELRIKKL TQNLSTTWKLNNNLLNDYWWH NEMKAEIKMLFETNENKDTTY QNLWDFTKAVCRGKYIALNAH KRKQERSKIDTQLTSQLKELEKQ EQSHSKASRRQEIITKIRAELEI ETQKTLQKINESRDWFFEKINKI DRQLARL I KKKREKNQIDTIKN VLEFLAKAIRQDKEIKGIGLGE EVKLFLFAEDMIVYLENPIVSA QNLLKLISNFSKVSGYKINVQK SQAFLYTNNRQTESQIMSELPFT IASKRKYLGIQLTRDMKDLFK ENYKPLLNIKEDETKKKWKNIPC SWVGRINIMKMAILPKVYRFN AIPIKLPMTFFTELEKTTLKFTW
16910	47278	A	17014	292	699	
16911	47279	A	17015	269	803	ALGPCSEALPTWVNENGEE MAQEIDL SALKELE R E A I L Q V L Y R D Q A V Q N T E E E R T R A A G N * K H T C SISGGKGPKNTDWEHEKCCA RCQQV LGFLLH RGA VCRGCSH R V C A Q C R V F L R G T H A W K C T V C FEDRNVKIKTG EWFYEE RAKKF PTGDN S V A R T S C T G K H E T V G G Q LLQSYQK
16912	47280	A	17016	1	1173	
16913	47281	A	17017	349	718	AGPEGTTTAECPI/CQQQRPILS LRYGTISWG/DQSATWWQVVDY IRTLLSWK WQSAKTTTGHLT KCLIHHDIPHSIASD*GTCFMAK EVWQWYCFSHSQDSRVQESRG GIGSCTTHHPCSFN

SEQ ID NO: NO:	SEQ ID NO: of peptide sequence	Met hed	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
16914	47282	A	17018	196	577	GSSGQSESAQPQGLWVLPSTS LAILSTDVNV*QPCFPAGAHQG QPLAWPVPFLAWLSSWQQKRC* KQQRSSRNLDHHRNGPWLHEE GDKTPFFHHPPQLQGSLSQS LLPAGRR*ARGPQQLPSPP
16915	47283	A	17019	1	2523	
16916	47284	A	17020	236	558	
16917	47285	A	17021	1610	2004	VTWSAQQMPWAIKNCPTHSPL GQGCLPQPQKM*VVQNDFQ*G* WTHCRKGIGKGGQRVGVWPWQ TQNRKGKGTFLTPLHSAVADAM LYAL*RGSDLDAAQTLPTAAQ DALYAVVPGEPTGQLQVRHN EFALGQ
16918	47286	A	17022	1	735	
16919	47287	A	17023	88	1871	
16920	47288	A	17024	1	1299	
16921	47289	A	17025	2	260	
16922	47290	A	17026	144	1737	
16923	47291	A	17027	1	1182	
16924	47292	A	17028	262	1132	
16925	47293	A	17029	1	484	
16926	47294	A	17030	3	382	LKGAPDLELDGESRRTWRERK GRKRKERALGRWQV*RSRCA* P/STPAALNAPLQGASHSPFLR NCWKGRSVRASSLLRQLAKGG CAARRLSWNLQCIVQMYEGHS QQPGLQPRLQRWSSQTLRTA
16927	47295	A	17031	1	2022	
16928	47296	A	17032	209	403	
16929	47297	A	17033	213	1993	
16930	47298	A	17034	1	378	
16931	47299	A	17035	64	1180	SASHSGAPATSLYERGVCPPL RRPPAVLVCRRAASCTLLAMS DLQEEGKNAINSPMSPALVDVH PEDTQLEENEERTTMIDPTSKEDP KFKELGKVLLDWINVLAERI IVKQLEEDLYDGQVLQKLF/EK NLAGLQLSINVAEVTQSEIGOKQ KLQKVLEQLHDLLRPRSWALR WLGNSIHGKNLVGNPQLLVS AMHFRAPIRLPEHVTQVVVV RKREGLLHSSHISEELTTTEM MMGRFERDAFDTLFDHAPDKL SVVKSLITFVNKHJLNKLNLEV TELETQFADGVYLVLLMGLLE DYFVPLHHFYLTPESFQDKVHN VSFAFELMLGRRPSRNPRLVK TWLTWDLKSPLRVLYNLFTKY
16932	47300	A	17036	3	764	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met cod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, !=possible nucleotide deletion, !=possible nucleotide insertion)
16933	47301	A	17037	I	1230	
16934	47302	A	17038	I	313	
16935	47303	A	17039	145	263	IFLLYLLKNKVQNK*EIKQHFLG KIMSRDNNTYLTWGTE
16936	47304	A	17040	5	982	PTFSRAVATMFSRAGVAGLSA WTLQPQWIQVRNMMATLKDITR RLKSIKNIQKITKSMKVMVAAK YARAERELKPARIYGLGSLALY EKADIKGPEDKKHLLIGVSSD RGLCGAIHSSIAKQMKSEVATL TAAGKEVMLVGIGDKIRGILYR THSDQFLVAFKEVGRKPTFGD ASVIALELLNSGYEFDEGSIIFN KFRSVISYRTEEKPUFSLNTVVAS ADQHGVSMTDIDADVAAKITQ EY/NWANIILLTLWKESTTSGG RSARG*QFWDNGQARIAFWRM DLDNLDIWTFNR/TRQAVITKE LIEIISGAASSVKKENSAS
16937	47305	A	17041	I334	1790	
16938	47306	A	17042	I	930	
16939	47307	A	17043	2	477	SGLGRLPGPWQEAGSSRGPSG DMAGVKALVALSFSGAIGLT/ LHMLGCALEDYGVYWPFLVLI FHAISIIPHFIAKRVTYDSDATS SACRELAYFFTTGIVVSCI.WISP VILARVALIKWGACGLVLAIG NAVIFFPYNNSRGFLSYLGRGDDF SWEQW
16940	47308	A	17044	130	434	
16941	47309	A	17045	I	1365	
16942	47310	A	17046	656	839	
16943	47311	B	17047	16	149	

SEQ ID NO: NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion,  =possible nucleotide insertion)
16944	47312	A	17048	1	1317	MTLNEHAAFKHLFNKAHLAPP LIHLTLSGHSTCFREHRVGVICS HFAQDLWPEQGREDSFQKVILR RYEKCGHENLQLKIGCTNVDES LTYKRIHTGEKPCKCEECDKAF SKFSILTGHKVIHTGEKHYKCE ECGKAFTRSSSLIEHKRSHAGE KPYKCEECGKAFSKASTLTAHK TIHAGEKPYKCEECGKAFNRSS NLMEHKRIHTGEKPCKCEECG KAFGNFSTLTGHKVIHTGEKPY KCEECGKAFSWPSSLTEHKRIH AGDKPYKCEECGKTFKWSSTL TKHKGHTGEKPYKCEECGKAF TTFSSLTKHKGHTGEKHYKCE ECGKVFSWSSLTTHKAIHAGE KLYKCEECGKAFKWSRLSEH KRIHTGEKPYKCEECGKAFSW VSVLNKHKKIHAAGKKFYKCEE CGKDFNQSSHLTHKRIHTGE KPYKCEECGKAFSKASTLTAHK TIHAGEKPYKCEECGKAFNRSS NLMEHKRIHTGEKPCKCEECG KAFGNFSTLTGHKVIHTGEKPY KCEECGKAFSWPSSLTEHKRIH AGDKPYKCEECGKTFKWSSTL TKHKGHTGEKPYKCEECGKAF TTFSSLTKHKGHTGEKHYKCE ECGKVFSWSSLTTHKAIHAGE KLYKCEECGKAFKWSRLSEH KRIHTGEKPYKCEECGKAFSW VSVLNKHKKIHAAGKKFYKCEE
16945	47313	A	17049	2	2183	

SEQ ID NO: NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USNN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, ==possible nucleotide insertion)
16946	47314	A	17050	3	1440	IKVLLGENRVPNTMAVWLAQ WLKGKASLTSFPPCPMASLRR LGEHIQQFQESSAQGLGLSLGP GAAALPKVGWLEQLLDPFNVS DRRSHLHQRYWVNDQHWVGQ DGPFLHLHLTSPPTHTLFTGH PAALAPAWGALVISLEHRYFVG SIPAGGRALSLRFLNISSSPWC FGGSYAGSLPSHHAPTFPRAQR IS*HFRPSSAVRPQVVSRLSMS TAIGGSLE/CRRWGLVRGGLGG KRGKGCGQRGCPA*VLADIASC FPQCRAAVSVFAAEVERRLRS GAAQAALRTELASCAGPLGRAE NQAELLGALQALVGGVVVQYD GQTGAPLSVRQLCGLLGGGG NRRGGIYVLCMYIV*IVLHSLG QKCLSFRAETVAQLRSTEPEQL SGVGEAPIYLAPSYPFFPGDTP WHVLSVTQALGSSESTLJRTG SHCLDMAPERPSDPSLRLGRQ NIFQQLQTWLKLAKESQIKGE
16947	47315	B	17051	41	2709	
16948	47316	A	17052	874	1024	
16949	47317	A	17053	1	1602	MDSLWGPAGSHPFVGHNRSL SPDLCPGKIVLRLAKESGAGMP EQDKDPRVQENPGDQRRVPEV TGDAPSFRPRLRDNGGLSPFPV GPGLQTLHQAQRSEIRYDQSS QTSWTSSCTNRNAISSSSYSTGG LPGLKRRRGPASSHQCQLTSSS KTVSEDRPQAVSSGHTQCEKV AEKAPGQTALRNDSRSEASR PSTRKFLLPHRRGEPLMLPPPV ELGYRVTAEDLDWEKEAAFQC IKSALQVEDKAISDCRPSRSPSHT LSSLATGAS/DSAQVTSLIPAPFP AASMDAGMRRTRPGTSAPAAA AAAPPSTLNRTLGSLEWMEA LHISGPQPOQLQQVPRGQNQRSQ TSRTSSCPK/LKCHLELLQLYGR PPGTKAEEAAPASSHCQLTSSS TVSEDGPEAVSSGHTQCEKTAD TAPGQTLGPRGGSPRSQSSPR RHKFPLLPRRRGEPLMLPPPLEL GYWVTAEDLDREKEAAFQRIN SALQVEDKAISDCRPSRSPSHTLS SLATGASGLPAISKAPSMDAQ ERHKS
16950	47318	A	17054	1	1155	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met/hd	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, ^=possible nucleotide insertion)
16951	47319	A	17055	1	1237	MDSLWGPGAGSHPFGVHNTRL SPDLCPGKIVLRAKESGAGMP EQDKDPRVQENPGDQRRVPEV TGDAPSFRPLRDNRGLSPFVP GPGPLQTDLHAQRSEIRYNQTS QISWTSSCTRNRAISSYSSMMG LPGLKRRRGPASSHQCQLTSSS KTVSEDRPQAVVSSGHTQCEKA ADIAPGQTLALRNDSSTSEASRP STHKFPLPRRRGEPLML/PPSL EVGVPGSLVKELDREKEAAFIQ RINSALQVEDKAISDCRPSWPS HTLSSLATGTSGLPAISKAAPSMD AQQETHKQSQDCLGLLAPLASA AGVPSTAPMSGKKHRPPGFLFS SSDPLPATSSHSQDSAQVTSLIP APFPAASMDVGMRRTRGEPL MLPPPLELGYRVTAEIDLQKEKE AAFQRKISALQVEDKAIA
16952	47320	A	17056	132	835	
16953	47321	A	17057	1	2947	MPEQDKDPRVQENPDDQRRVP KVTGDARSARPLRNDNGVLSF VPRPGPLQTYLHAQRSEIRYNQ TSQNTWTSSCTRNQNAISSYSS VGGLLGLKWRRGPAQGQESGAG MPEQDKIDPRVQQNPPDDHRTV PEVTGDARSASFWPLRDNGGLSP FVPRPGPLQTDLHAQSSEIRYN QTQSQTWTSSSTKRNAISSYSS TGGLPGLKQRRGPASSRCQTL SYSKTVSEDRPQAVVSSGHTRCE KAADTAPGQTLAPR
16954	47322	C	17058	229	624	
16955	47323	A	17059	1	1011	MVSTPATLPSLPKPALMASWG VPYDQLTKEEKTRVWFTDGSAR RYAGTTQKWTAVALQPLSRTS LKDSEGGKSSQWAEIQLAQVYL VHFIAKEKWPDVGLYTDWSA VANGLAGWSETWEKQDWKIG DKEIWGRGMWMMDLSEWSKAV KIFVSHVSAHQRTVSAEEEFNN QVDRPL/PVFTQWAHEQSGHSG RDGGYWSAQQTGLPFTKADL AMATAECPICPQQRPTLSPLYS TIPQGDQPATWWQIDYIGPLPS WKGQKFLTVIDTYSRYRFAY PAHNASAKTTIHGLIECLIHCYG IPHSIASDQSIIHF/TTKEVQ*WAH AHGIIHWSYHVSHHPEAAGL
16956	47324	B	17060	10	597	
16957	47325	B	17061	6	297	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Mer/	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion,  =possible nucleotide insertion)
16958	47326	B	17062	1	474	
16959	47327	A	17063	1	2712	
16960	47328	B	17064	1	738	
16961	47329	A	17065	3	772	DPADPMVLEVSEADRDA VPIS ESQRPLGFWSKALPSSANNYS FFKRQLLACYWVLVIEHTLM GHQVTMRELPINCVLSDPCSH KVGHAQHQHSIKWRWYIHYQA QAGPEGTSNLHEEVQAQMPTVS TSATLPSLPEPTQMALWEVPY D QFTEEETKGTAWFTDGSAYHT GTT KWTVAALQLSRTTLLKDS CEGKSPHHPVIAQWAHEQSGH GGRDGGYLWAQOHGFLTKA DLAMATAECPICQQQQKRTLNP
16962	47330	A	17067	1667	2012	LSPHWPPGLPFSALIYAFGLRSS RNKRRRLMKTMKVEACEEDLSAP KYLRIQLPTGSPRRRSEAPEVC FQGSSVFLSVHPPPLLSVPSARR* PQTTPRPPRHPPLSLHPLHPSAQ
16963	47331	A	17068	5	1074	RHSALGTGGSSSCRQRQPRDT WVPETTILTAWSS/RLQQLGPW LQVTVAGQVNLTAGIQTHTIAE HCNVTERPPTGHEALAPPCEQ GPPQVLDSNAVAPTAADCGYQL STAINRNQELCGRKPAVSPSR/G ISPQSPILRPAVHPGHYCLQQLR SGQKSNRRTTQKSFQKLHVDK RKPNENFSKESDHLLIYSREGNPD VASLATPPGIWMMMSATDLFYG DPFAFPGGGPFTLSLERGPSVIL GTDASEELLFTKASLAVENTSVF QFSTGKIYTEWWVWQKNNKSFLSP HFPTKPMASPVKGHSTSSLQR LNYRDRWQCLQEGAGLALLSA HMKVPTGSKEPQQAGKLPSPK RKQTTPITFKD
16964	47332	A	17069	2	699	CSACPVSHPWLPPWQSGSAFL P RALQRPPQHGHRLSKPMQSP RISVLLRPWPRRPLPTDLY*PS TRGHIIHLHDRHHGAPSRRW GDKASPPQPRYSRDSK/RRPPQ HGEVGTVFITNNKGQS/PATST WEVQSAECQKAPEAGPTPPSTA GDAEGANALRQESEGNWGSEA KSPHVAEGSWRPOQGSCHHL HPPDKTKDAARKTHSPGDNGC QPRPPRCPCKTLWSLSR
16965	47333	A	17070	223	1611	
16966	47334	A	17071	12	310	

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16967	47335	A	17072	31	430	LQAVRLFTLPLTSSGL*KLRTVP TWPSPSPCFPHFQSQPRTRAPT PSTI <sup>W</sup> PGVSGYSSGPPSLCPRTS RRAPPRHRVPAGRERLHIRVPP YPRPERHLLRVSRRGILGNNRV GRLPESRAIAGRKEEKTDK
16968	47336	A	17073	1	474	
16969	47337	A	17074	153	1224	RVFSESVCPVRNLEFLWRFAF PLAPAGRCPGPVPLQTSPRDTD AHRSSPLPPARASPQVAAAYR WARCPGCGGRKPKRSSGSWQLC RCPTLPPPGRGSRSSGRC/RTWP SPPSCFPHFQSQPRTRAPTPTSI PGYGSYSSGPGR*GLSPLHAA/ VSPPLPPGGP*GSWARAGLGSI ASAHPSPCLCRSLIRSR\$*QTCT RSPT*NCEVPPSAP*AASPLRTM FALVRTAGLKVHLLPLGYCTT MS*SSSMQTVPVVVVKVSNIPS VHPP*PCCKDCTISRSRSIFTRSP CNPPGFLLPFCSPSTGQ*SL*KEP PLASWTHFRSDVLLLFSVSMNG STLSLGCPSQKAVIALVQVT
16970	47338	A	17075	215	1246	
16971	47339	A	17076	566	675	QPCRQQ/CLQPQGSPPRFHARTLT VTLVHTRTHAHAH
16972	47340	A	17077	184	584	
16973	47341	A	17078	1	1167	
16974	47342	A	17079	849	2266	
16975	47343	A	17080	1505	1891	DAEKAFDEIQQ/PFMKILSRJSI QGTYLNVIKTIYDKPTANTILN VEKLKTFPLRTGTRQCPLSAL LFNMVLEVIARAIQEKGIGQI ISKKEVKLSLFADDMMVHIENPK DSSRKLLIKEFSKV
16976	47344	A	17081	1	842	
16977	47345	A	17082	155	531	GNLWSVDLRPGTPLRQNFRGTI RQQHRSRFTKNHCSQTPLIIPRQ TGSGVDSLKLQQTC\$*GSLVC TIDLANAAFFSIPVHKAHQKQFA FSWQYTTFTVLPRLTWLQPC*V PNLPAAEINTNEPESGNT
16978	47346	A	17083	1	1773	
16979	47347	B	17084	598	1428	
16980	47348	A	17085	3	227	
16981	47349	A	17086	1	207	

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16982	47350	A	17087	1	789	RDLQPFTSVTVHCRKGNQTF GGPLDAGSELTLPGDPKHHCG PPVKVGAYGGQVINGVLA HPL IWL VQKTDGS/WRMTVDYCKL NQVVIP AAAASDVS VSLLEQINT SPGTWYAAIDL ANAFFS PVHK AQQKQFAFSWQGQQY FTVLP QWY NSPALCHN LIRRDLDCFS LPLDITLVH Y DDIMLIGSSEQE VANTLDLFVRHL RARGWEINP KIQGPSTS VKFLG FQWC GACQ A PSKMRD KLLH LVPPTTK KEAQ
16983	47351	A	17088	1	435	
16984	47352	A	17089	2	808	PLIWL VQKTDGS/WRMTVDY C KLNQV VPI AAASDVS VSLLEQI NTSPGTWYAAIDL ANAFFS PVHK HKAQ QKQFAFSWQGQQY FTVLP LPQWY NSPALCHN LIRRDLDC FSLPLDITLVH Y DDIMLIGSSEQ EVANTLDLFVRHL RARGWEINP TKI QGPSTS VKFLG FQWC GACQ A PSKMRD KLLH LVPPTTK KEAQ QCL QLLACY/WALVETE HLTIS HQV TMRPELPIMN WVLFDPSSH KVGCAQ QHSI KWKWY VHDW ARAGPEGT
16985	47353	A	17090	2	544	
16986	47354	A	17091	1	633	MTVDYRKFNQVVTPMAA/AVP DAVS LLEQ NTFPGT WYAAIDL ANAFFS PVHEAQKQFAF LPQ GY NFPALCHN LIRR ELDF FLL QDITLVH Y DDIMLIGSSEQEVV NTL LL H KRSKEA EHTA ASR R V SCL PEQKS HEQ TLP WEQVPSS GDIKEY FPNAF VLL TTASL QGQ DNTSQL LTW KAP EDI KMS KT DAD AEE EAL R
16987	47355	A	17092	1	3228	MVTSS TV AITS L VVV ITS L V V  TSF VVV T TSL VV V ITS L VV V ITS  A IA ATL VV V L T FT VV V L T SL V V V T TSL V MV T PP A V T S L G V V  I T S L V V T C L V L V T A L G V V T S  L G V V T S L V M V T P L V A V T P L  G V V T S L V V V T S L V M V T S L T V V T S L V V T P L V M V T S L T V I T S  L F V V T P L V M V T L V V V N T S L V V V L T L V S P P S L C S L V V V T F L V V A T S L V V V T S L V V V T S L
16988	47356	A	17093	1	471	
16989	47357	A	17094	1	1590	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, ^=possible nucleotide insertion)
16990	47358	A	17095	332	1704	RGYVFCSWKKTDGS/WRMTVD YCKLNQVVIPAAAVSDVVSLL EQINTSPGTWYAAIDLANAFFSI PVHKAQQKQFASFWQGQQYTF TVLPQWYINSPALCHNLIRRL DCFSLPLDITLVHYIDIMLIGP RQLLACY/WALVETEHLTISHQ VTMRPELPIMNWVLFDPSSHKV GCAQQHSIIKWKVYVHDWAR AGPEGTTTPVISQWPHEQCGHG GRDGGYAWAQQCRPLTKAD LNTATAKRPICQQQRPTLSPQY GTIPQGDQPATWWVWDYMGS LPSWKGQRFVLTGIDTYSVYGF AYPACNASAKTAICGLTECLIH HHDIPIHSIASDQGTHFMAKEVR QWAHDHGIIHWSYHVSHHPEA AGLIEWWNGNLLKSQQLQCOLGD NTWQGWGKVQLQKVYYALNQH PIYGTVSPIAKIHRRVADSLKGG SGSWVWGFSTLAAALDNDLGT RKVRAPSTN
16991	47359	B	17096	I	2061	
16992	47360	A	17097	I	1623	
16993	47361	A	17098	I	741	
16994	47362	A	17099	213	679	
16995	47363	A	17100	33	853	
16996	47364	A	17101	3	1249	
16997	47365	A	17102	17	770	
16998	47366	A	17103	130	469	
16999	47367	A	17104	I	1425	
17000	47368	A	17105	I	882	

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17001	47369	A	17106	227	1519	VTLIKMNAMLETPTLS\AVSDG VKLSAVA AVLYVIVRCMNLKS ATAAPDLYLQDSGLSRFLLKSC PLLTKEYIPPLI W GKSGH QTAL YGKMGVRSPHPYGH RKFITM SDGATSTFDLFEPLAEHCVGDD ITMVICPGIANHSEKQY RTFVD YAQKNGYRCAVLNHLGALPNI ELTSPRMFTYGCTW FGAMVN YIKKTYPLTQLVVVGFSLGGNI VCKYLG ETQANQEKVLCVSV CQGY SALRAQETFMQWDQCRR FYNFLMADNMKKIILSHRQALF GDHVKKPQSLEDTDL SRLY TAT SLMQIDDNVMRKFHG YNSLKE YYEEESCMRYLH IYVPLMLV NAADDPLVHESLLTIPKSLSEKR ENVMFVLPLHGGHLGGFEGSVL FPEPLTWMDKLVVEY ANAICQ WERNKLQCSDTEQV EADLE
17002	47370	A	17107	21	385	SRSSSVVRQEPGRADGQR RRRR GGPGLRSPGERQQP PAPCR AHHPGDPAGAQ/PPP KTGKTCG APKATTRSTRCSISR*PPFPRSSC PTSPRATPSSSASSTAAMRRWL VTCRMPNWRA
17003	47371	A	17108	158	423	
17004	47372	A	17109	1	1851	
17005	47373	A	17110	1	1104	
17006	47374	A	17111	66	432	
17007	47375	A	17112	103	3531	
17008	47376	A	17113	1	1311	
17009	47377	A	17114	1	750	
17010	47378	A	17115	183	373	QPQATTLVH PVHVA*LF*VHW QNRYRAPDNQGYRHW RCLLPA LPDAGR/VRLSASC*KPPNSRG
17011	47379	A	17116	344	480	SPKDQE PSISKV***TSLPTSSR SLCLPPARMHF WVLAALLSFA
17012	47380	A	17117	3	3565	HEARRGLKMAACGRVRRMFRL SAALH LLFAAGA RNSPARA SHSQGQGP GANFVFV VGQAGG GGPAAGQQLPQLPQSSQLQQQQ QQQQQQQQPQPPQPPP PAGGPP ARRGGAGAGGGGW KLAEEESCR EDVTRVCPKIH TWSN NLA VLEC LQDVREPE NEISDCNHLWNY KLNLT TDPKFESVAREVCKSTIT EIKECADEPVGKGYMVSCLVD HRGNITEYQCHQY ITKMTAI IFS DYRLICGFMDCKNDIN

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USNN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion,  =possible nucleotide insertion)
17013	47381	A	17118	1	495	PDRRRGCPALSGS*SGPAPRL/C LCNPTLTFHPGSVIGVCL*RHW LCRANTRHPSYRGRLSSR
17014	47382	A	17119	1	1479	
17015	47383	B	17120	67	8652	
17016	47384	B	17121	67	9183	
17017	47385	A	17122	1	1440	
17018	47386	A	17123	1	422	FRWKELLDRPLEPSPETAQPPPP WLQK/NPTAVERANLLNMAKL SIKGLIESALSFGRRTLDSDYPPPL QQFFVVMEHCLKHGLKVRKSF LSYNKTIWGPLELVEKLYPEAE EIGASVRDLPGLNEFYEYHALM MEEEAVIVG
17019	47387	A	17124	2	587	WMGSCGLHRAWLQMRWWPE SAWKELLDRPREPPETAQPPPP WLQK/NPTAVERANLLNMAKL SIKGLIESALSFGRRTLDSDYPPPL QQFFVVMEHCLKHGLKVRKSF LSYNKTIWGPLELVEKLYPEAE EIGASVRDLPGLKTPGLRARA LRLALMQKKMADYLRLCLIIQR DLLSEFYEYHALMMEEGAVI
17020	47388	A	17125	312	493	
17021	47389	C	17126	102	278	
17022	47390	A	17127	2	140	KAHNCSGLERPPLDNPVSNR FASFLSPRDLKGRIICSD*SQVL
17023	47391	A	17128	1	2051	
17024	47392	A	17129	1	498	
17025	47393	A	17130	2	340	
17026	47394	A	17131	140	396	
17027	47395	A	17132	703	912	
17028	47396	B	17133	201	912	
17029	47397	A	17134	1	1382	
17030	47398	A	17135	2	431	
17031	47399	B	17136	99	1151	
17032	47400	A	17137	1	891	
17033	47401	A	17138	15	2722	

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17034	47402	A	17139	476	2934	TEPKTKTT*LSQ*MQKKPLTKF NNPSC*KLSIN/IVLEVLRALARQ EKEIKGIGLQKKEEVKLSLFADD MIVYLENPIVSAQNLKLISNFS KVSGYKINVQKSQAFLYTNNR QTESQIMSELPFTI/ASKRIKYLGI QLTRDVVKDLFKENYKPLLKEIK EDTNWKWNIPCSWVGRINIVK MAILPKVIYRFNAIPIKLPMTFF TELEKTTLRFIWNQKRARIKAKI LSQKNKAVGIGLTPDFKLYYKAT VTKTAWYWWYQNRDIDQWNRT EPSEITPLIYNQIFDKPEKNKQ WGKDSLWNKWCWDNWLAICR KLKLDPFLPTYTKINSRWIKAL NLRPKTICKTLEENLGITIQDIGTG KDFMTKTPKAMATDKDIDKW DLIKLKSFCATAKETTRIVNRLPT KWEKIFATYSSDKGLISRIYNEL KQIYKKKTNPIKKWEKDMNR HFSKDDILAAKKHMKCKSSLAI REMQIKTTMRYHLPVRMIAIK KPGNNSQKDIDPWRNGPKRKD RQITTFRGPTKLQVVVPTLGAAPGRCGPWPRPRCPGREGEELH PALGGERGQRQAAGSGGGARRL APSAGDGLCVGPV рEDTGETQT WKTGQPLGLREPWWGWRPTEPP PAPSSHSEEWPRRPVVRAPR P AGEHAGEGGAAVADTTAFSPW LPRVGGWHLQVHRGGRSCAGA RRFGGSRGWDLGDLSSAPV рASL
17035	47403	A	17140	1	2298	
17036	47404	A	17141	3	482	
17037	47405	A	17142	1	1026	
17038	47406	A	17143	1	623	
17039	47407	A	17144	25	392	ESLKGADPKFLRNMRFANKHN KKGLKKMQANSARATSARAD AIKALVKPEGKPDIPKGVSRK LDPLAYIAHPRLGKCAHSCIAK GLKLCLRLQAKDKDQTKAQAAP A PA*APKGARTPTKASE
17040	47408	A	17145	1	507	

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17041	47409	A	17146	2	811	YRFSGPTIRSIQNHHTHNNQGRK WHKKGIKKPRAQRYESLKGPE V*PSGQGVTCLLRADWLSPLLG SGTY\VGPKFLRNTRFAKKHNK KGLKQMANNAKAMSARAE A\IKALVKPKEVVKPKIPKGG\SR KLRSILPDIVHP\KLGKSRAPY LPRGFRLCLPNANAKSISSQQG GQQQQGGSNQGPQPKPQLQVP ASGVPNVPRALTKGFQSRYSLA QHEGQERTWVRRPPTPRPWGYH FAWGWGSPVIACTNKPEAGKR RNEKEKLCQGDGY
17042	47410	A	17147	I	636	
17043	47411	A	17148	169	410	
17044	47412	A	17149	385	1359	QTNSPNCVRGRVSPVLPGSSS MDVLASYSIFQELQLVHDTGYF SALPSLEETWQQTCLELERYLQ TEPRISETF\GEDLD\CF\JHFP SPCIEESFRRLDPPLL\PEVAAICE KSSAVDILLSRDKLL\SETCLSLQ PASSSLDSYTAVNQAQLNAVTS LTPPSSPELSRHLVKT\TSQTLSAV DGTVTLKLVAKKAALSSVKVG GVATAAAA\VTAAAGAVKSGQG DSDQGGLGAEACPENKVRVHR CQFN\GCRKVVT\KSSHLKAHQR THTGEKPYKCSWEGCEWRFAR SDEL\TRHYRKHTGAKP\PKCNH CDRCFSRSDH\LAHMKRHI
17045	47413	A	17150	1	948	
17046	47414	A	17151	400	446	PSFLR*PSFWSREFH
17047	47415	A	17152	7212	10914	ADSGCKL\PSSC*HVLC\WA\WVTY MVM\MAILHKL\LDQLDASRGRAI PFCGQRGRFKY\ELVKT\TGWGR GSGTTAHVGIMLYGVDSRSGH RHLDGDRAFH\RNNSLD\IRIATP HSLGSVW\KIRV\WHDN\KGLSPA WFLQHVIVRDLQT\TARSAFFLVN DWLSVETE\ANGGLVEKEVLA SDAALLR\PRLLVAEL\QRGFFD KHIWLSI\WDRP\PRSR\FT\RI\ORAT CCVLLICLFLGANAVWYGAVG DSAYSTGHV\SR\LSPLSV
17048	47416	B	17153	I	14934	

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17049	47417	A	17154	999	3009	ADSGCKL/PSSC^HVLCA/WVTV MVMAILHKLDQLDASRGRAI PFCGQRGRFKYEILVKTGWR GSGTTAHVGIMLYGVDSRSGH RHLDGDRAFHRNSLDIFRIATP HSLGSVWKIRVWHNDNKGSPA WFLQHIVVRDLQTARSALLVN DWLSVETEANGGLVEKEVLA SDAALLRFRRLLVAELQRGFD KHIWLSIWDRPPLRSRFTRIQRT CCVLLICLFLGANA^VWYGAVG DSAYSTGHVSRSLSPLSVDTVAV GLVSSVVVPVYLAILFLFRMS RSKVAGSPSPPTPAGQQVLDIDS CLDSSVLDSSFLTFSGLHAEVRT LLGLVGWAGGPAALAAQLGLKT LCTSQQAFVGQMKSDLFLLDD KSLVCWPSGEGTLSWPDLSSDP SIVGSNLRQLARGQA^HGLGPE EDGFSLASPVSPAKSFSASDEDL IQQVLAEGVSSPA^TQDTHMET DLSSLCAEVHTALPLHCSCLQ DSVQWHA^VQGLPAFCRGDPVT QEAOETARPA^AAQNLVLIPLHAA PHQVAEIDALYDVYLDVIDK WGTDDMLFLGDFNADCSDYVR AQDWAAIRLRSSEVFKWLPIDS ADTTVGNSDCAYDRIVACGAR LRRSLKPOSATVHDFQEEFGLD QTQASGPWGGAGLGSPPPGR QAAGRALAJSDHFPVEVTLKFH
17050	47418	A	17155	242	363	TKRQENGRRKKQDRPTEQQLR VK^KSRSTKKRRKQSRSES
17051	47419	B	17156	1	12879	
17052	47420	A	17157	3	596	NLLFPVRSERGPHRPTPLSWLW LRPCELNKLAAGGLAAGSSRA GALYLLIYIPRRP^ARAAPLCPAA ATGAPGASAGSASPASARPGL ARAAPGPLRGRPRPSRPTPFCV/ WLGVSSLSSYQHYFAEFPESFQ VCCRHCIGILCLTIRVHFPLCSAN PFHFSQLHLGPRPGKACHSVGL QIYNSQAHSHPSQQERQLFC
17053	47421	A	17158	1	235	FFFVLYNLFLFVITISPLQKVSI TQRQLVAEENVKCCTV^PEPQ** *LSNYPFVEMGFCHVPGWST TPTPKSVSR

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17054	47422	A	17159	256	4064	ADSGCKL/PSSC*HVLCA/WVTY MVMAILHKLDQLDASRGRAI PFCGQRGRFKYEIILVKTGWR GSGTTAHVGIMLYGVDSRSGH RHLDGDRAFHRSNLDIFRIATP HSLGSVWKRIVWHDNKGSPA WFLQHVIVRDLQTARSAILVN DWLSVTEANGGLVEKEVLA SDAALLRFRRLVAELQRGFFD KHIWLSIWDRPPRSRTFRIQRT CCVLLICLFLGANAVWYGAVG DSAYSTGHVSRSLSPLSV
17055	47423	A	17160	2	347	LTSRGPLCCVLLICLFLGANAV WYGAVGDSAYSTG/LCVAEP AERRHSRCWPGVQRGCLSRP GHPLSLPDVPSEQGGWEPEHTC RAAGAGRRQLPGLNPCTAPS SRSEASTLR
17056	47424	A	17161	9415	9994	ADSGCKL/PSSC*HVLCA/WVTY MVMAILHKLDQLDASRGRAI PFCGQRGRFKYEIILVKTGWR GSGTTAHVGIMLYGVDSRSGH RHLDGDRAFHRSNLDIFRIATP HSLGSVWKRIVWHDNKGSPA WFLQHVIVRDLQTARSAILVN DWLSVTEANGGLVEKEVLA SKASFRVPTPSRSVPALPAPAGG
17057	47425	A	17162	1030	1222	
17058	47426	A	17163	2	2762	
17059	47427	A	17164	25	115	
17060	47428	A	17165	1	383	
17061	47429	A	17166	120	596	IKAPCASFPTSGFPGQRSSFVGR SSSTPEECGHSELGRNEDKASR GRIRQQ/PFAVLKYLLFCSLRW* YPGKQGLEWTSSKLQQTCRKY RERHKDTPQEEQLQDT*LSG/V TK/G*NEGKNVKGSQRERSGYS QREAHQTNRSRSLGRNNTSQKRV GASIQRS

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17062	47430	A	17167	1	2236	RPSGPQLPGSVRHPRPPVRLRPLPRAQGSSSSFRPRPPFAPDTMDKFVWHAAWGLCLVPLSLAQIDLNITCRIFAGVFHVEKNGRYSISRTEEAANLCKAFNNTLPTMAQMEKALSIGFETCRYGFIEGHVVIPRIHPNSICAANNTGVYILTSNTSQYDTCYCFNASAPPEEDCTSVIDLPNAFDGPITITIVNRDGTRYVQKGEBRTPNEDIPSNPTDDVSGSSSERSSSTSGGYIFYTFSTVHPIPDEDSPWITDSTDRIPATSTSSNTISAGWEPNEENEDERDRHLSFSGSGIDDDDEFISSTISITPRAFDHTKQNQDW\TQW\NPSH\NSNP EVLL\Q\TTTRMTDVRDNGTTAYEGWNWPEAHPPLIHHHEEEETPHSTSTIQATPSSTTEATQKEQWFGNRWHEGYRQQTREDSHSTTGAAASAHTSHPMQGRTTPSPEDSSWTDFNPNISHPMGRGHQAGRRMDMDSSHSTLQPTA\NPNTGLVEDLORTGPLSMTTQSNSNSQSFSTSHEGLEEDKDHPHTSTLTSSNRNDVTGRRDPNHS EGSTTILEGYTSHYPHTKESRTFIPVTSAKTGSFGVTAVTVGDSNSNVNRSLSGQDQTFHPSGGSHTTHGSESDGHSHGSEQEGANTTSGPIRTPQIPEWLIILASLLALALILAVCIAVNSRRRCGQKKKLVINSGNGAVEDRKPSGLNGEASKS
17063	47431	A	17168	1	1980	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met/hd	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, !=possible nucleotide insertion)
17064	47432	A	17169	362	2551	EDFSTSATTTPSSPRELPSGQGL WLCWLELLPSFTRNGVVHTGP C*GLC*RWQQLSPQPSLPSNFGM KISDMATLITTVPAAFSSSDW NTPAPTQSPEEVRLHLCTSFN DMLKVGGQGEGAAAGLVQNP SGHALGCLDSAASGISDPSVAV LLENVPNQRGESLRCVPVYLGQ WNCSETGMDSQFGEEKGAH DPSPTYYHACLSTQWWPSPEP YPQPSGPQVKEPRNPGKSIIML CLWIRYHAADSGSSRAKLPLEE RLRPFSPTHDCLAFPLPLEKRPE GNVGSRCPSGTKLPEEGGSNI CCSAIFPVQLQPPVLIPRQTRSGV DLQQPTTDLQLRDLTRSSLPA MEQSWIENDFDELNRSRQLKA NKLENLEETDKFLDTYTLPRLN QEETESLNRPITGSEIEAIINNVP TKKSPGPDGVTAKFYQRYKEE LRTVKNKNHMIISIDAEEKAFDNIQ QPFMLKTLNKLQIDATYLNKIIRA IDDKPTANIIHLNGQKLEAFPLKT GTRQGCPLSPLFNIVLEVLR AIRQEKEIKGIGQLGKEEVKLSLF ADDMIVYLENPIVSAQNLLKLI NNFSKVGSKYKINVQKSQEFLYN NNRQTEQIMSELPTFTIASKRK YLGQQLTRDVKDLFKENYNPPLL NEIKKDTNKWKNIPCSWIGRINI MKMAILPKSGPSAARLLEFAGG PLQTLFAWVSPPEAAEQQILPN
17065	47433	A	17170	1	483	
17066	47434	A	17171	52	321	
17067	47435	A	17172	274	393	
17068	47436	A	17173	304	415	
17069	47437	A	17174	321	796	
17070	47438	A	17175	1	198	
17071	47439	A	17176	2	454	CRPVPAATNGRCFPATPRDPGP RMRRACA WGRSKGAGRCLRR ATRRDKMAKKESILDLSKIYID KTIRVKFQGGRKVASGILKGFP NLLUNLVLVTVI*YMRDPDDQY KLTEDATRQLC\LVVFRG\TSVL VCPQDGMEAIP\NPFIQQQDA
17072	47440	A	17177	1	1806	
17073	47441	A	17178	1215	2065	
17074	47442	A	17179	217	441	
17075	47443	A	17180	117	296	DWSDIQKLG*SLSLSKEIFQL*IV SPPALIHPAKLLHRSAs*LSVPQIG RECQCGCGWTAMC

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met/Asp	SEQ ID NO: in USN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, V=possible nucleotide insertion)
17076	47444	A	17181	2	138	LRTAPEFPGRFRGCAAAAESVAALL*STPPCRSGDSDLGKSR
17077	47445	A	17182	222	760	
17078	47446	A	17183	192	244	YIQPVF*GWTLGCCQFF
17079	47447	A	17184	1	990	
17080	47448	A	17185	1	2196	
17081	47449	A	17186	459	1387	
17082	47450	A	17187	2	454	
17083	47451	A	17188	1	957	
17084	47452	A	17189	398	553	
17085	47453	A	17190	2	293	
17086	47454	B	17191	53	182	
17087	47455	A	17192	3	1114	
17088	47456	A	17193	1	1024	SVVEFIPSCAVVLWSSVLLSPVRLLSYLSGVPPGHPMEDSMDMDMSPLRPHNYLFGCELKAGQDYHFKVDNDENEHQSLRTVSLG\AGAKDELHIVAEAMYYEGSPIKV/THLATLKMSPQPTVSLGG\FEITPPVVLRLKCGSGPVHISGQHLVAVEEADESEDEEEEDVK/LSLSISGKRSAP/GGGSKVPQKERKTCMLMKDDDD\DEEDEDGYDDEDDDDDDFDDEEAEEKAPSERNLYRDTP\AKNAQKSQNQNGKDSKPSTPRSKGQESFKKQEKTPKTPKGPSVVEDIKAKMQASI/A/EKGGLPKVEAKFINYVKNCFPMTDQDAIQDLWQWRKSL
17089	47457	A	17194	2	291	
17090	47458	A	17195	185	307	
17091	47459	A	17196	3	392	VRGGQAFRQRPAAPPLPVTRSAHGRRRPTRASQPSSLFHILLREGKMESSSSKSSQPLASKQEKDGTEKRGGRPRPKQP\PVSPGTALVGSQKEPSEVPTPKRPRGRPKGSK/NKLEKEEEEIGISQESSEEQ
17092	47460	C	17197	76	378	
17093	47461	B	17198	1803	1905	
17094	47462	A	17199	1	416	
17095	47463	A	17200	30	407	
17096	47464	A	17201	1	993	
17097	47465	A	17202	1	1287	
17098	47466	A	17203	1	2004	
17099	47467	A	17204	1	1368	
17100	47468	B	17205	1	3035	
17101	47469	B	17206	1	981	
17102	47470	A	17207	1	2017	
17103	47471	A	17208	1	1069	
17104	47472	A	17209	1	2463	
17105	47473	A	17210	1	324	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met/ codon	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion,  =possible nucleotide insertion)
17106	47474	A	17211	51	1528	GREASKMAQTQGTRRKVCYY YDGDVGNYY*G QGHGPMK HR IRMTHINLLLNYGLYRKMEIVRP HKANADEMTKYHSDDY KFLR S /RVPDINVGSTSKQMQRFNVG EDFPSIPMACFEFCQLSTGGSVA KCL*NFNKQQTIAVNWAGGL HHAKKSEASGFCYVNDIVLAIL ELLKYHQRVLYIDIDI HGDRV EEAFYTTDRVMTVSFIHKYGEY FPGTGDLRDIAGKGKYYAVN YPLRDGIDDESYE A FKPVMSK VMEMFQPSAVVLQCGSDSLSG DRLGCFNLTIKGHAKCVEFVKS FNLPMLMLGGGGYTIIRNVARC WTYETAVALDTEIPNELPYNDY FEYFGPDFKLHISPSNMTNQNT NEYLEKIKQRLFENLRLMPHAP GVQM QAPIPEDA PEESGDEDED DPDKRISICSSDKRIACEEEFSDS EEECEGGRKNSSNFKKAKRVK TEDEKEKDPEEKKEVTEEEKTK EEKPEAKGVKEEVKLA
17107	47475	A	17212	1	492	
17108	47476	A	17213	1	1851	
17109	47477	A	17214	1	753	
17110	47478	B	17215	427	614	
17111	47479	B	17216	1	711	
17112	47480	A	17217	750	1173	
17113	47481	A	17218	1	1224	
17114	47482	A	17219	1242	1743	
17115	47483	A	17220	423	1739	
17116	47484	A	17221	117	1183	
17117	47485	A	17222	1	377	FRRGAW/VPLLTRWGRPRRGCG ISNDSPRRS/IHYRETKEPPVVR CARGLQRTPSAGHRRAVLRMPR RGRTRPGAPQGGAALGGPARD RECACAGRGAQTFALKRNVC KMPSGRGRGRTCSKNFSYFPS
17118	47486	A	17223	331	1134	
17119	47487	A	17224	178	1200	
17120	47488	A	17225	1	367	
17121	47489	A	17226	85	3360	
17122	47490	A	17227	8	930	
17123	47491	A	17228	1	765	
17124	47492	B	17229	120	509	
17125	47493	A	17230	232	3187	
17126	47494	A	17231	1	999	
17127	47495	A	17232	1	325	
17128	47496	B	17233	1	535	
17129	47497	A	17234	271	634	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met/	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, ^=possible nucleotide insertion)
17130	47498	B	17235	301	523	
17131	47499	A	17236	1	1185	
17132	47500	A	17237	178	497	LPVPAYELNGSQLPLLLGAAAGLYLAYKRFYVKDHRNKAMINLHIQKDNPKIRHAFDMEIDLGDKAVYCRCWRSKKFPFCGDAHTKHNEVGTGDNVGVPLIIKKKET
17133	47501	B	17238	184	395	
17134	47502	A	17239	1	103	PAWHEGQPQPESECPCPQRQCICSHGRGTPARCGVSY*ART/PAGESP*TQQDLRAS*LGTTRANHSQRASARHKDSASAATVGAGHQRD AE
17135	47503	A	17240	447	667	HRPRRRFQIKPQSQVPEHAPLPLPTASDPP/AHSRPCPSESRLSPGGQRLGFPSSVLNCNSKCSWQLAACMGFSP
17136	47504	A	17241	265	890	
17137	47505	A	17242	1	1374	
17138	47506	A	17243	1	6189	
17139	47507	A	17244	1	8277	
17140	47508	A	17245	178	1177	
17141	47509	A	17246	1	447	
17142	47510	A	17247	1	465	
17143	47511	A	17248	3	3910	
17144	47512	A	17249	2	1871	
17145	47513	A	17250	1	666	
17146	47514	A	17251	1	635	FPGRRFRRAVWCTHCCAPTPSPVLPHSAAMSLKSPPPPGPAEGLLRQQPDTEAVLNKGKLGTTGTLVIAESRLSWLDGSGLGFSLEYPTISLHALSRDRSDCLGEHLYVMVNAKFEEEESKEPVADEEEEEDSDDDVEPITEFRFVPSDKSAF*FPCSVTEAMFTACMCQALHPDPEDEDSDDYDGEEYDVVAHEQGQGDIPTFYTYEEGLS
17147	47515	A	17252	1	2796	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met/Asp	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, !=possible nucleotide insertion)
17148	47516	A	17253	1	2393	MEIRGALDLRKQVQLFLVLLG LSRAGTESAHYSAEETEIGSFV ANLARDLGLGVEELSSREARV VSDDNNKKYLHLDLLTGNNLLN EKLDRDELCGSTEPVCVLFHQV LENPLQFFRFELCVKDINDHSPT FLDKEILIKISEGTTVGAATFLME SAQDLDVGSNSLQNYTISPNSH FYIKIPDSSDRK1YPELVLDRAL DYEQEAEELRLTLTAVDGGSPPK SGTILVLIKVLIDNNAPEFPQS LYEVQVPEDRPLGSWATISAK DLDAGNYGKISYFFFHASEDIR KTFEINPISGEVNLRSPFLDFEVIQ SYTINIQAATDGGGLSGKCTLLV KVMIDINDNPPEVTTISITKRIPE NASETLVALFSILDQDSGDNGR MICSIQDNLPPFLKPTFKNFFTL VSEKALDRESQAENITITVTDL GTPRLKTEYNITVLLSDVNDNA PTFTQTISYTLFVRENNSPALHIG SVSATDRDSGTNAQVNYSSLPP QDRHPLASLVSINADNGHLFA LRSLDYEALQEFEFRVGATDRG SPALSSEALVRVLVLDANDNL PFVLYPLQNGSAPCTELVPRAA EPGYLVTKVVAVGDGDSGQNA WLSYQLLKATEPGLFGVWAHN GEVRTARLLSERDAAKHRLVV LVKDNGEPPRSAATLHVLLVD GFSQPYLPLPEAAPAQAQADLL TVYLVVALASVSSLFLSVLLF
17149	47517	A	17254	89	1283	
17150	47518	A	17255	1	276	
17151	47519	A	17256	2	259	WQGGILGSDPTPPLTSPNLLQT ACFRERDV/RRERGQPLGDHS ALCLP芮RGVPVPCDGILLCWWG PPDAAEPLRGPSPARAGPVPLG
17152	47520	A	17257	624	4055	
17153	47521	A	17258	3	1784	
17154	47522	A	17259	1	1272	
17155	47523	A	17260	3	576	
17156	47524	A	17261	1	1017	
17157	47525	A	17262	1	1107	
17158	47526	A	17263	256	634	
17159	47527	B	17264	76	1340	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met cod	SEQ ID NO: in USNN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
17160	47528	A	17265	1659	2107	NLLCCTCSPFSSPVASAPQTCTN CIALLVHQQQWLVSSILQKHF LHLHIFLAALIVFNFSLHSF*1PDF DPWKLP*PISPTLSSLPSNRHIA LILPCSCMTEDDFKMPAAVAR YMTSPQAVHIIAVCPFKASRKV SHSSKLWLFKSV
17161	47529	A	17266	248	540	KFFSLRMLNINPHCLLACRVSA ERSAVSLMGFPCLCISRPFLSAAI NIFSFISTLVNLMIISLGVALLEE YLCGILCIS*IGMLACLARLGKF SWIIR
17162	47530	A	17267	4880	5121	
17163	47531	A	17268	468	602	CLQLCSFGLGLTW*CGLFFYST *TLK*FFPIL*RMMVVF*WGLH
17164	47532	A	17269	359	462	
17165	47533	A	17270	457	600	LWWFNALFLCWLTSLTTTLL LHECLPVWRD*TRRHLTGWSK GSCTN
17166	47534	A	17271	2405	2830	TPVFRFIALSYTFADSDGEYF*IL LSENPQRFFKCCFNMRSNKIPW DTFANSIKGAEFSGKHFTEFISS SESESESESTRFRDFRGLGETSSL SLDSFSLLGDDFLSFLLSFTIDA VSSKRLSKEIRKARLCWRFPRI
17167	47535	A	17272	1	2172	
17168	47536	B	17273	446	625	
17169	47537	B	17274	1	2604	
17170	47538	A	17275	1	3039	
17171	47539	B	17276	1	1383	
17172	47540	A	17277	1	993	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met/hd	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, !=possible nucleotide insertion)
17173	47541	A	17278	3	2494	RSTRQKVNLKDQELNSALHQADLIDIYRTLHPKSTEYTFVSAPHHTYSKIDHIIVGSKTLLSKCKRTEIITNYLSDHSAIKLELRIKNLTLQSRSITWKLNNLLNDYWVWHNEMKAEIKMFFENENKDFTTYQN LWDAFKAVCRGKFIALNAYKRKQERSKIDTLTSQKLEKQEQTHSKASRQEITKIRAEKIEETQKTLQKINESRSWFFERINKIDRPLARLJKNKREKNNQIDTICKNDGDITINPTEIQTITIREYYKHYLA NKLENLEEMDTFLDTYTLPRLNQEEVESLRNPITGESEIVAIINSLP TKKSPGPDGFTADEFYQRYKEELVPFLLKLFQSIEKEGILPNSFYE ASIILIPKPGRDFTTCKENFRPISLMNIDAKILNKILANRQHQHKKL IHHDOQVGFIQPMGQGWFIHKSI NVIQHINRAKDKNHNMIISIDEEKAFDKIQQPQFMLKTLNKL/G/DKI PRNPITYKGCEGQPLQGELOQTAQGNKRGHKQMEEHSMILMGRKNQYHENGHTAQG/IL*IQCHPHQATNDFLHRIGKNYFKVHMEPKKSPHRQVNPKPKEQSWRHTT *LQTILQGYSNQNSMVLMVPKQRYRSMEQNRALRNNAAYLQLSDL*QP*EKQAMGKGFP*MMVLGKLASHM*KAETGSLPYTLYKNQFKMD*RFKR*T*NHKPNPRKP RHYHSGHRHGQGLHVQNTKSN
17174	47542	A	17279	285	502	
17175	47543	A	17280	1	3189	
17176	47544	B	17281	1	1235	
17177	47545	A	17282	1	3139	
17178	47546	B	17283	1	1779	
17179	47547	B	17284	1	3127	
17180	47548	A	17285	1	3325	
17181	47549	A	17286	1	3145	
17182	47550	A	17287	1	1095	MIMGDFNTPLSTLDRSTRQKVNDKIQELNSALHQADLIDIYRTLHPKSTEYTFVSASHLTYSKIDHIVGSKALLSNCKRTEIITNYLSDHSAIKLELKIKKLTPNRSTTWKLNNLLNDYWVHNEMKAEIKMFFETNENKDFTTYQNLWDTFKACERGKFIALNAYKRKQERSKIDTLSQKLEKQEQTHSKASRQEITKIRAEKEMETQKTLQKINESRG/WKKFLEKLCFIELS*ARRI

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met/hod	SEQ ID NO: in USNN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, ^=possible nucleotide insertion)
17183	47551	A	17288	1	3229	
17184	47552	A	17289	1	1205	
17185	47553	A	17290	1	986	
17186	47554	A	17291	1	3170	MGDFNTPLSTLDRSMRQKVKK DTQELNSALHQADLIDIVRTLH PKSTEYTFSSAPHHHTYSKIDHIL GSKALLSKCKRTEII^TNYLSDGS AIKLERIKNLTQNRSTTWKLNN NLLNDYWVPNEMKAEIKMFF ETNENKDTTYQNLWDTFKAV CRGKFTALNAHKRKQERSKIDT LTSQLEKELEKQEQTHSKASRRQ EITKIRAELEKEIETQKTLQKIN^S QSWFFERVKKIDRPLARLIK REKNQIDTIKND
17187	47555	B	17292	1	2148	
17188	47556	A	17293	1	1416	
17189	47557	A	17294	1	3099	MGEIJTPLSTLDRSTRQKVNKD TQELNSALHQGDLIDIVRTLHP KSTEYTFSSAPHHHTYSKIDHILG SKALLSKCKRTEII^TNYLSDHSA I <sup>KE</sup> LERIKNLTQNRSTTWKLNN L <sup>LL</sup> NDYWHNEMKAEIKMFFET NENKDTTYQNLWDAFKAVCR GKFTALNAHKRKQERSKIDT SQLKELEKQEQTHSKASRRQEI TKIRAELEKEIETQKTLQKINESR SWFFERINKKIDRPLARLIK KNQIDTIKNDK
17190	47558	A	17295	1	3345	
17191	47559	B	17296	1	3122	
17192	47560	A	17297	1	2118	
17193	47561	A	17298	965	4091	
17194	47562	B	17299	15	2762	
17195	47563	A	17300	1	3049	MTVKVRJTVTSGKKPPWLPRQ TGYGVDLWQTPPTDLQLRVLTV RRKTNKQKGHPHQNPCTSPSS KTKDRSTRQKVVKNDIQLNSAL HQEDLIDIVRTLHPKSTEYTFSS APHHHTYSKIDHIVGSKALLSKW KRTEITANCLSDHSAIKLERIJK KLTQNW <sup>S</sup> ATWLNNNNLNDC WVHKEMKAEIKMFFETK <sup>EN</sup> K DTTYQNLWDAFKAVCRGKFT LNAHKRKQERSKIDT <sup>L</sup> SQLKE LEKQEQTHSKASRR

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met/hd	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, !=possible nucleotide insertion)
17196	47564	A	17301	3	4101	PLSTLDRSTRQKVNKD1QELNS ALHQVLDLIDYRTLHPKSTEYTF FSVPHHNSYKIDHIIVGSKALLS KCKRTEIITNCLSDYNAIKLELR TEKLTQNRSTTWKLNNPLLN YWVHKEMKAEIKMFFETNENK DTTVQNLWDAFKAVCRGKFA LNAHKRKQERSKIDTSQLKE LEKQEQTHSKATRQEIJKTRA ELKKIETQKTLQKINESSRWFFE KTNKIDRLLATLKKKREKNQI GARKNDEGAITT
17197	47565	A	17302	1	3234	MANKNNQCREVLKGPDELKT MAREPHDKCTSFSQFDQLEER VSAMEDQMNEMKREKEFREK RIRKNEQLQEIWVDVYVCRPNL LIGVPESDGENGTKLNTLQDII QENFPNLARQANIQIQQEIQRM QRYSLLRRTTPRHIIVFRFTK VEMKEKMLRAAREKGRVTHKGKPI RLTADLSAETLQARRESTRQKV NKDIQELNSAQHQADLTDNYR TLHPKSTEYTLFSAPHTYSKID HIVGSKALLSKCRTEI
17198	47566	A	17303	1	3390	MLTLNHNRLLTDAILNISTCLSR HLDLNNTGGKKRISYKRNLYLME EHLEGGLCSNEFTWENSTIMTDS QMLMHREEPGLSPNIPILSIVFT NNRSRKQKVNKD1QELNSALH QADLIDIYRTLHPKSTEYTFSA PHHTYSKTDRIVGSKALLSKCK RTEIITNCLSDHSAIKLELRKKL TQNCSTTWKLNNLLNNDYWV HNEMKAEIKMFFETNENKDTT YQNLWDTFKAVCRGKFI LNAHKRKQERSKIDTLLS
17199	47567	B	17304	1	2427	
17200	47568	A	17305	1	4257	
17201	47569	A	17306	1	3726	MVVKTNARELRDECTSLSSPFN QLEERVSMENQMNKMKQEE KPREKRKRNEQSLQEIWVDYVK RPNLCLIGVTESDGENGTKLEN TLQDITQENFPNLARKANIQIQE TQRTPQRYSSRATLRRHIIVRFT KVEMKMLRAAREKDFPTPK IKRDKEGHYIMVKGSIQQEELTI LNIYAPNTGAPRFIKQVLSLDLQ RDLDLSDHTLIMGDFNTSLLLTDR SMRKVNKDTQELNSLLHQAD LIDIYRTLHPKSIE
17202	47570	A	17307	1	1059	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met/Asp	SEQ ID NO: in USNN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, !=possible nucleotide insertion)
17203	47571	A	17308	130	1092	
17204	47572	A	17309	1	924	
17205	47573	A	17310	1	1206	
17206	47574	B	17311	1	1257	
17207	47575	A	17312	1	685	MEIILRICKLTISKELLDGSSRL TMTHYKHRYFSHSAEEQIISEEL NESEMICQHHHTAENDFDELRE EGFRRSVITNFSKLKEDVQTHF KEAKNLEKRLDEWLTRINSVEK TLNDLM*LKTV*ELRDTYTSF NSRFDQVEERVSVIDQMNEM EREKFKREKRV*RNEFQS/LQEIW NYVKRPNLHIGVSEIDRENGT KLENLQDIFQENFTYLARQAN IQIQEI
17208	47576	B	17313	70	1227	
17209	47577	B	17314	640	751	
17210	47578	A	17315	1	2328	MGVSGAQPGRCSCWHRSSSGQ GLGPVPEPADCGGEAAGRARE EGTVSLTMGTADSDEMAPEAP QHTHIDVHHQESALAKLLTC CSALRPRATQARGSSRLLVASW VMQIVLGLSAVLGGFFYIRDY TLLVTSGAAIWTGAVAVLAGA AAFIYEGRRGTYWALLRTLTL AAFSTAIAALKLNEDFRYGYS YYNSACRISSSDWNTAPTQSP EEVRLHLCTSFMMDMLKVGGQ GEGAAAGLVQNPGSHALGVCLD SAASGISDPSVAVLLENVPNQR GESLRCVPVYLQWNCNSKETG MDSGQFGEEKGAHDPSPTYYH ACLSTQWWPSPESPYQPQPSGPQ VKEPRNPGKSISMLCLWIRYHA ADSGSSRAKLPLEERLRPFSPTH DCLAPPLPLEKRPEGNVGSRCP SGTKLPEEGSGSNICCSAIFPVVL QPLLVIPRQTRSGVDLQQPTTD LQLRDLTVRRKTNKQKGPHQ NPMCTSPSSKTKELKEDVRTHH KEAKNLEKRLDKMVNRINSVE KTLNDPMELKTQARELHDKCT SFSSRFDQLEERVSVTDEDQMNE MKREEKFREKRVKVNNEQSRLQE IRDYVKRPNLCLTGVPESDGEN ETKLLENTLQDNIQENFPNLARQ ANIQIQEIQRTPORYSSSRATPR HIIVRFVKVEMKEKMLRAAGE KGQVTHKGKPIILTADLLAETL
17211	47579	A	17316	508	666	
17212	47580	A	17317	622	780	

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17213	47581	B	17318	1	777	
17214	47582	A	17319	1	508	MSGFEKQYKKIRLDKTLDENE GLELPVPAKRSNLGVRLYACC GLLLCPAYPQHFAHGVVDKIPG YPRAGTGLHMPQVCRCCR QAPCLKSNNALIVILGTVTLDA VGIGLVMPVLPGLLRDIVHSDSI ASHYGVLLALYALMQFLCAPK YKLPSENTNTSMQIN
17215	47583	B	17320	310	1047	
17216	47584	A	17321	1	1101	
17217	47585	A	17322	577	735	
17218	47586	A	17323	337	642	
17219	47587	A	17324	2	653	
17220	47588	A	17325	2	935	
17221	47589	A	17326	532	729	
17222	47590	A	17327	1	675	
17223	47591	A	17328	1	684	
17224	47592	A	17329	2	641	
17225	47593	A	17330	1	808	
17226	47594	A	17331	562	675	
17227	47595	A	17332	2	1687	DTGNNEWKQQEGLSHNNWLG LGCLFGPETPIFYPATLGHHTSSY YERKKEDKNGMKEEHDTSA MFITLNFNQISVENIRKGPMVV GESIAQSYLNVVQEIFRSRNHQ LLQDLTRDLCNDNLKTCHTSHGS VMAETAVINHKKRKNSPRIVQS NDLTEAAYSLSRDQKRMLYLF VDQIRKSDGTLQEHDGICEIHV AKYAEIFGLTSAEASKDIRQAL KSFAGKEVVFYRPEEDAGDEK GYESFPWFIKQRSNLGVRLYAC CGLLCPAYPQHFAHGVVDKIP GYPGRAGTGLHMPQVCRCCR RQAPCMKSNNALIVILGTVTLD AVGIGLVMPVLPGLLRDIVHS SIASHYGVLLALYALMQFLCAPK VLGALSDRFGRRPVILLASLLGA TIDYAIMATTPVRGHSVLSKGKQ HKSVENLQPDNVIEKKKIPFSGEK FKPAAEICKSNRELNVNHQDNG ENVSRACQRPLLQPLPSQAWRF RRKRNWFCCGPWSPFVQSRS LVPCVPAAPALTKRGQGTAQA VASEGGSPKPWQLPHGVEPAG AQKSRAEVWEPPRFQKM
17228	47596	B	17333	12	60	
17229	47597	B	17334	253	2103	

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17230	47598	A	17335	469	2512	PTSA <sup>Y</sup> ERGQRFASRQLQMNLL <sup>E</sup> FLRWLM <sup>A</sup> IKFPQAPCMKSNN <sup>A</sup> LIVLGT <sup>T</sup> VTLD <sup>A</sup> VGIGLVMPVL <sup>L</sup> PG <sup>L</sup> LRD <sup>I</sup> VHS <sup>D</sup> S <sup>I</sup> A <sup>S</sup> HYGV <sup>L</sup> LA <sup>L</sup> YALMQFL <sup>C</sup> APV <sup>L</sup> GAL <sup>S</sup> DRFGR <sup>R</sup> RPV <sup>L</sup> L <sup>A</sup> SLLGAT <sup>I</sup> DY <sup>Y</sup> AIMATT <sup>P</sup> VLW <sup>I</sup> YPLVNV <sup>S</sup> KS <sup>D</sup> DTLK <sup>I</sup> KINGV <sup>G</sup> EDH <sup>K</sup> T <sup>I</sup> F <sup>D</sup> GDGK <sup>T</sup> YQNVQQFID <sup>D</sup> EGNYTSGDNH <sup>T</sup> LRDP <sup>H</sup> YVEDK <sup>K</sup> GH <sup>K</sup> YLV <sup>F</sup> EANTG <sup>T</sup> TEN <sup>G</sup> YQ <sup>G</sup> EE <sup>K</sup> SLFNKAY <sup>Y</sup> GGGT <sup>N</sup> FRKESQKL <sup>N</sup> QQSAKKRDAELANGALG <sup>H</sup> IELN <sup>N</sup> NDYTLKKVMKPLITSNTV <sup>T</sup> DEI <sup>N</sup> ERANVF <sup>K</sup> MNGK <sup>W</sup> YLF <sup>T</sup> DSRGS <sup>N</sup> KMTIDG <sup>I</sup> KLNDIYMLGF <sup>V</sup> NSL <sup>N</sup> TG <sup>P</sup> YKPLNKTGLV <sup>L</sup> QMVLD <sup>P</sup> N <sup>N</sup> DVTFTNFYLPGPQAKANMWLL <sup>N</sup> QAHDKKSFSR <sup>I</sup> KGT <sup>G</sup> FPAL <sup>N</sup>
17231	47599	A	17336	2393	2945	
17232	47600	A	17337	980	1732	

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17233	47601	A	17338	1	2400	GRPFPRPPRLCQRRRLRGGRMK MTGDFEECLKDSPRFRAALEEV EGDVAELELKLDKLVLVKLGIAIM DTGKAFCVANKQFMNGIIRDLA QYSSNDAVVEETSLTKFSDSLQE MINFHIL/L*PNSEINLRHSFSN FVKEDLRKPKDAKKQFEKVE EKENALVKNAQVQRNKQHEVE EATNIIATTRKCFRHALDYVL QINVLSKRRSEILKSMMLSFMY AHLAFFHQGYDLFSELGPYMK DLGAQLDRLVGDAAKEKREME QKHSTIQKDFSRDDSKLYNV DAANGIVMEGYLFKRASNAFK TWNRRWFSIQNNQVYQKKFK DNPTVVVEDLRLCTVKHCEDIE RRFCFEVSVPTKSCMLQADSEK LRQAWIKAVQTSIATAYREKG DESEKLDKSSPSTGSLDSGNE SKEKLKKGESALQRVQCCIPGNA SCCDCGLADPRWASINLGIITLCI ECSGIHRSLSLVHFSKVRSLTLDT WEPELLKLMLCELGNDVINRVY EANVEKMGIKKPQPGQRQEKE AYIRAKYVERKFVDKYISLSPP EQQKKFVSKSSEEKRLSISKFGP GDQVRASAQSRSNDSGIQQS SDDGRESLPSTVANSLYEPEG ERQDSSMFLDSKHLNPGQLYR ASYEKNLPKMAEALAHGADV WANSEENKATPLIQAVLGGSLV TCEFLQNGANVNQRDVQGRG
17234	47602	A	17339	1	782	
17235	47603	A	17340	1	475	
17236	47604	A	17341	1	852	
17237	47605	A	17342	432	696	
17238	47606	A	17343	3	296	ETEIFALKKEELLFLKKNNQEEEV KGLQAQIAISGLTVEVDVPKSQ DLAKIMADIRWA*DELEDGEDF SLRDALDSSNSMQTIRKTTTRPI VSGWQSGV
17239	47607	A	17344	2	292	SQKKGLVGALTLPNPPHFCPCHL *EVKGQLQAQIASSGLTVEVDAP KSQDLAKIMADIRAQYDLEAR KNREELDKYWSQQVREGKGM GCQGVGGRQE
17240	47608	A	17345	1	908	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met/hd	SEQ ID NO: in USNN 09/540,217	Nucleotide location of first codon for last amino acid of peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, /=possible nucleotide insertion)
17241	47609	A	17346	1	1452	TGPEFHDLRLVRRRPQLSPVL LLSSPDMSFTTRSTFSTNYRSL GSVQAPSAGPRAARPASY AGAGGSGSRISVSRSTSFRGGM GSGSLATGVIAGGLAGMGVGIQ NEKETMQSLNDRLASYLDRVR SLETENRRLAESKIREVHLEKKG PQVRDWSHYFKHIEDLRAQIF ANTVDUNARIVLQIDNAPSCVR DDFRVVKYIETELAMROSCWRT DIHGAPQGPFDTNYHTDLQL/ EKTIERGSSRRELLFQ*RRNHEE /EKLKGLQAAQIAQFLGLTRGRRL DCPQFRDLRQDSWADIRGPIID ELASEEPRGSLDKYWSQQIIEE STTVTTQFAEVEAAETTLTE LRRTVQSLENDLDSMRNLKAS/ LENSLREG*RPAYALQMEQLN GILLHLESELAAQTRAEGQRQA QEYEALLNIKVLEAEIA TYR LLEDGEDDFNLGDA LDSSNSMQ TIQTTTRRIVDGKVVSETNDT
17242	47610	A	17347	467	843	
17243	47611	A	17348	114	1363	
17244	47612	A	17349	2	281	
17245	47613	A	17350	1	588	
17246	47614	A	17351	184	354	
17247	47615	C	17352	391	657	
17248	47616	A	17353	1	2010	
17249	47617	A	17354	2	443	VPDLPPSHRGFRAAQGGLPPKN KVAALPSWGSANQNSARWEL VSPPIHRRGGS*GPGETDLDGSS IQRAVELRLVQAFVVPKSSLRD PSREGRGWAG*VQTKGAA*AR PTLLWAPKR/DRGGKAAPTSTW NSPKAGCPSARSSPAPP
17250	47618	A	17355	1	1359	
17251	47619	A	17356	260	380	
17252	47620	A	17357	153	273	
17253	47621	A	17358	270	484	AKYRG TGSSRKALGAH WVPKQ PIPAWQHKDPSGRPEEQGVKL YREKEFSS*TL*/RI*TOPDAWA YAWADAW
17254	47622	A	17359	2	941	
17255	47623	A	17360	1	615	
17256	47624	A	17361	911	1472	
17257	47625	A	17362	2	442	
17258	47626	B	17363	76	235	
17259	47627	A	17364	38	190	
17260	47628	A	17365	134	523	
17261	47629	B	17366	1	1776	

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17262	47630	A	17367	394	554	
17263	47631	A	17368	22	831	
17264	47632	C	17369	1	1191	
17265	47633	A	17370	199	647	PSVPTEGSRNRTTAVAVEERQS DGSGSLSPGKLQTTTGIIPALL HITGAPVSSDFRLDWLIERPKG GRRRAELSISSLALPLPQHCGSD NDWIPLQLRLLSRAFSFHSDDL GFGAYRRLALHILCHSSKEALE LNTFQPVTLNAFSK
17266	47634	A	17371	1	2697	
17267	47635	B	17372	25	1698	
17268	47636	A	17373	2	218	ASLRSSPPFSRSLRCQGKNTPERS GLPKALFCTKPSR ADLGPAGH RRPLPSVQPG* AIPGRVSRGEKN LTNR
17269	47637	A	17374	2	2543	
17270	47638	A	17375	198	403	PQALREHSPSV*TGRQDRQLLF KDCTCQRQRDVDSVQKGKRL HISSPQGLNSFPAVSLKLEHNV KAE
17271	47639	A	17376	58	543	VLYRSSRMCRKIRVLISRPFSIV KICERVLSQTSGGRHDYAAAA VSKTGQKRIHSSGTRGSGAPHS PGWWEPSPDRVGVSICFLSLK YRLFSSCLVQPCLGVLGNNSC SPEGPREPSPSHGLGFPKMC* TQVPASTTQSDNGQNHPNGCP MPISPD
17272	47640	A	17377	14	701	
17273	47641	A	17378	91	309	GRKQFPHLATGKEGCVGGQRL PCVTVELIFPAPAGAAVPRRP*L PRTAPS*LHCLPVCRMPGEAPT ARHAAWV
17274	47642	A	17379	2	2625	
17275	47643	A	17380	I	1752	
17276	47644	A	17381	3257	3412	
17277	47645	A	17382	I	1091	
17278	47646	A	17383	233	1148	
17279	47647	A	17384	I	1716	
17280	47648	C	17385	162	356	

SEQ ID NO: NO:	SEQ ID NO: of peptide sequence	Met no	SEQ ID NO: in USN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, ^=possible nucleotide insertion)
17281	47649	A	17386	836	2106	AKKFRKRWPLEEPQQEQNVPDGG AAPVTALRKRTVSQRCSELPLE DAVGCPAQRYTPPSAPSSTTP LGLPLT/TCGARGSWEEKSDLC PLPCRTKHTSGSPRHKGGLKTH FIKNMRQYDTRNSRIVLICAKR SLCAAFSVLPYGEGLRISDLRV DSQKQRHPSGGVSVSSEMVFEL EGVELGADGKVVSYAKFLYPT NALVTHKSDSHGLLPTPRPSVP RTLPGSRHKPAPTKSAPASTEL GSDVGDITLEYNPNLILDDPQWP CGKHKRVLIFASYMTTVIEYVK PSDLKKDMNETFREKPFHVKLT LSKIRSLKREMRSLSEECSELPEV TVAMAYVYFEKLVLQGKLIKQ NRKLCAGACVLLAAKISSDLRK SGVTQOLIDKLEERFRFNRRDLIG FEFTVLVALELALYLPEPNQVLP
17282	47650	A	17387	1	2531	
17283	47651	A	17388	1	1506	
17284	47652	A	17389	34	576	
17285	47653	A	17390	112	1840	EELRVREHVTGGICGGSQMMV DLLGATTLELVAWAPWVMSAA AGGKNLKSPHKVEVDIIDDNF1 LRWNRSDESVGNTFSFDYQK TGMDNWKLSGCQNITSTKCNF SSLKLNVYEEIKL.RIRAEKENTS SWYEVUDSFTFPFRKAQIGPPEVH LEAEDKAIVIHIPGKTDKDSVMW ALDGLSFTYSLLIWKNSSGVEE RIENIYSRHKIYKLSPETTYCLK VKAALLTSWKIGVYSPVHCIKT TVENELPPNIEVSQVNQNYV LKWDTYANMTFQVQWLHAF LKRNGPNHLYKWKQIPDCENV KTTQCVFPQNVFQKGYLLRVQ ASDGNNNTSFWSSEEIKFDTEIJQAF LLPPVFNIRSLSDSFHIIYGAPKQ SGNTPVIQDYPLIEEIJFWENTS NAERKIIIEKKTDVTVPNLKPLT VYCVKARAHTMDEKLNKSSVF SDAVCEKTKPGNTSKIWLIVGI CIALFALPFVIYAAKVFRLCINY VFFPSLKPSSSIDEYFSEQPLKNL LLSTSEEQIEKCFIIENISTIATVE ETNQTDEDHKKYSSQTSQDSG NYSNEDESESKTSEELQQDFV
17286	47654	A	17391	3	373	

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17287	47655	A	17392	1	432	LPRFVGQQPRPLGPLRSGSGSEGCRAPGEAVRAPDYAFPIPGTRA/S/PLNRLPGLGTAWPOAHPTNP/KPAPAPGAQLDDPPRYSRHGLSRWGLPLQLSLVLLPPLQRPMPLQ/AAAPNTPWWPWTLRAGRREN/AHAQRKLHLWAGKVE
17288	47656	A	17393	98	376	
17289	47657	A	17394	1	364	
17290	47658	A	17395	1	1230	
17291	47659	A	17396	892	2004	RRMSFMSEVVLVGEMLSPFDQSGLGAEEESLGLDDYL\EVAKH/KPHGFSSDKAKAGLLPGLAV/DGLVSPSNNSKE\DAF\SGTDW/DVGRKWLKEFDGCPCLGIE*PWEETIARLTFLTTFGIDICDSLLP/P*FQGRLIKAAPPRLNP1IGHLPLQFLTKPRPGLAPFT\QQLP\PLSPGVU\SSTPDSFPFSFRSGS*KWDIH*KGD*RKPDYTAYYA/MPQCIKE\EDTPSD\ND\SG\ICMSP/ES\YLGSPQHSP\T\RGSPNRS\SPSPVLCGSARPKPYDPPGKEMVAAVKGEKLDKLLKKMEQNK/TAATRYQQKKRAEQAELTGECKEKKNEALKERADSLAKEIQLYKLDDIEEVRKARGKKRVP
17292	47660	A	17397	43	1300	DSCCIQGTMRLSRQQRPVGEGSLKQHQRLHSNFSNINESVFIVS/FSNLNTIGSGGRGAEGEP/GREPLSRPQPPAGPLGGALPAPP/SLMPQL*SE*GRLQLLYLLQ/PAVCSCSRCASPRSRVCARPAARTGLPTPAPASSP/CSRSLSRSSRLSSSCRSSCCHSLSSCCRLSSSLSLSSSLSCSSCRLSSCSLSCNSFTSSSLSLSSSLSCSSCRLSCNSFTSSSLSLSSSLSCPGSFS/CSHSLSSCSRSLSSCSHSLSSCSRSLSSCSHSLSSCSRSLSSCSHSLSSCSRSLSSCSHSLSSCSRSLSSCSHSLSSCSRSLSSCLFRRLNI
17293	47661	A	17398	288	574	

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17294	47662	A	17399	230	648	VIAPGLWMMAADIPRVTTPPLS LVQVPQEEDRQEEEVTTMILED DSWVQEAVLQEDGPSEEPFPQS AGKGGPQEEVTRGPQAGLGRL RELCCRWRLPEVHTKEQMLTM LPKEIQAWLQEHRPESSEAAA LVEDLTQTL*DSWVQEAVLQE DGPESEPPQSAGKGGPQEEVTT RGPOGALGRLRELCCRWRLPE VHTKEQMLTMPLKEIQAWLQE HRPESSEAAAALV ред LTQTL
17295	47663	A	17400	105	381	SSGFWPLRFPLDVIAVSTIAVH EKEESLWPRVAVFSTLAP/ESP WGEAPQSAGR*SGVPEDHVHL RYRGTLSSLACCSSRHHPQAQLS HYKN
17296	47664	A	17401	1023	1915	
17297	47665	A	17402	3	277	QVLLQGALLLITVAQAGRVLK LGVSRREFQDLILWKGKETFRR/C PGCSPALHILQPGSSIP/SSQOLL *YLAEEQPLHRGPPRTPAPVSGAE
17298	47666	A	17403	3	299	
17299	47667	C	17404	46	398	
17300	47668	A	17405	171	403	GKNSTLQQFNNILHYSSITVAV NNPTLGNNSVSPFLYIILFTGIHQ LVKVLRLKG*RFGLELASLSL LFLPPVSLF
17301	47669	A	17406	291	467	
17302	47670	A	17407	2	395	DHAYVFLGRTACYLMKAYRK VNPRVIFSSNTIETHPKDLLHSC DHPFAEKQTQFTVSTLDDVKNSG SIRDNYCRTSEISAVIDTECVS VMLQAGTPPLQVK*RKNFQQR KQG*KMKWDPDSDISNSMAEV
17303	47671	A	17408	1	149	EKEIPGPWLLGAMRFRFCGDL CPDWVLAIEISTLAKIPL*SCGCS AARY
17304	47672	A	17409	555	1156	QFYNKTPSRSECNPNLLHHMRTE GPPGVVDQPDGHQAGWPPPPEP AGQQQRGRQSGCHLQQGQASPR PSCGTIVHARACTPPASCPCPCHR YRSHLQRGKWWPK/GLPQHTR LDHTEVLGAAEGSTVSAVPSAT RAARDHVRLLQTRKCFCKGAL LLLITAARAGRVLFGQQOLLQF TGQGFAIDTVLGRTEDETQHC HCGLHIA
17305	47673	A	17410	3	366	
17306	47674	A	17411	408	1702	
17307	47675	A	17412	1	2661	

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17308	47676	A	17413	2	2288	
17309	47677	A	17414	1	1992	MGDFNTPPLSTLDRSMRQKVNK DIQELNSAVHVQVLDIYRTLHP KSTEYTFFLAPHRTYSKIDHIVG SKALLSKCRTEIIRNCLSDHSA IKLELRINKLTQNCSTTWKLNN MLLNNDYWWHNEMKAIEKMF ETNENKDITTYKNLWDTFKAVC RGKFIALNAHKRKQERSKIDTL TSQFKELEKQEQTHSKASRRQE ITKIRAELEKEIETQKTLQKINESR SWFFEMISKIDRPLARLIKKE KNQIDTIKNDKGDIIHTDPEIQT IREYYKHLYAIKLEELMENDKF PYTNTLPRLNNEEEIESLNRTITGS EIEAIKSLPTKKSPGPDGFTAKF YQRYKEELVPFLLKLFQSIEKE GILPNSFYEAISIILPKP/DVGSS QGNQAGERNKGYSFRKRGSQI VPVCR*YDCTFRKSHFLSPKSP* ADKQLQQSLSR1QNQCAKITSIPI HHQQTNRREPNEH*TP1HNCFKE NKIPRNPTYKGCEGPLQGELQT TAQ*NKKGHKQMEEHSMILMD RKNQYRENGHTAQGNLQIQCQH PHQATNDFLHRIKGKNYFKVHM EPKKSPHCQDTPKQKE*SWRH HAT*LQTILQGYSQNNSMVLVP KQRYRPMEQNRLRNNTTHLQ QSDL*QT*QKEEMGKGFP1**M VLGKLASHM*KAETGSSLYIL
17310	47678	A	17415	1	1677	

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17311	47679	A	17416	1	2178	MGDFNTPLSTLGRSTRQKVNK DTQELNSALHQADLIDLYGTLH PKSTETYTFFSAPHHTYSKIDHIV GSKALLSKCKRTEIIITNCLSDHRA AIKLELRKKLTQNRSSTTWKLNN NLLLNNDYWVHNEMKAEIKMFF ETNEKDTTYQNLWDTFKAVC RGKFIALNAHKRKQERSKIDTL TSQLKELEKQEQTHSKASRRQE ITKIRAEELKEIEITQKTLQKINESR SWFFERINKIDRPLARLIEKRE KNQIDATKNDKGDIITDPTEIQT TTIREYYKTLANKLENLEEMDK KLLDTTYTLPRLNQEEEVESLRP TGSEVVVAINSLPTKNSPGPDGF TAKYYQRYKEELVPFLKLKFQS TEKEGILPNSFYEASIIILPKPGR DTTKKENFRPISLMNVDAKILN KILANRIQQHKKLIHHHDQVGFI PGMCGWVNICKSINVQHINRT KDKNHHMISIDAEEKAFDKIQQP MLKTLNKLVLLEVLAIRQK JKGIGLQKEEVVKLSLFADD YLNPIISAQNLLKLISNFSKVS GYKINVQKSQAFLYTNNRQTES QIMSELPTIASKRJKYLGQLTR DVKDLFKENYKPLLNEIKEDTN KWKNPICSWIGRINIVKMAILPK VIYRFNAIPIKLPMTTFELEKTT LKFIWNQKRARITKSILSQKNK AGGITLPDLKLYYKAIVTKTA WYCYQRNIDQWNRTEPSEIM
17312	47680	A	17417	1	1770	
17313	47681	A	17418	1	1101	
17314	47682	A	17419	1	1614	

SEQ ID NO: NO:	SEQ ID NO: of peptide sequence	Met no	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
17315	47683	A	17420	1	1878	MVLALTGNKADLASKRPLEFQ EAQAYADDDSWLFMETSAGK AMNVNEIFMAIAEKLPKKNPKQ NAAGAPDRNQGYLSACEFSGR KLKPQTTKHIKQSILRTKLCGAS YASSNLIPRKLYEPPLVIPRKTG SGVDLQQPTTDLQLWVLTVRR KSNKQKGYPHQNPICMLPSSKT KDFKPTKIKRDKDGHYIMVKG SIQQEELTVLNINAPNTGAPRFI KQALRDLQRDLDHSHTIIMGDFN TPLSTLDRSTRQKVNKDQIQLEN SALHQADLIDYIYRTLHPRSKDY TFFSAPHHTYSKIDHIVGSKALL AKCKRTEITRNCLSDHSAIKLEL RIKKLTQKCSTTWKLNNLLNND YWVHNEMKAEIKMFFETENENQ DTTYQNLWDTFKAVCRGKFA LNAHKRKQERSKIDILTSQALK LEKQEQTHSKASRQRQEITKIRVE LKEIKTQKTLQKINESRSWLFE KINKIDRQLARLIKKKREKNQID AIKNDKGDJITTDPTEIJQTIREY YKHLYAKKLENLEEMDKFLDT YTLPRLNQEEVESLNRPITGSEI EAIKSLPAKKSPGPDGFTAEFY QRCEKELAQFLRLFKSTKEGI LPNSFYEDSIIL/ILPKPGRTTK KENFRPISL
17316	47684	A	17421	1	1761	
17317	47685	A	17422	1	1875	
17318	47686	A	17423	1	1611	
17319	47687	A	17424	1	4539	
17320	47688	B	17425	1	6294	
17321	47689	A	17426	2	1913	
17322	47690	A	17427	1	1026	
17323	47691	A	17428	1	2112	

SEQ ID NO: NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USNN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, !=possible nucleotide deletion, !=possible nucleotide insertion)
17324	47692	A	17429	I	1884	MENGDELREEGFRRSNYSELQ EEIQTKGKEVKNIEKNLDECITR IPNTEKCLKKLMELKTKARELR EECISLRSRCDQLEESVSMED EMHEMKREGKFREKRKRNSEQ SLQEIWDYVVKRPNRLIGVPED RSMRQKVNKDTQELNSALHQ DLIDIYRTLHPKSTEYTFsapH HTYSKIDHIVGSKALLSKCKRT EIIITNYLSDHSAIKLEKKIKLTLQ NFSTTWKLNNLNLNDYVWHN KMKAIEKMKFFETENENKDTTYQ NLWDTFKAVCRGKFIALNAYK RKQERSKIDTTSQALKLEKELKQE QTHSKASRRQEIITKIRAELEKEIE TQKTLQKINESRSWFFERINKID RPLARLIKKREKRNQIDAIAKND KGDDITTDPTEQTTIREYYKHLY TNKLENLEEMDKFLDTYTLPRL NQEEEVESLNPITGESEIVAIHSL PTKKSPGPDGFTAQFYQRYKEE L/RNKIPRNPTYKGCEGPLQGEL QTTAOGNQKRGDKQMEEHSM MGRKNQYRENGHTAQGNLQIQ CHPHQATNDFLHRIGKNYFKV HMEPKKSPHRQVNPKPKEQSW RHHAT*FQILLQGYSQNQNSMVL VPKQRYRSMEQRNRLRNNATY LQLSDL*QT*EKQAI
17325	47693	A	17430	I	1695	
17326	47694	A	17431	I	3779	MELKTKARELREECRSLRSRRN QLEERVSAMEDEMNEMKREG KFRERKIKRNEQSLQEIWDYVK RPNLRLIGVPESDAENGTKLEN TLQDIIQEDFPNLARQANVQIE IQRTPQRYSSRATPRHIVRFT KVEMKQKMLRAAREKDFKPT KIKRDKEGHYIMVKGSIQQEEL TILNIYAPNTGAPRFIKQVLSL QRDLDSHTLIMGDFNTPLSTLD RSTRQKVNKDTQELNSALHQ DLIDIYRTLHPKSTE
17327	47695	A	17432	I	735	
17328	47696	A	17433	I	2541	
17329	47697	A	17434	I	1461	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met/	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, ^=possible nucleotide insertion)
17330	47698	A	17435	2	429	AACAAAMSLVPIEKFQHILRVL NTNIDGRRKIAFAITASSSSSSSS SSSSSSSSSSSSSSSSSSSSSSSSSSSS SSSSSSSSSVNLLSNGLYL/VKG VGRRYAHVVLRKADIDLTKRA GELTEDEVERVITIMQNPRQYKI PDWFL
17331	47699	A	17436	1	615	
17332	47700	B	17437	264	556	
17333	47701	A	17438	1	406	FFFFFLQKVQYIYLHIFTQQHRL WVTSAAFLSLSMAAVGTSSL SENSGPGHGGKQTF*GP/EGTDI PEGRHIFSAQAFSVVAGRTA AALLHGSHVPQGR^SRIGSRSGG PPSHPDTCSGSSHSAGRSCPHTC TG
17334	47702	A	17439	3	3484	
17335	47703	B	17440	42	367	
17336	47704	B	17441	203	382	
17337	47705	A	17442	22	266	YRDLPHFLLNSDLIFNMNSTSLRE TMILIRTLSRVP/PLHGVIQPIS KIQGLVLNALNQVQESIFQVSF NLFPDAFQHVIRA
17338	47706	A	17443	1	1137	
17339	47707	A	17444	1218	1482	QSPWPSLRLGDVSITPPLNIFSC SIGWPFCLV/SFC*PKK*TFQGV GSEVYDVKHFAASCVLCHKQMN KLNLYFRNTYFVALLSTELFEN
17340	47708	A	17445	2	377	
17341	47709	A	17446	1	211	
17342	47710	A	17447	2	732	CSSPSN/TILGVQKLNQSWRLA QDFRLINEAVIPLYPVVPNPYTL LSQIPEEAEASFVTLSDLKDAFFCIP LHSDSQFLFAFEDPTDHNSQLT WMVLPQGFRDSPHLFGQAAQ DLVHFSSPGTLVVQYMDLLL ATSSEASCQQATLDLLNFLANQ GCKRKGIALGVLTQTHGTTPQP VAYLSKETDVAAKGPLTAILL LAFGPCIFNLLVVKLVSSRIDA LQMVLQMEPQMSSTNNFYRGP

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met/Asp	SEQ ID NO: in USNN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=>Stop codon, /=possible nucleotide deletion, !=possible nucleotide insertion)
17343	47711	A	17448	I	3003	MPGAQDLQPTMPPEPPHPQWPATWPEPPRVRVPPAPRPPVPLTAQGLSVDQSRLGKFSDDPDRYIDVLQGLGQTFDLYTWRDVMLLLDQTIAFNEKNAALAAAREFKDWTYLSQVNDRMTAEERDKFPSSGQQAVPSMDPHWDLDSDYGDWSHRYLLTCVLEGLRRRKPKMVNSMMSTITQGKEENPAFLEQLWEALRKYIPLSPKSLEQLILKDFITQSAAIDRGLQKQLQSVLPENQNLEALLNLATSVFYNRDQ
17344	47712	A	17449	5	624	IOPILAYPHPKTLKQLWGFLGIT/GFCPVWIPRCNSKIAKSLSYTLIKE TQRANTHLVEWEPEAETAFKTLKQALVQAPTLSLPTGENFSLY VTERAGIALGVLTQTRGTTPQPVTYLGKDFEPMKCDCQIIQVQTYATQDDLLEVPLANPDLNLYTDGSSFVENGIRRAGYAIVSDVTILESKPLPPGTSAQLAELVALTRALELGKGE
17345	47713	A	17450	636	2628	SNDRTEDDCGKHPFMSSPPATEP WVCLIEGQEIDFLLDGTTFSVLIPCLGRLLSSRSVTIQGILGQPVTRYFSHLLSCNWETLFLSHAFHLVMPESPTPLLGRDILAKAGAIISMKTGNKLPICCPLEGINPEVWALEGQFRAKNAHPLQIRLKDPISFPYQRQYPLRPEAHKGQLDIVKHLKAQDSVRKCCSSPCNTPLIGVQKLNQSQRWLVQDLRLINEAVIPLYPVVRNPYTLLSQVPEEAEWFTVLDLKD
17346	47714	A	17451	2	568	CSSPSN/TILGVQKLNQSWRLAQDFRLINEAVIPLYPVVPNPYTLLSQIPEEAESFTVLDLKDAAFCICPLHSDSQFLFAFEDPTDHNSQLTWMVLPQGFRDSPHLFGQAAQADLVHFSSPGTLVVQYMDLLLATSSEASCQQATLDLNLFLANQGCKRKGIALGVLTQTHGTTPQPVAYLSKETDVAAK

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met/	SEQ ID NO: in USNN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, v=possible nucleotide insertion)
17347	47715	A	17452	254	849	LQPESLEIAGILVQ*MIE*QPKK GTNSIPVSKPSP/GVQKPNQW RQVQDQLRLISDAV/PLVPAVSNP YTLLSQILEEAEWFTVLDLKDA FFCIPLRSDSQFLLA/FEDPTDHT SQLTWTVFTQGFMDTPHLFGQ SLAQDGLGHFSSPGTLVQLVQYDD LLLAKQQATLDLLNFLANQGY KLSKLKAQLCELLVFSSCARMH
17348	47716	A	17453	1	369	
17349	47717	A	17454	1	1632	
17350	47718	A	17455	636	1837	SNDRTEDDCGKHPFMSSPP/TEP WVCLIEGQEIDFLLDITGTTFSV LIPCLGRLLSSRSVTIQGILGQPVF RYFSHLLSCNWETLLFSHAFLV MPESPTPLLRDILAKAGAIISM KTGNKLPICCPLEGINPEVWA LEGQFRAKNAHPLQIRLKDP1 SFPYQRQYPLRPEAHKGQLQDIV KHLKAQDSDVRKCSSPCNTPILG VQKLNSQWRLVQDLRLINEAVI PLYPVVRNPYTLLSQVPEEAEW FTVLDLKDAFFCIPLHSDSQFLF AFEDPTDHTSCLMWMVLPQRF RDSPHLFGQAQAOQLGHFSSPG TLVLQYSEIAKTLTYLIKEMER ANTHLVEWEPEAETAFETLKQ ALVQAPALSLPTGQNFAVYIE RAGIALGVLTQTHRITTPQPVAY
17351	47719	A	17456	2	52	EISFVENGIQRAGYAI/SDVTVL ESKPLPLGTSQALAEVLALTRA FELGKGKRINANTDSKYAYLIL HALAAIWKEREFLISGGTPKYH KEIMELLHAMQKPEVAVLHC QSHQKG*EWDTKGRLCHS
17352	47720	A	17457	1625	2505	PGVQKPGQWRLVQDILRLINEA V/PLYPVVPKPYT/LSQIPKEAE SFTVLDLKDAFFCIPLHSDSQFL FAFEDPTDHTSQLTWTVLPQRF RDSPHLFGQALVQDLGHFSSPG TLVLQFVDDLLAASSEASCQQ ATRDLLNFLANQGYKASKSKA QLCLQQVVKYGLGLIARGTRALS KKRIQPILAYPRPKTLKQLRGFL GITSFTRLQIPGYSKMARPLYTL IKETQRANTHLVEWEPEAETAF KSLKQALVQAPALSLPTRQNFS LYVRERAGIALEVLTQTHGTTL QPVAKG
17353	47721	A	17458	1	2415	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met/hod	SEQ ID NO: in USNN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=-Stop codon, /=-possible nucleotide deletion, <=-possible nucleotide insertion)
17354	47722	A	17459	2646	5167	KNSGHILGTCPGYRYAKGKET GKEIKGPQNPPGYRQLCPLQAV GGGEFGPTQVHVPPFSLSDLKQI RVDLGKFSDDPDRQYPLRPEAH EGLQDILRYLKVQGLVRKCSSP CNTRLGVQKPKGQWRLVQDL RFINEAVPLHHSVVPNSYIILSQI PEEVEWFTVLDLKDAFFCIPHLH SVCQFLFAFEDPTDIIITSQFTWT VLPOGFRDSPHLFGQLAQADLG HFSSPGTLVIQYVDDLLATSL EASCQQATLDLLNLLAQGYK ASKPKAQLCLQQVKYLDLSLA RVTRALSKERIQPILACPRPKTL KQLRGFLGITNFQCLWIPGYSE MARPLYTLIKEETQRANSHLVER EREAETAFKTLKQALVQALALS LPTGQNFSLYARERAGIALGILT QTHGTTPQPVTYLRKLISYFVE NGMRRAGYAIIVSDTVPEKPL PPGTSTQLAELVVLTQAELERK KKRINVNNTDSKYAYLILHAA IWKEREFLTSGGTNPKNYHKEMI ELLHAVQKPKEVAVIPCQSHQK GEEK/EAEGNRRADEAKIAA RRNLPTIPMEGFLVWNNPVQE IKPQYSLTKEWGLSQQGHFSFLP LGWLTTLEGKAGRATPNPRNV YFPLHLRLGLRTGRPLPSQSTRA QEMTLVRPPRPSSSPPPEKAAEG RGRRCSSETKLHRHRLRPLRTP LCATAPLAASVAAVLAAPAA
17355	47723	B	17460	1	2208	
17356	47724	A	17461	2	168	
17357	47725	A	17462	890	1034	
17358	47726	A	17463	386	619	TFITGDCLGTKN/IIIFDGCGVLS EVGLVLDCSNQRFKAGPA*LCQ SPFKNIL*ESLPMCMCRQLEKH AHPQGLCHTQVT

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met/hd	SEQ ID NO: in USNN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=>Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
17359	47727	A	17464	123	2169	DLGHGRSREMASVAVLEDVAV NFTREEWALLGCPQKNL,YKDV MQETIRNLDCCVGMKWDQDNIE DQYRYPRKRNLRCRMRLERFVES KDGTCQCGETSSQIQLDSIVTKNT LPGS/VGPYESRMSGEVIMGHSS LNCYIRVGAGHKPHEYHECGE KPDTHKQRGKAFSYHNSFQTH ERLHTGKPKPYDCKECGKFSSL GNLQRHMAVQRGDGPVKCKL CGKAFFWPSLLHMHERHTGE KPYECKQCSKAFTSYSSRLRHE RTHTGEKPYECKQCSKAFFPYS SYLRHERHTGEKPYKCKQCS KAFPDSSCLIHERTHTGEKPYT CKQCGKAFSVSGSLQRRIETTHS AEKPYACQQCGKAFHHLGSFQ RHMIRHTGNGPHKCKICCGKF DCPSSLQSHERTHTGEKPYECK QCGKALSHRSSFRSHMIMHTG DGPBKCKVCGKAFVYPSVQF HERHTAEKPYKCKQCGKAYR ISSLRHETTHTGEKPYKCTLG KAFIDFCSFQNHKTTHTGEKPY ECKEGKAFASRFRYLSRHKRTH TGEKPYECKTCRAFGHYDNL KVHERIHSGEKPYECKEGKAF SWLTCFLRHERIHMREKSYEC QCGKAFTHSRLFQGHEKHTTG ENPYECKECKKAFASLSSLHRH KKTHWKKTHTGENPYECKEG KAFASLSSLRHKKTHWKTKH
17360	47728	A	17465	1	1317	
17361	47729	A	17466	1	336	
17362	47730	C	17467	51	353	
17363	47731	A	17468	190	348	YAIHIMDVHTVRSLYYFNCFRY *ACYCCHYLTDIPEITKLSGCSY GGTSLIWG
17364	47732	A	17469	1	1716	
17365	47733	A	17470	1	840	
17366	47734	A	17471	699	1283	LLTARLTWVSARLMYSVLLMC *LFPRLLSLCLTPPHCSICFV C/FKNVLDKGFEPPDVRLLTJKY NSNGSQSPWMEEQIRDAGERV HSAFSLNWKGPLVFEKDRPYSV SFIGLFLPMAEKTGPLKGNGP GEFLFLRQIQLVWLPAGIMT EHYFPITATQALEINNAISTIMEI FPTVTSFASQWITASFSV
17367	47735	A	17472	300	461	
17368	47736	A	17473	1	2451	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met cod	SEQ ID NO: in USN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=-possible nucleotide deletion, !=possible nucleotide insertion)
17369	47737	A	17474	2	3542	
17370	47738	A	17475	1	1156	
17371	47739	A	17476	1	1176	
17372	47740	A	17477	1	257	
17373	47741	A	17478	295	1353	
17374	47742	A	17479	3	1772	
17375	47743	A	17480	2	284	
17376	47744	A	17481	1	141	
17377	47745	A	17482	1	506	PHSPLWKTLCSPPSGVCCGFVT LFCNDRFACLFQLTPPPSPAWM TAAASLLASLPPALPPLNLQDA KFVEERRKQLQNYLRTVMNKV IQMVPEFAASPKKETLIQLMPFF VMGLQVGMYGLFHFGVMMMDQ PQPSLTRADESPCDRVLSPCAA HRKQRDCCLSWKAEP*FLVK* KTLCSPPSGVCCGFVTLFCNDR FACLFQLTPPPSPAWMAAASL LASLLPAPPLPPLNLQDAKVEER RKQLQNYLRTVMNKVIQMVPE FAASPKKETLIQLMPFFVGMGLQ VGMYGLFHFGVMMMDQPOPST RADESPCDRVLSPCAAHRKQR DCCLSWKAEP
17378	47746	A	17483	1	741	
17379	47747	A	17484	1	993	
17380	47748	B	17485	277	416	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USNN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=-Stop codon, /=-possible nucleotide deletion, <=-possible nucleotide insertion)
17381	47749	A	17486	686	2400	TGMSVDEKPDSP/MYVYESTVH CTNILLGLNDQRKKDILCDVTLI VERKEFRAHRAVLAACSEYFW QALVGQTKNDLVVSLPPEEVTA RGFGPLLQFAYTAKVLLLSRENI REVIRCAEFLRMHNLEDSCFSF IQTQLLNSEDGLFVCRKDAAC QRPHEDCENSAGEEEDEEEETM DSETAKMACPRDQMLPPEISFE AAAIPVAEKEEALLPEPDVPTD TKESSEKDALTQYPRKKYQL ACTKNVYNASSHSTSFGFASTFR EDNNSNSLKPGLARGQIKSEPPS EEENEESITLCLSGDEPAKDR AGDVEMDRKQPSAPPTPTAPA GLCLERSRS/GNYQOPHI/VGQK EVSNFTMGS/PLRGPGLEALCK QEGETLDRRSVIFSSACDQVSTS VHSYSGGARFLATEHQEPGLM GDGMYNQVRPOIKCEQSYGTN SSDESGSFSEADSESCPQVDRG QETGSTSDRLRSLTKLQSCSGPM FKGPTATVAATESWGTVLQNP LGCAGTGEEVYTNPPIRGRAA LVPRSPLETVYSSLPEHQTSLKQ CAQAGPGVCLLVHNHWQLLEG
17382	47750	A	17487	1	1089	
17383	47751	C	17488	295	348	
17384	47752	A	17489	1	711	
17385	47753	A	17490	1	1248	
17386	47754	A	17491	135	259	
17387	47755	A	17492	434	506	
17388	47756	A	17493	3	227	
17389	47757	C	17494	3	236	
17390	47758	C	17495	25	153	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USNN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( N=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
17391	47759	A	17496	1	1557	MASPEAVASQNDNGFSQKPPPTPLFASRSVNRLLKSRQTPRGEVESVTIDGEKTDGSWRMTVDYCKLNQVVTPIAAAVPDVVSLLQEINTSPDITLVHYIDDIMLNGSSEQEVNTLDLLVRHLCATGWEINPTKIQGSSTSVFKFLGVQWCGDCCRDPVSKVKDKLLHLAPPTTKKEAQAHUTGLFGFRRKYIPLYGVLLCPIYQVTRKAASFQWRPEQEKAQQQVAAAMQAALPLGPYDPAGPMLLEIAVADTEAVWGH/WHSA SFPSHPCCHCPMGP*TKWP*WQGWRLCMGSATWTSTHEG*PGYGHQ*VPNLPAAEINTPEAIPHHS/SRRSASYLVAG*LYWTSIMERAEHLLIWIWVCLSCMQFCQDYHPWTHGMPYPLWYSTQLCL*PRHSLYH*RSVAVGSCSWNSLVLPCSPSS*SSRVDRTVERPFEITTTMPTSQESRVQESRGSGSGTTHHHP**STSNIFASCYGITFCWSRGSSRGRNAATRRQNNNSIKL*VKIATWTLWAPPTSKL
17392	47760	A	17497	2	1120	PSKVKKEKLHLAPPTIKKEAQRIVGQLGFWRQHIPHLGALLWLQYATQKAASFEWGPEQEKAHQVQVAVQAAALPLGPYDPADPMVLEVSVADRDAAVWSLWQAPIGESQQRPLGFWSKALPSTNDYS/CFRCAIY*FMGCCQ*FGWIVRDLEEA*LENW*QRNLGKRYVDGPL*VVKNWKDCICIPCECSPTGDL,SRGGF**SSG*DPPFCGHHSASFPSHPCCRPMPG*TKWPWWQE*RLCMDSATWTSTHQSPDYSHC*VPNLPAAEETNTETSIWHHFSG*SASYLLAG*LH*TSSIMEKAEVSPHWNKHSLLWIWVCLSSMQFCQDYHPWTHSMPYPLSWYSTQHCLSLQRERHSLYR*RSAAVGACS
17393	47761	A	17498	1	1908	
17394	47762	A	17499	1	915	
17395	47763	A	17500	2	670	
17396	47764	A	17501	1	1332	
17397	47765	A	17503	151	674	
17398	47766	A	17504	1	825	
17399	47767	A	17505	134	447	
17400	47768	A	17506	98	778	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met/Asn	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
17401	47769	A	17507	1	830	MHCFIFSAAWFCFLWISLHLVERPDMAVLLFPFGRLGLMLQCPRGYWPVLLGAEWLLIYWLTAQAVGLTHFPLLMIGSLLTLLPVALISRYRHQRDWRTLLLQGAAATAAALLQSLPWLHRGKESWNALLTLTG/EPDAGPDMMSGVLAQSRQ*HLAAARSVTGFSANQLARATSGVLAAVCYQSLAPVGIAVRTVALYAILSGAADYRAGLAQWLARGADCDVDERHADRDKQSWRDLWPWTYCSGDCDSRHGAQGQKARAPPKHDQFPHAIFRG
17402	47770	A	17508	2252	2772	RSKTTAFTPLRVRRTSAHARPGPAPIAATFLPVCFPTDISGRQPISNALSIR*RSMLPMLVTAPNSSSFRVQEPS/SQTVLRADSSANFRQGVGLVRQFRRFKNTPLVGELOQPVRDVVVYRAFPLAVVVAARQAAVSLRGFLAFGKRLVNFNKLNAFDLQRFLWRINALQVDKKLITF
17403	47771	A	17509	539	1077	
17404	47772	C	17510	192	396	
17405	47773	C	17511	10	294	
17406	47774	A	17512	2	379	KRPQSGITEATSSRRQRPTTRLQGQLPGQEKRVLKATEGIANPSWGWGGAVSPLRASLTSRLRKINNHYNTENWKLPKDSVHLIPSPQAPSMPFFPLANPPWAPHPREKMWNPQIQGTNCIIVVCGP
17407	47775	A	17513	291	590	
17408	47776	A	17514	187	589	VLSFLIHRWEGDKDSLLGPNFSQTPQPSRRFICAFPWENPS*EPSYPSISDPGLLILPSKGDWVWIHLGPIFSKKPLYS*SSFLVIFYPVTPSFLFLGYKFPLAHAVFRVPETLSLLIQNSHCHGCTYYPDGPE
17409	47777	A	17515	1509	1748	IGVVRREGIPVLCFLFSKGMLPVFAHSV*YWLWVCHR*LLLF*DTSHQYLIY*EFLA*SVVDFCQRPFHLVLDFFWLVSY
17410	47778	A	17516	152	568	CQLELSCMKCPSTPVGRSLPVGCTRSGTQLRWHSPWPWSWCTVLGESLLSGLVVLFRASRPE**NPALKLPPQLPLPPDALSQGQDGFSVCKHPTGAVTFPSSGMLPLGSMTIFKILILPIHEHGMFFSLSVSSFVSL

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met	SEQ ID NO: in USNN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, !=possible nucleotide insertion)
17411	47779	A	17517	152	568	CQLELSCMCKCPSTPVGRSLPVG CTRSGTQLRWHSVPWQSWCTV LGESLLSGLVVLFRASRPE**NP LKLLPQLPLPPDALSQGDGSFV CKHPTGAVTFPSGMLGSMTIF KILILPIHEHGMFFSLSVSSFVSL
17412	47780	A	17518	152	479	CQLELSCMCKCPSTPVGRSLPVG CTRSGTQLRWHSVPWQSWCTV LGESLLSGLVVLFRASRPE**NP LKLLPQLPLPPDALSQGDGSFV CKHPTGAVTFPSGCPHTLQA
17413	47781	A	17519	I	474	
17414	47782	A	17520	1326	1712	FLYVIKALGKKQLQFGQQQILIPS IELLDYLINPGSGCVCWLWKLNK PQCYCYLIHFSGLTTELWSKVHTIL LEGHYEFLEYAADR*PICLFWSK KERQLVSFLDYSLSLHLLGSFYV VFFFFFLYLLVRLCWDL
17415	47783	A	17521	18	236	
17416	47784	A	17522	281	1005	TGWSPLQLSKATVARLPLWIPP LWAGHGLGELWLASEGYPEPSGLK LPEEGTGSNLRCASAASAGDTQA NRVWSGPAANFSRPAAEGPFA HALRQPSVHCSPLCVHEFSSSS LISENNMQYLVFCSGVRFRLIMVI SSIHILCLVPKRTRVLGRLSLTC FRFLRGPKERPTIPHSAPPGLH VIAIPLP*SFMKPSPEADAPMTG SFLKSPSEADTGTATLPVQSVVPI PLSILPILEVGGVLFT
17417	47785	A	17523	I	1524	
17418	47786	A	17524	881	1108	SRKMGAPNA**SAWSWSREGL AAP*SMFSSLSADSSADCKLPE GKVQPASTGTLTARASKDLYFC CCFSISARAS
17419	47787	C	17525	I	867	
17420	47788	A	17526	203	514	SSSTARPSQTSSAEEPTSWYRG DNPSKPMDDPLVAGVFGAIVGA ASVLGNAPLDGIETGCGAWSST NAEHTGLWLQILRKEGLKDL*N GTVPRLGRWTASPWM

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17421	47789	A	17527	1	1578	MAKKEQLLSAAPS KTN AEGQE PSGVY TTR ALGF KHK TQ PGQ TPS YP QEF ILY TND T W NASK T E PFTPLER GLK PG S Q ESS G W H L V G T P L G R S F Q R K E Q A A I F A V L Q P P L V I P R Q T G S G V D L Q Q T P T D L Q K R V L T V R R K T N S I N N K K D D H A K T T S K G H Q Q R P K V D K S T K M R K N Q C K K A T N S K N Q N V S S P K D H N S S T A K E Q N W M E N E F D K L T E V G F R S S Q F D Q V E E R I S D E K L N E I K H E D K I R E K R M K K E Q S L Q E I W E Y V K R P N L R L I G V P E S D G E N G T K L E N T L Q D T I Q E N F P N L A R Q A N I Q I Q E I Q R T P Q R Y S S R R A T P R H I I / E * H Q Q * N E G K T V K G S Q R E K * G Q E I P S G V Y T T R A L G F K H K T G Q P F G Q T P S Y P Q E F I L Y T N D T W N A S K T E P F T P L E R G L K P G S Q E S S G W H L V G T P L G R S F Q R K E Q A A I F A V L Q P P L V I P R Q T G S G V D L Q Q T P T D L Q K R V L T V R R K T N S I N D K K D D H A K T T S K G H Q Q R P K V D K S T K M R K N Q C K K A T N S K N Q N V S S P P K D H N S S T A K E Q N W M E N E F D K L T E V G F R S S Q F D Q V E E R I S D I E D K L N E I K H E D K I R E K R M K K E Q S L Q E I W E Y V K R P N L R L I G V P E S D G E N G T K L E N T L Q D T I Q E N F P N L A R Q A N I Q I Q E I Q R T P Q R Y S S R R A T P R H I G R F T K V E M I K E K R L R A V R E K S R V T H K G K L I R L T A D L S
17422	47790	A	17528	738	1323	A T G G H S N Q R Q R S * K L S K K F R R M Y N * N N Q Y R E V L K G A D A G E N Q G S T T E T L C M * R M R Q S L Q F D S D L V R H Q R K H S G E K P Y E C C E C G K A F R G S S E L I R H R R I T G E K P Y E C G E Y K S Y E C I A C G K A F G R S S T L I E N Q R I H T G E K P Y E C N E C G K S F N Q S S A L T O H Q R I H T G E K P Y E C S E C R K T F R H R S G L M Q H Q R T H T R
17423	47791	A	17529	1	656	M A G K P E Y D K T I S T I V L N A L N A L G V S A E A S G R N D L V V K T V E G D R K V S G S A Y R E T K D R G F H I H G T L L L N A D L S R L A N Y L N P D K K K L A A K G I T S V R S R V T N L T E L L P G I T H E Q V C E A I T E A F F A H Y G E R V E A E I I S P N K T P D L P N F A E T F A R Q S S W E W N F G Q A P A F S H L L D E R F T W G G V E L H F D V / G K R P Y H P R P G V Y R Q P Q P R A A G S P R R T T A R L P F L S L

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17424	47792	A	17530	1046	1401	LLDIRMLCHGKGVIHVLRLQF LLGRPAPHLRAALQLPGLSLH GTALGLWLQLRQLLILQGPF GISCGGSGCDPEQDCV/DCGRG CWPRKCPQGSAPRSRGAPHR PRPQQRAAGRQ
17425	47793	A	17531	112	1170	YPFFHLIDSTIDTCVCFTKPLCC VFQLHQVIVVLL*TGYSLFADAD DLWMGFLRGHPFC*CYCFLFVS FPSNSQAPLLQVCWSLLEVHSR PCSPGYHQRRLQNSKDCCLLLP LEALSQSGTHQMPAGALLYEM SVNPCWEEHQTDQLFTHESTFI RSKTQKKVPDKLLSDSTVTPLF KITENIGCVMGMTADSRSQVQ RARYEAANWKVYGYEIPVD MLCKRIADISQVYTRNAEMRPL GCCMILIGIDEEQGPQVKCDP AGYYCGCKATAVGVKQTESTS FLEKKVKKKFDWTFEQTLETAI TCLSTVLSIDFKPSEIEVGVVTV ENPKFRILTEAEIDAHLVALAER
17426	47794	A	17532	2244	2432	DGQQLIALHRLALRELQQAVH AGIAPAGENPV*WWFRNRQNP LIALRSLPAFQSGNLSQCLH
17427	47795	A	17533	251	546	SSISDILSSA*SIRLLILVYAS*SS RAVFFSTIRSFIFFSKLVILVSPSC NLLSRFLASFHWWVRTCSFSKEF VIITHLPLTSVNSSYSSLFSFVHF G
17428	47796	A	17534	597	1092	FTNQKESRTRWIHSRILPEVQG GTGTIPSETIPINRKRGNPP*LIL* GQRHSDTKAG\RDTTKKENFRP ISLMNIDAKILNKILANRQQHII KKLIIHDQVGFFPGMQGWFNIR K/CNKCNPAYKQSQRQK/HT*L SQ*MQKKPLTKFNNPSC*KLSIN *VLVGRISK
17429	47797	A	17535	I	2153	
17430	47798	A	17536	2164	2427	
17431	47799	A	17537	I	322	GPRWGPRVHRAPDPVRIPSSGP LLPPIRFYPRYVLP^PPSASTSRPC QRTSASGRCPCPMH/DTVKATM PIWV/DPPVPDHYEGEAEHQGIL VTHPHHQRCPAGHRHRVVF
17432	47800	A	17538	I	627	

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17433	47801	A	17539	583	1145	GNGRTVDTQVCQAPITSQSLR PADPNPGEQDAEAGPASRRDT EAERLRFRQFQYHVVASGPIHLA VGQLWTLCRQWLRPEARSKEQ MLEVLVLEQFLGALPSKMRWT VQSQQPRSCREAASLVEDLTQ MCQQEGLAAHPSHDTAIRGIPR LAASWETASAMEATADARQKR THTEKEAWLLEAPHELA
17434	47802	A	17540	1	1301	
17435	47803	A	17541	1	1232	
17436	47804	A	17542	1	549	MNTANVEKPYVQKYQTAFVLV MKHRQCQLASHLVQNYRS/IQL WAWEKIQDPGTTCPFSFTTQG SKKPYPDFVARLRDAAQNSITD ENARKVIVELMAYGNANPECQ SATKPLKGKVPTGSDVSDQKA VGVQAAKRRNRTDTGLGRSAR KSGKGVTRMLPKHASMILDGG GPATSPSCRCR
17437	47805	A	17543	146	510	SPYWNKGKSPGWLAESIFKRPV FRQGAKIEPYPDFAASLQDAAQ KSIITNENARKVIVELMAYNAN PECQSAIKPLKGKVPGVSDVSR GFQQQOPPLSQQVLQGMGQLPQ YSNCPRPQAAVQQ
17438	47806	A	17544	2	828	
17439	47807	A	17545	1	420	
17440	47808	A	17546	1	1947	
17441	47809	A	17547	1	399	PLKVNIYPDSKYAFHIIHLHHIER GFLTTQGSSIINASLKITLLKAA LLPKEARVIHCKGHQRASDPIA QDNAIHTDKIAKKAAASIPTYTPH FQFFSSVATPTYSPAETSTYQS LPTQGKWFLDKETYFLPASQ
17442	47810	A	17548	1	2382	

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17443	47811	A	17549	1	2194	MAPEQGRVSILQLTLFIEYHGYSIFVVKGDLPDCEADQLLQMIRVQQMHRPKLIGEELAQLKEQRVHKTDLERVLEANDGSGMLDED EEDLQLRALSRQEIDMEDEEEA DLRRAIQLSMQGSSRNISQDMT QTSGTNLTSEELRKREAYFEKQQQKQQQQQQQQQQQQGDLSGQSSHPCERPATSGALGSDLALLTQSLSFGSLFTWTRVTFGAEDPGQEDSFRRRVPCPCPHSVRRSTYDLGSSDQPAQGTSHFQIGILLTRLSQVPILPQPPVPHPIIILSPPPHTVSGLQFLSVPSPPLPAQQFLLKEVAGAEGIAKVIPTCPVPLIGQDILTKLSASLIPIGLQPHLJATL LPNPKPPSPLPLVSPVNLPQVWDTSTPSLATDQTPTIPPLKPNHPYLAQCHYSIPQLALRGLKPVITRLLQHGLLKPINSSYNSPILPVQKPDKSYRLPQDLDLINQIVLPIHPVASHPIIPDTTPDPHDICSLIHLAFTFPHTSFPPIPHPDHTWFIDGSSTWPNRHSPAKVGYAIVVSTSILEATALPSTTSQQAEIALT RALALAKGLHVNIYTDISKYAFHILHNAVIWAERGLFLSTQRSSIHASLIKTLKAALLPKEAGVIHCKGHQKASDPIAQGNAYADKS DNGLAFTSQII/HKQFLRLLVFS GTIPLTVNLQERTGQYFYLLPFTELEPVLEKLQGTVHLNFYMD
17444	47812	A	17550	1	355	
17445	47813	C	17551	99	335	
17446	47814	A	17552	21	447	LGPLPFSLSPCCLHCQGKRLCGHHEEARRRKNVSPRKEAGIHC KGHQK/A/SDPIAQGNAYADKT KFLDLAFTPRLSFTCQITQAVSQALGIQWNLHTLTILNLNQKRIRACPODATGYSPELLYGCSFLLGPSLIPDTSP
17447	47815	A	17553	119	239	TQKGQRAALFLICILSPSPLPTLGKNFKN*IPALKPHNRI
17448	47816	A	17554	1	798	
17449	47817	B	17555	460	1059	

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17450	47818	A	17556	3	1476	IPTCPVPLLGQDILTKLASLII <sup>P</sup> GLQPHLIATLLPNPKPPSPLPLV SPNLPNQPVWDTSTPSLATDQTP ITIPLKPNH <sup>P</sup> YLAQCHYSIPQLA LRLGKPVITRLLQHGLLKPINSS YNSPILPVQKPDKS <sup>Y</sup> RLPQDLD LINQJVLPIHPVASPHJPD <sup>T</sup> PD <sup>P</sup> HDCISLJHLAFTP <sup>F</sup> HTSSFP <sup>F</sup> IPHP DHTWFIDGSSTWPNRHSPAKV GYAIVVSSTSILEATALPPSTS QQAE <sup>L</sup> IALTRALAKLGLHVN <sup>I</sup> YTDSKYAFHILHHN <sup>A</sup> VIWAER GFLSTQRSSIII <sup>A</sup> SLIKTLLKAAL LPKEAGV <sup>I</sup> HCKGHQK <sup>A</sup> SDPIA QDNAYADK <sup>L</sup> LAKKAASVPTSV <sup>P</sup> HGISQAPPPLPTHQARYWQIDF THMPVRK <sup>L</sup> KYLLVVWVDTFTG WVEAFTP <sup>G</sup> SKKATAVISLLSDI IPQFSLPTSIHSDSLRAFISQITQA VSQALGIQWNLHISYRPQSSGK VEQTNGLLKTHLT <sup>K</sup> LSQLKK DWTVLLPLALLRIRACP
17451	47819	A	17557	24	594	VGSGDL <sup>P</sup> WEGNP <sup>L</sup> SSCLLHEK DPPTTSGPQTDQPK <sup>E</sup> HLTNFKS GCSSPGPARSQFFL <sup>S</sup> RSRSTL*SF YHLPSSHLVCLTVSFRD*PSPTC PAIDS* <sup>K</sup> GG/CE <sup>L</sup> KA/RVKEHFC HDL <sup>P</sup> ASSMQSNYPVHDSGHLT TGPSLFKPTLNIEYSTGH <sup>A</sup> PYHV RSACFPFA <sup>F</sup> CHDCQFPEASPEAE AAAILSVQPAEP
17452	47820	A	17558	1	1152	
17453	47821	C	17559	301	462	
17454	47822	A	17560	1	423	
17455	47823	A	17561	421	856	KLINLFSNFC <sup>S</sup> YSRQFLSFSSTL YFWWVF <sup>C</sup> YNRCCFSK*RMIVH <sup>I</sup> TNRDINCQIAYARIEGDMIVCA AYAHELPKYGVKVGLTNYAAT YCTGLLLAHRLLNRF <sup>G</sup> MDKIC YLDAGLARTTTGNKV <sup>F</sup> GDLDG GLSIPQ <sup>S</sup> TK* <sup>F</sup> PGYD

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17456	47824	A	17562	3	1082	GPLCIALALQEFGTRRRWACRS LSSSGRRSLFRRMGSVKAVKNK AYFKRYQVKFRRRREGKT=DYY ARKRVLVIQDKNQYNTPKY=RM VRVTNNDIMCQMLYARRIEGD MIVCAAYCTPNLPKIWW*RVGL TNY=AAAY(CTGLLLVARRLLP*/ RFGMDKIVEGQVIELTGDEYNV ESIDGQPGCLPPAYLIDAGPCSE PTHWPLKF GGAPEGKLWMMGL SIPSQYPNRFP(GYDSEKQRNFN AEVHRKAHSWGWQNCCRFTWR YFMEED\EDAYKK\QFS\QYIK\ NSVT\PDMM\EEEMY\KKAHAAI RENPV\WKRKP\KEV\KKKRW NRPKMS\LAQ\KKDRAV\QKKKAS FLQSSRSGLLES\TPAIP
17457	47825	A	17563	2	4967	
17458	47826	A	17564	56	284	RQTTRRAAGIVRGDCPASSPTNC DLGQC\NSTS\LEPRFVQTVHLL CPWT\GGSSPLLAARGSLPVSSL GPLKPMVSCAGR
17459	47827	A	17565	1	3525	
17460	47828	B	17566	35	3691	
17461	47829	B	17567	80	3787	
17462	47830	A	17568	225	507	
17463	47831	A	17569	2	2621	
17464	47832	A	17570	14	1658	
17465	47833	A	17571	1	3654	
17466	47834	B	17572	1	3570	
17467	47835	A	17573	1	3663	

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17468	47836	A	17574	485	2347	TEPKTKTT*LSQ*MQRPLTKF NNTSC*KLSIN/IVLEVLRALARQ EKEIKGIGQLGKEEVKVSFLADD MIVYLENPTVSAQNL.LKLIGNF SKVSGYKINVQKSQAFLYTNRR QTERQIMSELPTIASRKJYLG QLTRDVKDLFKEENNPKPLKEV KEDTNEWKNIPCSWVGRNIVK MAILPKVIYRFNAIPIKLPMTFF TELEKTTLKFIFWNQKRCACIAKS FSQKNKAGGITLPDFKLYYKAT VTKTAWWYQNRDIAQWNRT EPSEIMLHIYNYLIFDKPKEPNKQ WGKDSLFBKWCWENWLAICR KVKLDPFLTPYTKMNSRWKD LNVRPKTAKTLEENLGLITQD VGKDFMSKTPKAMATKAKIDK WDLIKLKSFCTAKETTIRVN PTTWEKIFATYSSDKGLISRIYN ELKQIYKKKTNNPIKKWAKDV NRHFSKEDIYAAKKHMKKCSS SLAIREMQIKTTMRYHLPV AIIKKSGNNRKIQ/GGIWCDRIL* R*TTCRVAKEIQSL*RRI/WKRL QRTLSIPVLD AV*PPMF*ASVID TMTI*CFEARDTCFTLTLESFW D MHRCLAAKGIGLLLC*PLIWH MSLMGVKSPPFVFSCLWTS AV
17469	47837	B	17575	1	3354	
17470	47838	A	17576	1	3297	

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17471	47839	A	17577	I	2563	MKAEIKMFFETNENKDTTNQN LWDAFKAAEVEESLNRPITGAEI GAIINSLPTKKSPGPDPGTAEEFY QRYKEELVPFLLKLFQSIEKEEI LPNSFYEASIIILPKPGRDTTKKE NFRPLSLMNIDAKILNKLANRI QQHIKKLIHHHDQVGFFPGMQG WFNIRKSINVIQHINRAKDKNH MIIISDAEKAFDKIQQPFMLKTL NKLGIDGTYFKIIIRAIYDKPTAN II LNGQKLEAFPLKTGRQGCPL SPLLFNILEVLAIRQEKEIK GIQLGKEEVKLSLFAADMIVYL ENPIVSAQNLKLJSNSFSKVSGY KINVQKSQAFLYTSNRQTESQI MSELPTIASKRKYLGQLTRD VKDLFKENYKPLLKEIKEDTNK WKNIPCSWVGRINIVKMAILPK VIYRFNAIPIKLPMTFTELEKTT LKFIFWNQKRAHITKSIISQKNK AGGITLPDFKLYYKATVTKTA WYCYQNRRDIDQWNRTEPSEITP HTYNYLIFDKPEKNNQWGKDS LFNKWCWENWLAIWRKLKD PFLTPYTKINSRWIKDLNVRPKT IKTLEENLGITIQQD!GMGKDFMS RTPKAMATAKAKIDKWDLKLK SFCTAKETTIRVNRQPTTWEKIF ATYSSDKGLISRIYNELKQIYKK KTNNPIKKWEKDMNRHFSKED IYAAKKHMKKCSSSLAIREMQI KTTMRYHLPVPRMAlIJKSGNN
17472	47840	A	17578	I	3514	MELKTTKARELREECRSLSRSCD QLEERVSAMEDEMNEMKREG KFRERKIRKRNEQSLQEIIDYVK RPNLRLIGVPESDVENGTKLEN TLQDIQENFPNLARQANIQQEIQ QRTPQRYSLRRATPRHIIIVRFTK VEMKEKMLRAAREKDSTRQK VNKDTQELNSALHQADLIDIYR TLHPKSTETYTFSAAPHHTYSKT DHIVGSKALLSKCKRTEIITNYL SDHSAIKLELRIKNLTKRSRTTW KLNLLNNDYW
17473	47841	A	17579	I	3693	

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17474	47842	A	17580	1577	3354	TEPKTKTT*LSQ*MQKRPLTKF NNLSC*KLSIN/IVLEVILARAIRQ EKEIKG!QLGKKEEVKLSLFADD MIVYLENPIVSAQNLKLISNFS KVSGYKINVQKSQAFLYTNNR QTESQIMSELPTIASKRKYLGI QLTRDVKDLFKENYKPLLKKEIK EDTNWKWNIPCSWVGRINIVK MAILPKVIYRFNAIPKLPMTFF TELGKTAALKF!WNQKRARITKSI LSQKNKAGG!TLPDFQLYCKAT VTKTAWFPSGDVGLEADFSPSH TLKTQFFSCLAEFAAACSCFFQR MNGFGMAMTTTGSTGAESPL PSCSIDQGDDTKLHRARSPGRT FPAAGIPAAAAPDGPPLSLH KLWFPVELGGRALPRAEESHGE VAALGVMVVAQGGKNQGEAA RSTPWLRPTSHLPPCSSSSAWW TEQTDAHPLLFLCLGIYLLNA LSNLMSMVALVRSRGALRSPMY YFLGHLSLVDVCFITVTPRLL AGLLHPGQAISFQACFAEMYFF VALGITESYLPAAAMSYDRATAA CRPLRYGALVTPWALRLAARY DRLASVYVAVITPTLNPFINSLR NKEVKGALKRGLRWRAAPQE
17475	47843	A	17581	I	3042	
17476	47844	B	17582	I	3384	
17477	47845	B	17583	I	3264	
17478	47846	A	17584	I	3780	
17479	47847	A	17585	I	3165	
17480	47848	A	17586	I	3894	
17481	47849	A	17587	I	3345	
17482	47850	A	17588	523	3981	
17483	47851	A	17589	I	3429	
17484	47852	A	17590	I	3921	
17485	47853	B	17591	I	4797	
17486	47854	A	17592	I	6499	MVKGSIQQEELTILNIYAPNTG APRFIKQVLSLDLQRDLDHTLI MEDFNTPLSTLDRSTRQKVNK NTQELNSALHQADLIDIVRTLH PKSTEYTFFSAPHHTYSKIDHIV GSKALLSKCKRTEIIINTYNSLDSH AIKLELRINKLTQSRSTTWKLN NLLNDYVWHNEMKAEIKMFF ETNENKDPTYQNLWDAFKAVC RGKFIALNAYKRKQERSKIDTL TSQLKELEKQEQTHSKASRRQE ITKIRAEKIEJTQ

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17487	47855	A	17593	1359	2520	IQCHPHQATNYFLHRIGKNYFK LHMEPNKSLHSQDNPKQKGTK LEV/CTLPDFKLYYKATVTKTA LYLYQ/NQRCRSMEQNRLRN NATYIINYLYIFDKPEPKNQWQG KDTLFNKWCWEN/WLAICRKLK LDPFLTPYTKINSRWIKDNLNVRP KTIKTLEENLGNTIQD1GMGKD FMSKTPKATATKAK1DKWDLIQ LKSFCATAKETTIRVNQRQPTWE KIFGIYSSDKGLISRIYNELQQIY KKKTNNP1KKWVKDMNRYFSK EDIYAAKRHMKKCSSLAIREM QIKTTMRYYLPLRMA1IKKFG NNRQETVR3EMA1LSSGTMDFR HRACFVLSPDFSTRWPAGA QRPPV1VVVALDSSLPPQASG QRPPSLVEDVDGAGALVAPC
17488	47856	A	17594	1	1227	
17489	47857	A	17595	2	2774	NLC5LI1PLREVTIVEKADSSSVL PSPLSISTRNRMRTFLFANLKD FLVQRISDFLQQTTSK1YSDKEF AGSYNNSSDDEVY5RPSLLVSSSP QRSTSSDADGERQFNLngNSVP TATQTLMTMYRRRSPEEFNPKL AKEFLKEQAWK1HFAEYQQGIC MYRTEKTRRELVKGIPESMRGE LWLLLSGAINEKATHPGYYEDL VEKSMGKYNLATEEIERDLHRS LPEHPAFQNEMGIAALRRVLT YAFRNPNI
17490	47858	A	17596	1	3472	
17491	47859	A	17597	1	900	
17492	47860	A	17598	1	1290	
17493	47861	A	17599	153	3834	
17494	47862	A	17600	299	1184	
17495	47863	A	17601	1	729	
17496	47864	A	17602	1	2232	
17497	47865	A	17603	36	224	TQWGPSVCWCLIPWPSFPDQ*P GF*AVLLPWRCOGFWPLLAC APAGPATAAEPAVSSPAEP
17498	47866	A	17604	1	624	
17499	47867	A	17605	1	578	RDLDLFLSPQDITL\WVYVDGIM LIGSSEQEVASTLDDLVVRHLHA RGWEINLTK1QGLATSVKFGLV QWYGA CRDIPSVKDKLHLA PPTTKEA QHLLA SFWGPEQ KGLQQVQVAVQAA1PLGLYDP ADPMVLEVSADRAVWSLW QAPIGESQWRPLGFQNKALPSA DNYS PFERQLLACYWALVETE

SEQ ID NO: NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, !=possible nucleotide insertion)
17500	47868	A	17606	1	282	PIYRVSRAAANFEWSPEQEKA QQVQAAVQAAWPLGPYDPAD PMVLEVSVDRADWSCWQA SI/GHKVGHAAQQHSIIKWKYI RDWARADPEGT
17501	47869	A	17607	1	338	SIYLVTKAA/SSEWGPEQEKA LQEVAQAVQAALEPYDPAGP VVLEVSLADRDAVWSLWQAPI GESQRPLGFWSKALPSSA/DH KACHAQHSIIKWKYIHDRA RAGPEGT
17502	47870	A	17608	1	757	
17503	47871	A	17609	1	1317	
17504	47872	A	17610	2	24	LCQRLLLAEPNEKPGSLGNVM AVARIEIGICEYYHEKTTKALD SHGVLAGSTIKGVRSFQRNLLE KLPATERATANAIELLTVLDQA YENFAPQILPSTGSPSQETAQF KANQNKPVLVRGKGSPHEAIRYI SAAHREWKPAILTSAIRFCST WLVFTSKNFPKLVTQHGHSIAG NGQSSDETQVQGAAWKSDSRG TKRQIPTWILAEGNNAGAQLDI PGPTIPAPNCNSLKVQPSWSTTPS MPSSLGKAYWLLACYWALVET E/RLAMGHQVTM/KPELPVMN WVLSDPSSHKVGGAAQHQHSINK WKWYIRNRARAGPEGTS*LPAP LIG
17505	47873	A	17611	1	1815	
17506	47874	A	17612	875	1916	PGKQGLEWTPRKLQQTCRGA GQLEEKLANRKQ*HQH*QKG*P /PQKLNAKDIINSSPTEQNWTE NEFDLTVFGFRRVITNSSL KEHVLTQCKEAKNFDKRLEEL LIQITSLEKNISDLMELKNTARE/ LLEAYTSINSQIDQAEMDR*PD* *RRKERRIK*HNKK**RGYHN*S  QEIQTTIREYYKHLYANKLENL EEMDKFLDTYTLPRLNQEEVEP LNRPITSSE EAVINSLPNQKSPG QTNSQLTSTRDAEKAFNQKIQHP FMLKTLNKLDDGTYLKITRAI/ S*QTHSQCHTEWAKGASIPFEN RHKTTRMPSLTTPIQYSIGNSGQ GNQEFWKLHLVEREW
17507	47875	B	17613	1	1158	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met/Asp	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, ^=possible nucleotide insertion)
17508	47876	A	17614	851	1344	IILKPSPSPLYPWKNCPLRNPSSLVPKRQTGSGVDIWQTAADLQQRGILLEGKLTNRKE*YQHQKQRCPHQNP1*RSPTSNTKARE/QNWTENEFDELTEVGFRRLWITNNSQQLKEHLLTQCKEAKNLEKRLEELTRITSLEKNINDPMELKNTAAEPHEAYTSINS
17509	47877	B	17615	99	716	
17510	47878	A	17616	1	588	
17511	47879	A	17617	1	1140	
17512	47880	A	17618	1	774	
17513	47881	A	17619	3	527	AENSKKQNASSPPND/RNSS/EAQNWTENEFDELTEVGFRRLWITNNSQQLKEHLLTQCKEAKNINDLMEKLRLQELLTRITSLEKNINDLMEKLNTARELREAFTSFVCVNECAVSUITSLSREDSHWLEDSKGHMR/RHQE^KCEYFHPHPGLQFYQLPESDSHSDPLWPHGGSFLSSVV
17514	47882	A	17620	1	1383	
17515	47883	A	17621	1	990	
17516	47884	B	17622	337	1515	
17517	47885	A	17623	153	474	QTKSNNVNIKKQDVHTKTPSEGHQHQRPKIDHNSLPAREQNWIENEFDELTEVGFRRLWITNNSQQLKEHLLTQCKEAKNLEKRLQELLTRITSLEKNINDLMEKLNTAA
17518	47886	A	17624	1	771	MPFSDTERVITGPSTKVHSYPGLQALLLQLRLHSLMWRWSAAVAIGVHVRC DLLAVHPVWLWAVPQWQEPIEKMLTLIPGPRITATIIGLYQHEGIRAYCDSRVYYIKPS SGIESVLTTRPSTQDHNSSSPAREQNWWTENEFDELTEVGFKKWWITNSFELKEHVLTQWKEAKNLEKRLANLLTRITSLENNINDLMEKLNTAQUELHEAYASINSRQSEERISEIEDQLTEIEQVQDKIREKRIKRNEQSL*EIWDYV

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met/Asp	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, I=possible nucleotide deletion, V=possible nucleotide insertion)
17519	47887	A	17625	53	814	PGKQGLEWTPRKLQQTCRGA GQLEEKLANRKQ*HQH*QKG*P /PQKLNNAKDHNSSPTREQNWTE NEFDELTEVGFRWVITNSSEL KEHVLTQCKEAKNFDKRLEEL LIQITSLEKNISDLMELKNTARE/ LLEAHTSINSQIDQAEMDR*PD* *RKERRIK*HNKK**RKEQAAI FAVLQQLPLVITRQTCGVDPQK TPADLQKRCRTVRRKTSQQKA VASTLTKRITTQKLNNAKDHNS PTREQNCTENEFDELTEVGFR WVITNSSELKEHVLTQCKEAKN FDKRLEELLIQITSLEKNISDL ELKNTARERWKTQVSIAKSIK QKWTASQTNKEEKREESNSTIK NDKGDIITTDPTIEQTTIREYYKH LYANKLENLEEMDKFLDTYYTL PRLNQEEVEPLNRPITSSIEAVI NSLPNQKSPGQTNSQLTSTR
17520	47888	A	17626	I	1566	
17521	47889	B	17627	I	1005	
17522	47890	A	17628	I	2172	
17523	47891	A	17629	I	504	
17524	47892	A	17630	2	1601	
17525	47893	C	17631	132	278	
17526	47894	A	17632	380	828	EVLRVMIELNAVIYPYPKDTGC QPLV*HAAASLNSPEVMGATQ LKPLRPCCKKCPKIVLEGH*EW MEARHRNLGTLHGLPCSRTHF* TTAQGEWLCLCHCGEHPQG GRHPCIC*HCYSCHTLAPPVQW TPNVAEPDNKAGAQYKSPRV
17527	47895	A	17633	I	963	
17528	47896	A	17634	2	368	EFSDPHHTFDHMWRTKEHNE AGWLSSSVDKVMKENDELGD SISQLQKQILSLKSAKIALSESЛИ SCRERTEIVEK*T*ALIMLVA Q*KVHAQPHHAQPRQVSTVK RALIVLQEVTDP
17529	47897	A	17635	I	1881	
17530	47898	A	17636	755	939	ARKNTRIIYSYGVCKNVETWR* MFCTLLGRQQGCATVGKGDR GPLRYYASWRKGDVLDQD
17531	47899	A	17637	367	423	
17532	47900	A	17638	3	1925	
17533	47901	A	17639	I	1137	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met/Asp	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, ^=possible nucleotide deletion, V=possible nucleotide insertion)
17534	47902	A	17640	153	474	QTKSNNVNIKKQDVHTKTPSEG HQHQRPKVDHNSLPAREQNWI NEFDELTEVGFRRWVITNSSEL KEHVLTQCKEAKNLERQLKE LTRITSLEKNINDLMELKNTA
17535	47903	A	17641	1	1068	
17536	47904	B	17642	1	717	
17537	47905	A	17643	585	2302	VLQLLRQERLELFVPPGELVVS LASGVKLQTFAGGKAWLQLQTH SDLGEQKLITTFPISLSLKVLVIFC NWPEAKTAAYDGEQATCEPVK KAMFLADTHLLREFLGHWLDK LRREWQVERAFQTAWLQLQPE VVFILEDFVFDGEGWSTSEA WV DDVEQFRKMFRRHPSHVQLKVV AGNHDTGFHYETNTYEVERWR NRNNPSFIMGSITPTDYLASKH LPEDVVLIYCGVKLPDRIVDS KAGLLKLPLVKNVISTQLQFPSI MDQLLVYLNLFNETSPLVMCLD VMAMMSNRGNHHHLAATRLRKV LDHNSLPAREQNWTNEFDELT EVVFRRWVITSSSELKEC/DVLT QWKEAKNLEKRLDELLTRITS QKNIINDLIELKNTAQELHEAYT SINSQIDQVEERISEIEDQLNEIK CEDKIREKRMKRNKQTLQETW DYVKRPNPWCIGVPESDGENG TKLENTLQDHIIQENFPNLRARA NIQIQEIQRTPQRYSSRRAATPRHI IVRFTKVEVKEMKMLRAAGEKE DETNDNNEFFLWSQKGKRGATL NDHVEESCPPTKNACLGTPHI C
17538	47906	A	17644	1	282	PIYRVSRAKAAANFEWSPQEKKAL QQVQAAVQAAWPLGPYDPAD PMVLEHSVADRDADWSCWQA SI/GHKVGHAAQQHSIIKWKWyI RDWARADPEGT
17539	47907	A	17645	3	903	
17540	47908	A	17646	1	349	
17541	47909	A	17647	1	489	
17542	47910	A	17648	1	352	
17543	47911	A	17649	1	505	KTDGSRWRMTVDYHKLNQVAT PVAAVVPDVVSLLQINTSLDT WYAAIDLGNVFFSIPVHKVHQK KFAFSWQGQQYTFTVLPQGYIN SPALCRHIFVRRHLDRFLSPQDI TVVHYIDDIMLVGPILYRMT KAAIFEWGPEQKALQQVQAAV QAALPLGPYDPADPMRLR

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met/Asp	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, !=possible nucleotide insertion)
17544	47912	A	17650	1	1557	MASPEAVASQDNDFGSQKPPPTPLFASRSVNRQLKSQRTPRGEVESVTDGEKTDGSWRMTVDYCKLNQVVTPIAAVPDVVSLLEQINTPSDITLVHYIDIMLNGSSEQEVNTNLLDVLVRHLCATGWEINPTKIQGSSTSVKFLGVQWCGRDARDVPSKVKDLLLHLAPPTTKKEAQHLTGLFGFRRKYIPYLGVLCPYQVTRKAASFQWRPEQEKAQQVQAAMQAAALPLGPYDPAGPMVLEIAVADTEAVWGH/WHSA SFPSHPCHCPMGP*TKWP*WQGWRLCMGSATWTSTSTHEG*PGYGHQ*VPNLPAEETNTEPAI*HHS/SRRSASVLYVAG*LYWTSCLIMERAEHLLWIWVCLSCMCQFCQDYHPWTHGMPYPPWYSTQLCL*PRHSLYH*RSVAVGSCWSNLVLP CSPSS*SSRVDRTVERPFEITTTPMTSQESRVQESRGSGSGTTHHHP**STSNIFASCYGITCWSRGLSSGRRNAATRQNNSIKL*VKIAWTWLWAPPTSKL
17545	47913	B	17651	47	838	
17546	47914	A	17652	1	1566	
17547	47915	A	17653	1	981	MVAIAKVLJIAYKEDSDSHNQPNTRMTVSKGPVSAVEGGRRGQDSDDCVEENDAVRTWPPSRILRTESHPSHTCSWRHLLSSCPYTMGSFMPSSGNISSTHAVISFPLSEEMNPMLPKATVMTSLEAAA RQNLKSRQAPRCEVESVTIIEEVYYTRKELFEFSNLVRKKSGEQIREWILRKTDGSWRITVDYRKLNQMVTPIAAVPDVVVSLLQINTSPGTWLCHNLIWRDLDCLFLPQNITLVHYTDDIMQIGSSEQEVANTL DLLPALMASW/ENSP*SIDRGRED*SLVHKWFCITCRHHPKVDSCTTAPE*DIPEGQQL
17548	47916	B	17654	179	1219	
17549	47917	A	17655	1	2655	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met/hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
17550	47918	A	17656	1	942	MVGAKAKWPKPLEPLPLRKIVNQ KQHHIPPEGIAEIAATIKDLKDAG VVPIPTSPFNNSPIWPVQKTDGS WRMTVDYCKLNQVVTPIAAAV PDVVSFLEEINTSLGTWYAAID LANAFFSIPVHKVHQKPFAFSW QG/QQYFTTVLPQDYINSLAL*H NLIWRDLDYFLLLQDITLVHYI DDIMLIGSNDHKVGGAAQQHSII KWKLHYHDQAQTCPEGTTTSVI AQWAHEQSGPGSRDGGYAWA QQHGLPLTKADLATTAECPVC QQQRPTLSPRYGTIPSLPLTKAL TLQLKKCSSGPMLEFTGLAM FPIILKQLD
17551	47919	A	17657	1	868	
17552	47920	A	17658	83	346	
17553	47921	A	17659	1	643	MVGAKAKWPKPLEPLPLRKIVNQ KQHHIPPEGIAEIAATIKDLKDAG VVPIPTSPFNNSPIWPVQKTDGS WRMTVDYCKLNQVVTPIAAAV PDVVSFLEEINTSLGTWYAAID LANAFFSIPVHKVHQKPFAFSW QG/QQYFTTVLPQDYINSLAL*H NLIWRDLDYFLLLQDITLVHYI DDIMLIGSNDHKVGGAAQQHSII KWKLHYHDQAQTCPEGTTTSVI AQWAHEQSGPGSRDGGYAWA QQHGLPLTKADLATTAECPVC QQQRPTLSPRYGTIPSLPLTKAL TLQLKKCSSGPMLEFTGLAM FPIILKQLD
17554	47922	C	17660	38	202	
17555	47923	A	17661	3	410	LKSRRQAPRCEVESVTHEEVVYT RKELEFNSNLYRKKSGEQIREW/L RKTGDSWRITVDYRKLNQMV TPAAAAPDV/VVSLQEINTSP GTWLCHNLIWRDLDCCFLPQN ITLVHYTDDIMQIGSSEQEVTI DLL
17556	47924	A	17662	2	526	
17557	47925	A	17663	2	431	
17558	47926	B	17664	55	1506	
17559	47927	A	17665	1	753	
17560	47928	A	17666	73	310	QLAEPHFWLPD*KGAGFEWGP EQKKALQ*VQAAVQAALPLGP YDPAAPMVLLVSVADKDAVWI FHLSGSDRWRRTYRCL
17561	47929	A	17667	323	687	KTDGDSWRITVDYRKLNQVVTPI AAAAPDVVSLLHEHINISPGIWH HHQKQFAFS*QQQQFT/FTV/LPH GYINSLALCHNLIRRDLDFHFSLP QDITLVHYIDDI/VTGSSEQEVA GSLESTCRHTKV
17562	47930	A	17668	3	1363	
17563	47931	A	17669	1	1203	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, -=possible nucleotide deletion, .=possible nucleotide insertion)
17564	47932	B	17670	130	1374	
17565	47933	A	17671	1	1063	
17566	47934	A	17672	3	239	
17567	47935	A	17673	231	368	NKHQEDSLKPPIPGPSSWTA/P KPTLGQKGTCCTEKKKKKKK GRI
17568	47936	A	17674	1	1270	
17569	47937	C	17675	100	270	
17570	47938	A	17676	459	1978	
17571	47939	A	17677	35	347	VVRAWYPGWGQGSEKEWQW DQQEALGRVGRSGSKVGTGEWEGR AGPEGTGQNCEGPROILEVCGT TAPFCLAEQEWGPGCHPHHLL PPSPRPPPPQPPPTPPEPPS*PPSP PRPPPQPPPTPPEPPS
17572	47940	A	17678	236	397	NWLQPCG*AHPTGSFPAPKLC PASPQAPFSNEILSEPGPTLAPM PT/GAPCRSHGAGHSQDPGWP SSPTGEDTNSAGPQAARVQMG CGHCVSLVPR*/CCWTPGGA
17573	47941	A	17679	132	492	TDHRDRKDKHPPALPASAMD KNA/GQEGRPGASGRGSSPMATA TTGPQGVMPGYH*CSLRPKGSS VGLW*MLPGLGLTLQDGLPS GPRQVQNCPGAKALNQQGPOE PA*CKASNQRPSVYLPTREYPS EQHIVTEKTNILLRYLHQQWTS RTLPRRKTRSKQRKLTGYCH YRSTGSNARPLMFIKTQGF RLVVDAAWPGTHPSQGWAPF WPKAGPELLSRSQGESESCTSRA RLMFYPTMAAPVK
17574	47942	A	17680	618	755	
17575	47943	A	17681	796	1092	
17576	47944	A	17682	1	391	
17577	47945	A	17683	1	697	
17578	47946	A	17684	1	888	
17579	47947	A	17685	749	1667	
17580	47948	A	17686	1	2088	
17581	47949	A	17687	189	438	
17582	47950	A	17688	387	497	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met/Asp	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
17583	47951	A	17689	1	728	MAQEIEGDRRLFRARLTRLRVRQKGPCGPLKAPLGMVPECHSVKPSRDTFDSKTSFKALLSFLKIP AIDVHKPIDHPINFTFPDPGHRA PARHRHSTAAAVTMSPSGP/PA AAPSPCSPIPRHG*GPLRATSYC PVSWKQKQNSVSNKQTN EQTK TAKAEGARSRGPRNKIPGLPPG PRSGLRIWLPPPREGSQFQTPAR GHPQQPCSGKGTECQSIQNLASRISPVGTSRGRTSRQTIRVK
17584	47952	A	17690	1	819	
17585	47953	A	17691	1	2115	MSGSYSSVWAEDDIQFQDSRFLE LKGDTKIDLKRFSQGQYVEPGK YNLQVQLNKQPLAEEYDIYWY AGEDDVSKSYACLTPELVAQF GLKEDVAKNLQWSHDGKCLKP GQLEGVEIKADLSQSALVISLPO AYLEVTPWDWDPSSRWDDGQ GIIADYSITAQTRHEENGDD SNEISGNGTGVNLGPWRMRAD WQTNYQHTRTQLALGEDYLN DIFDGLNYVGGSVSTDQMLPP HLRGYAPDISGVAHTTAK
17586	47954	A	17692	1	1080	
17587	47955	A	17693	1	253	
17588	47956	B	17694	1	1069	
17589	47957	A	17695	1	764	
17590	47958	C	17696	136	990	
17591	47959	A	17697	1	1422	
17592	47960	A	17698	547	1017	
17593	47961	A	17699	176	431	
17594	47962	A	17700	1	846	
17595	47963	A	17701	1	1815	
17596	47964	A	17702	1	1578	
17597	47965	A	17703	1	1149	
17598	47966	A	17704	22	441	
17599	47967	A	17705	828	920	
17600	47968	A	17706	1	231	MESKRLDNA/CAGGGD*PQLHQCPRTAVD*RRNQTAF A*RDA STYRHESGGNASPECHGLYQR QKNADGGGQRRI
17601	47969	A	17707	1	563	
17602	47970	A	17708	19	372	
17603	47971	A	17709	134	491	
17604	47972	A	17710	1	969	
17605	47973	A	17711	59	839	
17606	47974	A	17712	186	725	
17607	47975	A	17713	1	251	
17608	47976	A	17714	1381	2217	
17609	47977	A	17715	357	804	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met/Asp	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /'=possible nucleotide deletion, /<possible nucleotide insertion)
17610	47978	B	17716	I	2361	
17611	47979	A	17717	I	2832	
17612	47980	A	17718	I	3477	
17613	47981	B	17719	I<143	3122	
17614	47982	A	17720	I	3018	
17615	47983	A	17721	I	4371	
17616	47984	B	17722	I	2010	
17617	47985	A	17723	I	2168	
17618	47986	A	17724	I	2067	MKEIEIQKSLPKINESRSWFFEKI HKIDRLLARLIKKKREKNQIDTI KNDKGDITANPTAIQTTIREYY KHLYANKLENLEEMDKFLDTY TLPRLNQEEAESLNTPTGSDIE AIINSLPTKKSPPGPDGLTAEFYQ RYKEELKKEGILLSSFYEASILLI PKPGRDTTKKENFRPISLMNID AKILNKILANRIQQHHKKLIIHHD QVGFIPGMQGWFVNICKSINVQ HINRTKDKNHTISIDAEEKAFDK IQQPFLMLKTLNKLGLIDGTYLKII RAIYDKPTANIIILNGQKLEAFL KTGTRQGCPVSPVVFTNVLEV AREIRQEKEIKG1QLGKEEVKRS LFADDMMIVYLENPIVSAQNLLK LISNFSKVSGYKINVQKSQLAF YTNNRQTESQIMSELPPFTIAPKR IKYLRQIOLTRDVKDLFKENYKL LLNEIKEDETNWKWNKIPCSWVGR INIVKMAILPKGIIHRFNAIPKLP MTFFTELEKTTLKFIWNQKRAR IAKSILSRKYKAGGSMLPDFKL CYKATVTKKAWWWYQNRDID QWNRTEPSEIMPHIYNYLIFDKP EKNKQWGKDSLFNWKWCWENW LTICRKLLKLDPLTPYTESINSRW IKDLNVRPKTIKTLEENLGTIQ DIGMGKDFMSKTPKAMATKAK IDEWDLKLKLSFCTAKETTVR VNRQPTEWETIFAIYSS
17619	47987	A	17725	I	3457	
17620	47988	A	17726	I	3630	
17621	47989	B	17727	I	3384	
17622	47990	B	17728	I	2199	
17623	47991	A	17729	I	3924	
17624	47992	A	17730	I	3345	
17625	47993	A	17731	I	2382	
17626	47994	A	17732	I	3720	
17627	47995	A	17733	I	3894	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met cod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
17628	47996	A	17734	1	2427	MGCVRQIIPLGTHPVVHQQLTSIP QNCQSPQKTRKDREIGQPRGAY GDMRSKCNVMLMMESWRNRR TLEIQTIREYYKILYTNKLENL EEMDKFLDTYTLPLRNQEEVES LNRPITHSDIVTIIINSLPTKKI:SPG PDRFTAKFYQRYKEELVPFLLK LFQSIEK/EGILPNFSYEASILIPK LGRDTTKKENFRPISLMTDAK ILNKILANRQQHIIKKLQHQDV GFIPGMQGWFNIRKSINIIQHIN RIKDKNHMIIISDAEKAFAFDKIQN PFMLKTLNKLGIIDGTYLKIIRAI YDKPTANIIINGQKLEAFPLKT GTRQGCPLSPPLLNFNIVLEALAR AIRQEKEIKGIQLGKEEVKLSLF ADDMIVYLENPIVSAQNLLKLIS NFSKVSGYKINVQKSQAFLYTS NRQTESQIMSELPTIASKRKY LGIQLTRDVKDLFKENYKPLLK EIKEDTNKWKNIPCSWIGRINIV KMAILHKALYRFNAIPKLPMT FFTELEKTTLKFIWNQKACRIA KSILSQKNKAGGITLPDFKLHY KATVTKTAWWVYQNRDIDQW NRTEPSEIIPPIYNLYIFDKLDKN KKWKGKDCLFNKWCWQNWLA CRKLKLDPLTPYTKNSRWIK DLNVRPKTIKTLEENLGITI:QDI GMGKDFMSKTPKAMATKDKID KWDLIKLKSFCATAKETTIRVNR QPTKWEKIFVTYSSDKGLISRIY
17629	47997	A	17735	1	3780	
17630	47998	A	17736	1	2808	
17631	47999	A	17737	1	4842	
17632	48000	B	17738	331	3282	
17633	48001	A	17739	1	2880	
17634	48002	A	17740	1	3213	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met/Asp	SEQ ID NO: in USNN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
17635	48003	A	17741	1	2561	MKAЕIKTFETNKNKDТTYQNL WDTFKAVCRGKFIAЛNAHKRK QERSKIDTЛTSQLKELEKQEQT YSKASRRQEITKIRAEЛKEIETQ KTLQKINESRSWFFEКINKIDRP LTRLIKKKREKNQ\DSIKNDKG DITTDPTЕIQTITREYYKHLYAN KLENLEEMDKFLDTYTLPRLNQ EEVESLNRPITGSE\EAJNSPLT KKSPGPДGFTAЕFYQRYKEELV PFLLKLFQSIЕKEGILPNSFYEA IILITKPGHRTTKKNFРISLMLNI GAKILNKILANRJQQHИKKLJHH DQVGFIPIGMQGWFNIRKSINVI QHINITNDKNHMIISIDAENAFD KIQQRFMLKTLNKLGIДGMYL KIIRAIYDKPTATQNLKLIGNF SKVSGYKINVQKSQAFLYTNNS QTESQIMTELPTIASKRKYLGI QLTRDVKDLFKENYKPLLSEIK EDTKGGKNIPCSWVGRNIMK MDILPKVIYTFNAPIKLPMTFFT EVEKTLKFIСNQKRARIAKSFL SQKNKAGGITPPDFKLYYKATV TKTACYWYQNRDIDQWNRTEP SEIMQHИYNYLIFDKPDKNKQW GKDSLFLNKWCWENWLAICRKL KLDSFLPTYTKINSRWIKDLNIR PКTICLLEENLGSIIQDIMGKD FMSKTPKAMATKAIIDEWDLIK LKSFCТАKETTMRVNRQPTEW EKIFATYSSDIGLISRIYNELKQI
17636	48004	A	17742	1	5042	MTGSNSHITIЛTLNINGLNSAIK RHRLASWIKSQDPСVCCIQETH LMCRDTHRLKIGWРKИYQAN GKQKKAГVAILVSDKTDFKPPT KIKRDKEGHYIMVKGSIQOEEL TILNIYAPNTGAPRFIKQVLSDL QRDLDHSHTLIMGDFNTPLSILDR STROKVNKDТQELNSALHQAD LIDIYRTLHPKSTETTFFSAPHH TYSKIDHIVGSKALLSKCKRTEI ITNYLSDHSAIKLELRKNLTQS RSTTВKLNNL
17637	48005	A	17743	101	471	MLSRLASRNRMRAFVEVVR VRE/RVGNDFIИYRLSMLDЛVE DGGTFAETVELAQAVEAAGATI INTGIGWHEARIPTATPVRGA FSWVTRKLKGHVSLPLVTTNRI NDPQVADDILSSTH
17638	48006	A	17744	161	311	

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17639	48007	A	17745	221	799	
17640	48008	A	17746	20	346	
17641	48009	A	17747	431	1578	
17642	48010	A	17748	1	771	
17643	48011	A	17749	3	863	AVI.RREM.RQMEGA.WLGSDLV DQGKERLNRLGFFETVDTDTQ RV/PGSPDQV.DVYKVIVSLGGR LFVNDFQADDADLSDYTNKKIE IJDASHADYFHIDIMDGHFVPNLT LSPPFFVSQVKKLATKPLDCHLM VTRPQDYIAQLARAGADFTLH PETINGQAFRLIDEIRRHDVMK GLILNPETPV.EAMKYYIHKADK ITVMTVDPGFAQQPFIPLEM.DK LAE.LKA.WREREGLYEIEVDG C.NQATY.EKLM.AAGADV.FIVG SGLFNHAENIDEAWRVMTAQIL AAKSE
17644	48012	A	17750	2	893	
17645	48013	A	17751	139	2057	
17646	48014	A	17752	2	361	
17647	48015	A	17753	497	897	PRSASFSAWLAF.CST/TKD.SHP.L LAQLLDG.VENLDHRQHLLFTA GHGARPLIRAHADVEENCDHPF ILIVHPSIHP.IYLSIHPSTIRGERL MTQIPLIKHFLAGVTGLKL.TQQ MRFCENVCPLIATAGNRQTH
17648	48016	A	17754	83	1038	PSRAGHLPPKIKSSMAGTT.PCL.S IMVRQK/PLVPAPLYQGMRDG KIVR.FEEITRTPL.EVQDC.LLASA LALGLALMGNA.QAVTTIPFWH SMEGEL.GKEV.DSLA.QRFNAEN PDYKIVPTYKGNYE.QNQLSAGIA AFRTGNAPTY.FAGHIM.QACGV ALSATIY.FIRR.KVV.SLDQ.KLNJ AMTFVGMSGALLV.QYV.QAD VLRQIPL.VICIGLY.FL.LMP.KLG EEDR.QRRM.YGL.PFALIA.GGC GFYDGFFGPAAGSFYALAFVTL CGFNLAKATAHAKLLNAT.SNIG GLLLFIL.GGKVI.WAT.GFVML.VG QFLGAP.HGV.PTCV
17649	48017	A	17755	571	1728	
17650	48018	A	17756	332	511	
17651	48019	A	17757	581	637	RALR*SLQDGSAKRGASVS
17652	48020	A	17758	1	1098	
17653	48021	A	17759	1	366	

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17654	48022	A	17760	321	611	GEGENYCDSSVMTWVVAI*QN WQCHCCSLRCASLRRQG*RQDV TDTREGTIKREMARNVW/WRA RVINAGFSRGSSLRGPISDHRRK RLSASIRQFYPRP
17655	48023	B	17761	95	645	
17656	48024	B	17762	1	3978	
17657	48025	A	17763	1	328	MLIAEGLMTAKNITVITNSLPA AFALSENKDDITLVVCGGTIVRHK TRSMHGSIAERSLQDINADLMF VGADGIDAVNGITTFNEGYSIS GAMVTAANKVIAVLDSKFNR RGFNQVLPFKEIDIIITDDAVSEV DKLALQKTRDTSLVYVLSLADF FRTASTIGERDGTQVEMILFAGF VYLVISLSASLLVLTDCSTEVK KGEVVVVCGPSGSGKSTLIKTV NGLEPVVQQGEITVDGIVVNDDKK TDLAKLRSRVGMVFQHFELFPH LSIENLTLAQVKVLKRDKAPA REKALKLLERVGLSAHANKFP AHYSGGQQQRVAIARALCMDP IAMLFDPESTSALDPEMINEVLD VMVELANEGETMMVVTHEM GFAVKWRIGSTQQGAQLHCNR WLHVRKHLLVAYYNLVGIKPG KESYMRNLNEKALDDFCQSLVD YLSAGHFSIYERILHLEGNGQ LARAALKIWPQLEANTQQIMDY YDSSLETAIDHDNYLEFQQVLS DIGEALAEAFVLEDKLILLVLD AAR*NLLKLKVIIIMIDGGFQTGI VVIIHNLLSIGFELRPNLRGAREL PVAFQLMKNALINTEMGRQV DQALTIKGGFV
17658	48026	A	17764	216	473	DALRVASGNCGYSALLPLFCRL L*AES*VPVQRPCGETLMRSS VVCLGGTAPECSSLGAEKSGR SWPRKVAHTLGSWTPVRES
17659	48027	B	17765	1	1570	
17660	48028	A	17766	1580	1764	PASSLVMR*CLNRIA*SRAHQPA VRAY*SASAPGIA*KENA*G*RL HHR*NPAKPDGGL
17661	48029	A	17767	1	1827	
17662	48030	B	17768	1	1281	
17663	48031	B	17769	72	1169	

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17664	48032	A	17770	20	552	SAGDA*DWFWHGGVAGGNG* RSP* A/VTSSALKC IHLARVRAW LLRMKVV*ATCA*CVTMLRLKC CIK*/CPDNSL RMVQLFFPD PW KARHNR RIVQVPAELVKSKL QLGGV FH M ATDWE PYA EHML EVMS SIDG YK NL SES NDY VPR ASRP VT KFEQR GHL GHG VWD LM FER KV
17665	48033	A	17771	3287	3568	CAFQR NIWHAKL N A SPTPV FVP **LLASL TIPM KPAAMP GKG KMD WW RVC RAS A SRPC QK*SLC QT PAS VNT L LTV TAVCCAS MASTT TRLW KI
17666	48034	A	17772	1	3126	
17667	48035	A	17773	249	3943	
17668	48036	B	17774	1	2178	
17669	48037	A	17775	263	434	
17670	48038	A	17776	619	1184	MRTSCGSFI KRRV MRR IAS GMV A EN RAV **PSG ICAIM VSTSS MK PMR SIS SASS RTRPL S L /AEV QSA TFQ VV QQT ARST DND LRPL TQ GA *LH VIT LAA VQS /IPHL R RAC V *RNP SLL QQ PVP V RGS V PAP ESV VLSA QD QDS ATE V KRM LQ FFRSPSG P YP E RRG HSA DVE YT LPELEM VFRNP D R
17671	48039	A	17777	1	1485	
17672	48040	A	17778	497	1838	
17673	48041	A	17779	534	922	
17674	48042	A	17780	1	458	MQQ LEE A L K QLA QG QG SSS QAL T QV R R W D S A C Q K L P D A N L A I S V A G E Y A A E L A N Q A L D R N L N V M M F S D N V T L E D E I Q L K T R A E K G L L V M G P D C /W Y V D D C R H T A G F C *R D A G R Q Y W R H W R F R Y R D S G A V F A D C A G R G G N Y S R D W P W R A R P O P
17675	48043	A	17781	2	270	QAG KYY GGA V FAP VFG A IM GG V L R T M N I E P D A L T S V D K N E F V I N H G E G T G G R S *F A R P S C S V G A R R T F A S T A R D D T R Q P C G C G G R S L C S
17676	48044	A	17782	1	1437	
17677	48045	B	17783	63	201	
17678	48046	A	17784	1016	1263	
17679	48047	A	17785	1	933	
17680	48048	B	17786	1	1888	
17681	48049	A	17787	845	2220	
17682	48050	A	17788	110	581	
17683	48051	A	17789	696	989	

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17684	48052	A	17790	199	573	
17685	48053	A	17791	1	3270	
17686	48054	A	17792	1	3018	
17687	48055	B	17793	1	708	
17688	48056	A	17794	264	512	FLAQWILPELPLSRHLRQCTWCR RHRNRW*VRSLLHRCWLADCRCP ELRIRSHDL*SLAQRSLYRDTR TPDRLRQLRTVLLHWLLC
17689	48057	A	17795	1	2109	
17690	48058	A	17796	1239	1854	YHDDRNQPDAGNPSNADSGPQI*QATGSPRRLVRR\RWKRVRNRLLAGKLAIVIDDFGYRPHENQVLAMPSAISVAVLPDSSHAREM <sup>ATKAHNSGHEVLIJHLPMAPLSKQ/TAGEKYATPGDEQRNN*AHYS*WVNPNPYAVGINNHMGSKMTSNLFGMQKVMQALERYNLYFLDSVTIGNTQAMRAAQGTGVKVITRKVFLDGFAK</sup>
17691	48059	B	17797	1	2243	
17692	48060	A	17798	74	295	TISVLUWMLSLNTSKRRLA*TSIGFFGLHSFTPGRNGLRGASGTAFFGGVVEVSTCGFSKLLAFTSVMSGGRV
17693	48061	A	17799	1	1872	MLRIHCMQHWYNNLSDGAMEDALYEIASMRLFARLSSLDSALPDRTTIMFRHLLEQHQQLARQLFKTINRWLAEAGVMMTQGTLVDATIEAPSTTKNKEQQRDPEMHQTKKGNQWHFGMKAHGVDAKSGLTHSLVTTAANEHDHDLNQGNLLHGEEOFVVSADAGYQGAPQREELAEVDVWDWLIAERPGBKRTLQHPRKNRTGISISIAYMTGSIRARVEHPFRIIKRQFGFTARYRGCLNTITNGDVFPPLATWFGG
17694	48062	A	17800	1	1269	

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17695	48063	A	17801	1	1988	MNDSEFHRLADQLWLTIERRLD DWGDGDSIDCEINGVGLTITFE NGSKIINRQEPLHQVWLATKQ GGYHFDLKGDEWICDRSGETF WDLLEQAATQQAGETITGFRV YTLQLNAQLRLGFLRLPYSVNL ATEVKSLTHYTKVPEATNPNSLE SSVDVKLSANRLKYPMMRKRL MKMWREAKALHSDPVEAWAS IIEDADKAKSFKQARGRGGFVR SSWQEVNELIAASNVYTINYG PDRVAGFSPIPAMSMVSYASGA RYLSLIGGTCLSFYDWYCDLPP ASPTWGEQTDPVPEASADWYNS SYIIAWGSNVPQTRTPDAHFFTE VRYKGTKTVAVTPDYAEIAKL CDLWLAPKQGTDAAAMALAMG HVMLREFHLDNPSQYFTDYVR RYTDMPMLVMLEERDQYYAA GRMLRAADLVDALGQENNPE WKTVAFTNTNGEMVAPNGSIGF RWGEKGKWNLESIARIENPHF RSVKNHNPVLVRQLPVKNLTLV DGNTCPVSVYDLVLANYGLD RGLEDENSAKDYAEIKPYTPA WGEQITRVPQYIETIAREFADT AHKTHGRSMILGAGVNHWYH MDMNRYGMINMLIFCCGVGQS GGGWAHYVGQEKLRPOTGWL PLAFALDWNRPPRQMNSTSFFY NHSSQWRYEKVSAQEELLSPLA
17696	48064	A	17802	3854	5726	
17697	48065	B	17803	1	1869	
17698	48066	A	17804	391	1246	
17699	48067	A	17805	58	1353	
17700	48068	A	17806	872	2123	
17701	48069	A	17807	1	1422	
17702	48070	A	17808	217	509	
17703	48071	A	17809	76	422	
17704	48072	A	17810	2	288	
17705	48073	A	17811	1	1626	
17706	48074	A	17812	779	832	
17707	48075	A	17813	1	1818	
17708	48076	A	17814	1	645	
17709	48077	A	17815	157	293	ALVCSSWPSEKCKSKPQ*DTIS HQLEWQSLKSQETTGAGEDVE K
17710	48078	A	17816	1	1446	
17711	48079	A	17817	1	306	

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17712	48080	A	17818	71	513	TIRSGLGWSQMEMRNMLGTAKKYKLPSENTINTSQIN*KI*KKRINSSHTLSQD*TRKQLNL*I DQ*QELKLWQ*SIAYQPKRVQDQMDSQ/RREFYQRYKEELHNRAKDKNHNHISIDEAKAFDKIQQRFLMLKTLNEVLMGRISK
17713	48081	A	17819	I	828	
17714	48082	B	17820	I	567	
17715	48083	A	17821	I	1224	
17716	48084	A	17822	I	897	
17717	48085	A	17823	207	547	NHFLQQLGPILLQFPPTSSESSPSET TSAWTLCPHHYQAFGQSHSTSL *EV/HKLSHIFMSSSEPSKLFQPL PVTQFQSRFHIFRFLFSSILPYW CQFTVLVHFPAADKDISVTITP
17718	48086	B	17824	I	1128	
17719	48087	A	17825	I	765	
17720	48088	A	17826	I	952	
17721	48089	A	17827	1570	2176	FLQSTHLTKG*YPESTMNSNKF TRKKQPNQRAKDMKRPFSKED IDAANKHMKKCSSSLAIREMQI KTTIMRVHFTPVRMIAIKKSGNN RCWRGCGEIGTLLHCWWDCKL IQPLWKSMWRFLKDLEIIPFD PAIPLLGIVPKDYGKSCYKDTCT HMFIALFTIAKTWNQPKCPTM IDWIKKMWHIYTMEYYGAIKR MSSCPL
17722	48090	A	17828	I	531	
17723	48091	A	17829	I	462	
17724	48092	A	17830	876	1111	
17725	48093	A	17831	2	276	LLPGFFCSNLAPVPPSGGHQHD LPYPSA*NPGASGTGQARMGQ SHQWAFLWRKDAHVRKESGY MYSLYDRAYGERTTGRRGRG GPIPRP
17726	48094	A	17832	I	1290	
17727	48095	A	17833	I293	1863	RSTPSMKE/QLATALPRHMTAE RMIRIANTEFRKVVPALGNCDTM SFVSAIVQCPQLGLEPGSASGH AYLLPFGNKNNEKGKKNVQLII GYRGMDLARRSGQIASLSARV VREGIDESFSEFGFLDEKLHHRPGE NEDAPVTHVYAVARLKDGGTQ FEVMTRKQIELVRSLSKADTDI* PWWMCPCPMKRKSAT
17728	48096	C	17834	I	786	

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17729	48097	A	17835	2	654	FCRQRQCQVYRRGRFTTHAAFTGTHRDNVLQVQSKLRADGCAL EDYFSQSEQVLPSELAFDEAPQDVVNKVFNTILRTIMEGQSIVN VDEIHRRAARFFYQARQRDLYGAGGSNAICADVQHKFLRIGVRC QAYPDAAHIMMMSASLLQEGDVVLVVTHSGRTSDVKAVELAK KNGAKICITHSYHSPIAKLADYIICSPAETPLLGRNASARILQLT LLDAFFVSVQAQLNIEQANINMQKTGAM^KRP*NWQKRTGQRLF V*PIATIHR*RNWP1IIFAHQPRKRRY*VVMPRQEYNN
17730	48098	A	17836	1	4806	
17731	48099	A	17837	1	466	
17732	48100	B	17838	193	1045	
17733	48101	A	17839	1196	2732	
17734	48102	B	17840	1	732	
17735	48103	A	17841	290	664	
17736	48104	A	17842	302	1716	
17737	48105	A	17843	249	909	
17738	48106	A	17844	36	340	
17739	48107	A	17845	902	1455	RRCVLRP/GLDIMRNRLNIRQQQRLEQAAAYEMTALRAATIELGP LVRGLPHLRTIHRQLYQDIDFWAGQRITLINHGFVPKSTTVVET NGPSDQSIAERMRRPGQTISRIHQVQKKLGIELTNCYEHSGLPDIKN VTGILICRQTHARPARLARLIFTANKNTINALVDIEVDDFTD CQIDCCCFETGSHSVLARLGGASAQDLQLDATSASHGSK
17740	48108	A	17846	1	1668	
17741	48109	A	17847	1	1080	
17742	48110	A	17848	1	907	MRAIGFTSNVLTFLTCSTSFLNT FRAADVANVQTATSNFRQIYQVF EDIITQYNGKYVLAVEGNPPGLE QGMFCISSGRPFIEKLKRAAAG ASAIIAWGTCAASWGCVQAAARP NPTQATPIDKVITDKPIKVPGCP PIPDVMSAIITYMVTFDRLPDVD RMGRPLMFYQGRHIHKCYRRA HFDAGEFVQSWDDDDAIPKV ACTKWAAKGLPPITPVPHTE* WVWSRLLAGGNGLDRGRFSGV DSSWISYSSAISVTMAPATTLN QTSKAALAAACAISTLCNGWPA VILAQHRWMKWSGLAS
17743	48111	A	17849	239	899	

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17744	48112	A	17850	155	249	CMRRKALTGGPDR*TAMR* HNKSPALTGS
17745	48113	A	17851	1	1326	
17746	48114	A	17852	1	1394	
17747	48115	A	17853	46	705	
17748	48116	A	17854	2	488	
17749	48117	A	17855	563	687	LLARTSRQ*KTSNCVNKL*MP SGQWAVLLLPCRCWWRWT
17750	48118	A	17856	1	1429	
17751	48119	A	17857	1	1037	
17752	48120	A	17858	2	276	LLPGFFCSNLAPVPPSGGHQHD LPYPSA*NPAGSTGQARMGQ SHQWAFI.WRKAHVRKESGY MYSLYDRAYGERTTGRRGRG GPIPRP
17753	48121	A	17859	1	1290	
17754	48122	A	17860	1293	1863	RSTPSMKE/QLATALPRHMTAE RMIRIANTERFKVPALGNCDTM SFVSAIVQCPOLGLEPGSASGH AYLLPGNKGNEKGKKNVQLII GYRGMDLARRSGQIASLARV VREGDEPSFEFGDLDEKLHHRPGE NEDAPVTHVYAVARLKDGTTQ FEVMTRKQIELVRSLSKADTD* PWMCPCPMKRSAT
17755	48123	A	17861	207	210	QLSLLNLPLDSIHHRLASSALK RVNDQVGAAPPRHOSPPPRNA VSLAPRPVPVEWSCAKLLCLSC RVNCQD*GNKALTSIHVFVWGE GIVGKMWLFYCTEAHFVDRPS GYSN
17756	48124	A	17862	2	654	FCRQRQCQVYRRGRFTHAFT GTHRDNVLQVQSKLRADGCAL EDYFSQSEQVLPSELAFDEAPQ DVVNKFVNITLRTIMEQGSIVN VDEIHRAARFFYQARQRLDLYG AGGSNAICADVQHKFLRIGVRC QAYPAHIMMMSASLLQEGDV VLVVTHSGRTSDVKAABELAK KNGAKIICITIISYHPIAKLADY IICSPAPETPLLGRNASARLQLT LLDAFFVSVAQLNIEQANINMQ KTGAM*KRP*NWQKRTGQRLF V*PIATIHR*RNWPJILFAHQPRK RRY*VVMRQEYNN
17757	48125	A	17863	1	4806	
17758	48126	A	17864	1	466	
17759	48127	A	17865	214	907	
17760	48128	A	17866	1288	2757	
17761	48129	A	17867	705	839	AGRSRENRRYRAKQPRCGKR*F *CVYRFYPSGRYAEPSAPNYT

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17762	48130	A	17868	199	1628	
17763	48131	A	17869	746	1013	TRARRRFITALRFSSLVSAASPCC NWAAAFSSVYFCQQIVR*PHFDR QEKRSQLVNQPDGSSSAQSQR QRPKSPQQPVQSAANPSLLCR
17764	48132	A	17870	2	331	
17765	48133	A	17871	1	591	
17766	48134	A	17872	1	1197	
17767	48135	A	17873	45	3402	NRFSHISVTSACGWWYHIPVEE/Q PEY/PGNLELERURSARIRWNAI MTVLRASKKDELGGHMASFQ SSATIYDVCFNHFARRNEQDG GDLVYFQGHISPGVYARAFLEG RLTQEQLDNFRQEVHGNGLSS YPHPKLMPEFWQFPTVSMGLG PIGAIYQAKFLKYLEHRLKDT SKQTYYAFLGDGEMDEPESKG AITIATREKLD/NLVFVINCNLQ RLDSPRWDELLRKDTSGKLIQL MNETVGDYQTFK
17768	48136	A	17874	452	1395	LAGATGTAIRLILHAPPLLPKIM RLP/TVSEGKPDSDPAAEKAFAAE NKNTYGALASLELAQQFVDKN ELEKAAAQLQQGLADTSDENL KAVINLRLARVQVOLKQADAA LKTLDTIKGEGWAAIVADLRGE ALLSKGDKQGKHQRAECEIQ GYIDMIKHLVAPLVFTSLILTGC QSPQGKFTPEQVAAMQSYGFT ESAGDWSLGLSDAIIFAKNDY KLLPESQQQIOTMAAKLASTGL THARMGDHTDNYGEDSYNEGL SLKRANVVADAWAMGGQIPRS NLTTQGLGKKYPIASNKTAQGR AENRRRAVVIITP
17769	48137	B	17875	1	1579	
17770	48138	A	17876	182	2069	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met/Asp	SEQ ID NO: in USNN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion,  =possible nucleotide insertion)
17771	48139	A	17877	1	2017	MESGVATRPIAIDFVVYIDKLTE FVYKTNLFMFKPIFSQARKAPKR VVLPEGEEARVLHATQELVTLG LAKPILIGRPNVIEMRIQKLGLQI KAGVDFEIVNNESDPRFKEYWT EYFQIMKRRGVQTQEQAQRALIS NPTVIGAIMVQRGEADAMICGT VGDYHEHFSVVKNVFGYRDBGV HTAGAMNALLPSGNITIADTY VNDEPDAEELAEITLMAAETVR RFGIEPRVALLSHISNFGSSDCPS SSKMRQALELVRERAPELMIDG EMHGDAALVEAIRNDRMPDSS LKGSA NILVMPNMEA RISYNL LRVSSSEGVTVGPVLMGVAKP VHVLTPIASVRIRVNMLVALAVL FVNADETTVNNFHACFACVEV FTVRHTTNRYQHGVVTLRFSG CFFAFHRHINA VFFRFNQAVFV ALRPEVIAIMHKLREQGHRVV LSNTNRLHHTFWPEEYPEIRDA ADHIYLSQDLGMRKPEARLYQH VLQAE GFSPSDTVFFDDNADNI EGANQLGITSILVKDKTTIPDYF AKDKARHHRTRPLWA WLKLLW QRIDE DNM ITL AGLN LAYV SLLS LVP LV AVV FAL F A FPM FSDVS IQLRH FIFANFLPATGDV I QRYIE QFVANSNKMTAVGA VASLA ISS YLLSLIA N V LMLMS * SVLRMS WNP KWA WSSI WYS
17772	48140	A	17878	31	312	RGTGHCALYRRAAARC AKITL TTFISL FSSYFVIY NILLIYLIFA ASFCLL VV* CII TV FITV CSAGD VSGMSATWC FVA ISVDHFTG FNRF
17773	48141	A	17879	1	1098	
17774	48142	A	17880	1	1015	
17775	48143	B	17881	1	1917	
17776	48144	A	17882	931	1773	
17777	48145	A	17883	785	956	KKWMHSAV*WRKRSIRR VSSL GY*TQAKDRR FALPELRRIVCS TV RRYVRRWRTNRT
17778	48146	A	17884	221	367	
17779	48147	B	17885	1	1318	

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17780	48148	A	17886	1190	1634	APSQTVSLP <span style="white-space: pre;">E</span> ASSMSGVMAG VEAVSSPGPYAVCAGSLLPSGW LCVKTSVIA <span style="white-space: pre;">I</span> ASAWSAPGAWS IKRSSAVSVRIWALCGA <span style="white-space: pre;">I</span> QPECA VRSLPSVPAFRQV <span style="white-space: pre;">I</span> LAPVTHAL* PRRSSGCP*CDYSLQLL <span style="white-space: pre;">I</span> QPAH *HLQGLLRKQL <span style="white-space: pre;">I</span> SCQR
17781	48149	A	17887	I	2499	
17782	48150	A	17888	454	1698	
17783	48151	A	17889	635	1665	KSIFWRAPADCEP/QVRQSAKV QFGDYQANGMMAVAKKLM APRQLAEQVLTHLDLN <span style="white-space: pre;">I</span> ASAKV EIAGPGFINIFLDPAFLAEHVQQ ALASDRLGVATPEKQTIVVWDYS APNRGFFGGAPL <span style="white-space: pre;">I</span> GTTLQDLTR PTKEDGLQAKPISFWASQALQF VN <span style="white-space: pre;">I</span> VKIIYGV <span style="white-space: pre;">I</span> TALSTFVLP <span style="white-space: pre;">I</span> PQTQ ALSWVVGVSV <span style="white-space: pre;">I</span> LAMIGTGFNV CWALAGHLFQRQLFRQYGRQLN IVLALLVYCAAFSKGTSNDNVA LLFRSRVKANC <span style="white-space: pre;">I</span> TYTDGQLR IFFRMLNCIFQS <span style="white-space: pre;">I</span> FATQNVNVQV LTTFNANFWFH <span style="white-space: pre;">I</span> F <span style="white-space: pre;">I</span> WNFTVFN TQFAYCNH <span style="white-space: pre;">I</span> FCITCFCN <span style="white-space: pre;">I</span> ADATPF AFFAVQQPERVHRKTA <span style="white-space: pre;">I</span> LL
17784	48152	A	17890	73	212	
17785	48153	A	17891	2049	2445	VFPVFLRIVYFWKPKGMKVNT ARNWQLKPLFTELPVILPDTQL HYVAVMELYSPA <span style="white-space: pre;">I</span> E <span style="white-space: pre;">I</span> ERIQ <span style="white-space: pre;">I</span> A* VWSWNIWLY* <span style="white-space: pre;">I</span> *R <span style="white-space: pre;">I</span> LIQ <span style="white-space: pre;">I</span> *IALT PVVRTGKTKLMSA <span style="white-space: pre;">I</span> LFN <span style="white-space: pre;">I</span> THR MKAMNLLSPKRRLPPRNGKK
17786	48154	A	17892	I	1476	
17787	48155	A	17893	332	572	RGGA* <span style="white-space: pre;">I</span> RQKHRRTSALSLSLP* NMATAVHLHRFSTRRAVTSSS ARKWTNSGAMSGLN <span style="white-space: pre;">I</span> RASA <span style="white-space: pre;">I</span> AV LRV*QSPEDGCCARIR
17788	48156	A	17894	80	405	PRNLRKSGPPISDAISPTSKP* <span style="white-space: pre;">I</span> T TEPISAPSLLATYKAAGCGGTT QCTAINAVHSGMASFNNEVLV FLAI <span style="white-space: pre;">I</span> EKARGINSTTPTSTNSVMP QIRPTSTIMTSESQRQR
17789	48157	A	17895	I	1392	
17790	48158	A	17896	I	1374	
17791	48159	A	17897	1971	2306	
17792	48160	A	17898	209	449	
17793	48161	A	17899	I	240	
17794	48162	A	17900	I	456	
17795	48163	B	17901	222	3807	
17796	48164	A	17902	3140	3219	
17797	48165	A	17903	240	298	

SEQ ID NO: NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *-Stop codon, /=possible nucleotide deletion, v=possible nucleotide insertion)
17798	48166	A	17904	1902	2047	NQPVYRSNGD/RJWRTGKLFP TVFRLIRTLSPRAFPFTSYRRC VAY
17799	48167	B	17905	1	1994	
17800	48168	A	17906	1	2151	
17801	48169	A	17907	3	1127	GTPYASQPVIRPVEGSKPLIKQV LDIGAHGTDKTIAQKLARVAR MHFARQRLAAVATFACSAQNA IALMEEIAANFSYEMIRLTECIL GFTWNRLYQGINVHNAEVRRQ LAHDGHELVVVPCHRSMDYL LLSYVLYHQGLVPPIAAGINL NFWPAGPIFRRLGAFFIRRTFKG NKLYSTVTFREYLGEFLFSRGYSV EYFVEGGRSR/TGRLLDPKTGM LRGGTRPITLPIYIGYEHVMEV GTYAKELRGATKEKESLPQML RGLSKLRLNLGGYVNFGEPM LMTYLNQHVPDWRESIDPIEAV RPAWLTPTVNNIAADLMVRIN NAGAANAMNLCTALLASRQR SLTREQLTERQLNCYLDLMRNVP
17802	48170	A	17908	192	486	PVLVVLWVFSWLCGRSLVCD AFGCVLCVLCFWCGVCWGW SRCLVLVRVLDCVAVA GVGIGLWV/RVLP CCDV LARFRV DL CWG

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17803	48171	A	17909	1	2470	MFQPSDSGKSFIFNMSVGYNLE GIKQPPMQQFIDNMMADSDHP KFAQYRDTLNKLLQDDAFLAR HGLQEKRSLQALPARIPTSMV HGVTLSSTMHGCPPEHIEACRY MLEEKGLNTFVKLNPTLLGYA RVREILDVCGFGYIGLKKEESFD HDLKLTTQALEMLERLMLAKAE KSLGFGVKLNTLGTINNNKGAL PGDSTSGVLRTYERLLTAWML TCPCADEHQGRGESVKLATALT WWLRGSQNRDEITKDGQFSNH AGGILGGISSSGQQIAHMALKPT SSIDVPGRTINRFGEEVEMITKG RHDPVCVGIRAVPIAEAMLAIVL MDHLLRQRAQNAADVKTIDPRC AQSIGSFNSNGCIVGADTLPIQSE HYQVMRTDQRRYFGHPDLMV FQRLSSQSVNLGMGTVLJGDM GMPAGGRFNGGHASHQTLGDLV DIFLQLPKTRWTSQAQLRPQAL DLVSRDGKHVVSTLWKPEPISL IKLAAQDKDVTRIFVNPAIKQQ LCLDACTIATGCAKCDPGVSIG AYAYLLTTRAQCLAHLDPLDPLE PLEIDGTLPLRYYFIHGGPVRVFT YYTPKEESIKLFLHDYLDLHRSN PNLDVQMVPPVSVMFGRAPGRE KGEVNPPLRMLNGVQKFFAVL WLGRDSFVRSPSPSVLRRMADE HGTDKTIQKLVARVARVMHFA RQRLLAVGPRPLPARQDFNKL
17804	48172	A	17910	1	734	
17805	48173	A	17911	1	962	
17806	48174	A	17912	1630	2633	
17807	48175	A	17913	1360	1600	HSTGRWATTINVPITCGTKARH STSSICKTGMLLWANALKQHC LLSRNL*KGESINVANSLSYF NLRPQCNQIRTQD
17808	48176	A	17914	1	816	
17809	48177	A	17915	703	1546	
17810	48178	A	17916	209	485	QVIRPTFIPSTSSNGAISLPASTR RDS*MANAS*RCSLA*RATMFP A*SATSIIFHARPVGVEGT*IVRIV VIMLRLLSRRKVRGIRLPAAVL
17811	48179	A	17917	619	1167	

SEQ ID NO: NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion,  =possible nucleotide insertion)
17812	48180	A	17918	1	764	DSGQQLDDVQLARYLLSGQNZ PKSDR PYRVR*LTGAMLKLI LT L/VIEGNVTLGIIRVKIGTGCVIK NSGDWR*LRNQS VYRCGRCES GSGLYHWARLPVCVLVLCWK VLTSSLVPPD
17813	48181	A	17919	3	1462	
17814	48182	A	17920	122	983	
17815	48183	B	17921	1	1287	
17816	48184	A	17922	289	958	
17817	48185	A	17923	1	5079	
17818	48186	A	17924	1	255	
17819	48187	A	17925	1892	2448	TESRCADGAGSVDVGVTEPVVP RVELVAKWPGSRAGCTGTLGC PWVGAGCVGGGLGPQARLSGPT ASTEASAKAASLASMWLRL RL*GACP FARTGATA PSSSKGP ELGVSGLRKATWMGRGSGCCT RGLGAGEWRAV PESCGLDESS EDSDRDHAVPFSSSSCRSML RPRRVARGLCRRGV
17820	48188	B	17926	52	888	
17821	48189	A	17927	929	1148	TVWNGTCGLPSSLMKCMVIM IMRAIQKMMMSKPTITLVGW N*RRASVFSQPRVEKVHSAE NQVSRTSSS
17822	48190	A	17928	125	937	RISMVFPWCFCSCSR LATTPAP TVRPPSRIA KRRPSSIA QIGWIRVT TILMLSPGITISTPSGSSMVPVTS VVRK*NCGR*PLKNGV*RPSS LDRMYTSDSNLHGLRPAVSPVT NTPA/SDGYYSHDGLSLAQVDSL ANYHEGQYTSAGLSSLQGGATL TTHGGALHRTQNMGGTRLLID ADGVADVPVEGNGAAVYTNM FGKAVVSDVNYYRNQAYIDL NKLPENAEATQS VVQATL TEG AIGYRKFAVISGQKAMAVVN AEGKVSLAVV
17823	48191	A	17929	3992	4213	VPAIQQKFPRSWKLGGERPPKA FRLRLSAA*RKSVP*AQRSLAD/ SGMLPLRKCLDTF*TQIV*SAF KIQREGS
17824	48192	A	17930	1	1636	
17825	48193	A	17931	1	900	
17826	48194	A	17932	1	939	
17827	48195	A	17933	427	1250	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met/ codon	SEQ ID NO: in USN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, !=possible nucleotide insertion)
17828	48196	A	17934	521	805	LCPSNTSPLSCLLCDLVASTEM APMRVFQPKPVNA**LFATIEP PYSVNKLKPY**PAWTKSCL IAPSIWLRPAAKSYFDTPGCSIF GTAA
17829	48197	A	17935	1	2052	
17830	48198	B	17936	1	573	
17831	48199	A	17937	1	1278	
17832	48200	A	17938	161	659	
17833	48201	A	17939	1	588	
17834	48202	A	17940	695	1281	KLKPYSWAFSRQSGRSVILTPPR VTVVVVAGFGPIPVGFTVMVRP GWAAP*FLPVASVYFP*AGLAG FLKKNRGCCANPAPPPIRPPIMY PP/MQRLQEPPADWWACAWFS GKD*WKKSPNCTRCA
17835	48203	A	17941	261	2045	
17836	48204	A	17942	1	637	
17837	48205	A	17943	31	280	
17838	48206	A	17944	1	582	
17839	48207	A	17945	1	2496	
17840	48208	A	17946	330	507	
17841	48209	A	17947	1087	1875	
17842	48210	A	17948	1	476	
17843	48211	A	17949	1	537	
17844	48212	A	17950	2	492	
17845	48213	A	17951	1	1101	
17846	48214	A	17952	2538	2833	TRRNWRPIQSSEESWRAAGSST PLTTQNROQTAGIY*RSR*TAA RR*SPALPRRNPRLA TAG!WQY ATQTRQQRVPQL*LSAPATRK NRLLANAWLTM
17847	48215	A	17953	125	1831	
17848	48216	A	17954	2	825	
17849	48217	A	17955	1	840	
17850	48218	A	17956	1	1725	
17851	48219	A	17957	463	1824	
17852	48220	A	17958	2	117	
17853	48221	A	17959	1	2640	
17854	48222	B	17960	223	1560	
17855	48223	A	17961	638	746	RIP*MT*WS*KPWHKNYMMHA QASVDNLIKWKKGYQ
17856	48224	A	17962	385	514	
17857	48225	A	17963	17	225	SSPSKFTVAFFASLVMASAVSL ALSLRSLLTTLIS/CGLVLQEERT DDALVEQFSPIRRARGHAPQQE ATEM

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17858	48226	A	17964	1	521	LVFLVLFVGFLSCFKSTYLTLYGDSPSLCDGLLII*IIISRIDTNKPA DNSISGIRDVGWVAKSYQVA/V GERLHNRTPGTSHQSDFTRDF* LC*PGSACPNLVSEHERPQANM LVEASGRLAA*YQNALSCSFGY GVGLVRRQDFSSLGRFLQSAFA SNRY*QVVVVFEEFQQVS
17859	48227	A	17965	267	554	LRFRFRTRAVGRIFHLRDLVLGCNRYGRGGGDHGLCSVLPRLSRLGRLPQGDSSAADAQSRHREKCR*DGVLVCDDDQNRRQTPVWKPHQEDVQV
17860	48228	A	17966	1	915	
17861	48229	A	17967	1226	1399	SDSNISICTCAQIH*KHFRII*NCI L*EVEP*RLS*M*LQRKCVQGEP SKVHSLWGI
17862	48230	A	17968	828	1070	SFFDYQTSALEHARR*LHCRT*NAGWLPHRTDRSSGYHGRTCSAAGRCSSGDHSSYQQQNPAEK LPAGHPQRSGSPERTG
17863	48231	A	17969	45	1198	
17864	48232	A	17970	348	508	RLFRWCPMS\WASYFPPESQSLPDSYWLFECLNLTAYNSQNAIIRESHAIYS
17865	48233	A	17971	251	601	MAKKMSLSIAVFWRRLYAY\YPHI.R*K\\$*TNW/QWWRSALS*A V*PNRS/IDSRWSIIWSVLFGMLV/AT/ALAPAFWLRY*KKSFSAWNPTKSPRCLSNAACPCCSLSKKASLPWTIAARSR
17866	48234	A	17972	1	2121	
17867	48235	C	17973	1	1710	
17868	48236	A	17974	1	1335	
17869	48237	A	17975	1	1497	
17870	48238	A	17976	2	824	
17871	48239	A	17977	1	1965	
17872	48240	A	17978	1	3555	
17873	48241	B	17979	197	2021	
17874	48242	A	17980	1	348	
17875	48243	A	17981	1	891	
17876	48244	A	17982	1	679	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met/Asp	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, !=possible nucleotide insertion)
17877	48245	A	17983	3	2502	EAIREVSNPIVPQEEIWTHREAVPVQILTGWCVTAKAPPDISAISALTAVKHGNCSSLTPLLNPPGSDVIVCAEMDEQWGVYVGAKSRQRWLFIAYDSLRLKTVVAHFGERTMATLGRLMSSLSPFDVVIWMTDGWPLYESRSLKGLKHLAILVTFEEKFQEEPVKKQIMVSISVSDTGGKEEKPKLNLNLSKTNGLQNTTEAQLCETKSDFELSGFNPISIDTEDMKTGCCCQFQSVRRAYFKATSSPRRLIITKLITRVDGYVADDPSRRYSGHGDLLWPNAGNSCVETTVGSLLCEVQAAPTHTLEGKHGCRNKEKKRLTHSGACTYTFSELGLELWAWNCGKTENVNLGAVGKGVGDDRGFKKIHAKSOFCTCSVLYFTTIKQGQISLTLWSKVVMHILEHLKENSKQLTSICTRYQRVFGPTWLHETIFCKVALTATLAELEKSTSTLQTFLDKIWLGAQQHTGSQEPMQALLTCDCPAWKKALRKVTQKGGAAFFGVDNLGSSLSPTTDLLYEEQRLTSLSGSWFPICVMVELTLRAGSSPGRILYVEFDQAVTKEPRFLQYKHYWDGAIVAGSSIRQDSFVAEASTTITRIESPVPSRSSTFLDDFSITQQHRRRHAGLSVMLSIIISPPVRLCQERTLRRDFRERLMLDLEYQSGYCRRLRTAGSEMQMVPDVLIFAHRSLAGLFPGLDERRLVNA
17878	48246	A	17984	10	211	GSQSTIFTFAARWVNLTWANENTDTISPLGVGEQRHCSSP*RFPDSDRCSPPSPRSQQQNQSPQTWQ
17879	48247	A	17985	1	1725	
17880	48248	A	17986	1	379	
17881	48249	A	17987	3	273	
17882	48250	A	17988	3	1157	
17883	48251	A	17989	76	378	
17884	48252	A	17990	1527	2005	
17885	48253	A	17991	578	1312	
17886	48254	A	17992	1	1758	
17887	48255	A	17993	1	2433	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met cod	SEQ ID NO: in USN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, !=possible nucleotide insertion)
17888	48256	A	17994	I	537	SQEELLQQALVAQLA/HSEQLE GVQLPEPDEPSARHALPANEPRI VLNNNGVVSYNDRPILNLLSWQ HIGYVSSLHLDYRVSTTVRN ILSGYFDISIGYQAVSDRQQKLV QQWLDILGIDKRTADAPFHSLS WGQQRLLALIVRALVKHPTLLL DEPLQGLDPLNRQLIRRFVDVLI
17889	48257	A	17995	I	536	
17890	48258	A	17996	I	1319	
17891	48259	C	17997	74	341	
17892	48260	A	17998	3	103	
17893	48261	A	17999	I	745	
17894	48262	A	18000	I	663	
17895	48263	A	18001	2	297	
17896	48264	A	18002	8	340	VPANSLSAIALFRRESVTPLAAL AASPVCAGRFVLLKNHRRDLP* ISVPVNSSNSARSLVWHSGRQ QIAPDWSSKDDFMRLGKPNRFS VLLLATWIR*STVIRRSPFTS

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met/ codon	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, !=possible nucleotide insertion)
17897	48265	A	18003	I	1341	MVHRFGIRVRFVALGFYQDVIL PVRAIRHEWGHYVHLCASIQR QIDVSFARDATSHSSCPVTGVR FWGYPFAANKVVIAGFELEGET MTRPGLICAEGGLLVMIVSRLS ELYDSYHEFTRQRVTEIVEKAA NHLPAVVEMMTLHRCAINRHN FVRRVGPAGISTFFASSPDGVN AGFSTFRVVFTCQRSPRLQRHS HADVQTATLLNTVNLEQKQA NAILSGLSDMIPNSPESAPEIQL LQSRMILGKTIAELNLRDIVEQK YFPIVGRGWARLTKEKGELAI SWMHIPQLNGQDQQLTLTVGE NGHYTLEGEETVNGMVGQRL EKDGVALTIADIKAKGPTQFVL SQRTELEAINALQETFTVRSERSK ESGMLELTMTGDDPQLITRILN SIANNYLQNIARQAAQDSQSL EFLQRQLP*TLSKNRPTPFSAA*/ DDMIPNNSPESAPEIQLLQSRM LGKTIELNLRDIVEQKYFPI/D GSRLGEINQRKTR*AGDQLDAY STTEWSGSATDTQVGENGHYT LEGEETVNG/NGRPASGKWR CADYRGH*GQDQQLTLTVGEN GHYTLEGEETVNGMVGQRL KDGVALTIAIDIKAKGPTQFVL QRTELEAINALQETFTVRSERSK SGMLELTMTGDDPQLITRILNSI ANNYLYQNIARQAAQDSQSL FLQRQLPENVSELDQRKKNSTF
17898	48266	A	18004	414	893	VFAQHGLTVAAIAAHARDRWF VGRTAHANPPVRCSTDGSGRVP VTRYSGFVAAVILLTASPRGG ECSREAPLCVSEYLLLQSAGE YAPAPRCVLRCPVSVDDEFVPV VPD*APP*EVALFLLRLTPVAR PADGGWLLAAIRPDALTSLAIV VLAAR
17899	48267	A	18005	432	1108	
17900	48268	B	18006	I	753	
17901	48269	A	18007	46	282	
17902	48270	A	18008	I	1201	
17903	48271	A	18009	I	618	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met/Asp	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, !=possible nucleotide deletion, !=possible nucleotide insertion)
17904	48272	A	18010	I	1045	MLCTKWDKLGLEKAGKNKNAYKWKYGWPANAPDEPHIEQLVGECRVMRQLKRLISRAPSPPSSMVVGESGTAIPVVSHAEFKGGFADIGVHYLDWTSRTTEKSSTSKSHKDDFGYLEFEGGANFSWGMYGFFDWENFYNGRINKPGSEQRYTFKNTNRIYLGDTGFNLYLHAYGTYGSANRVNHFDDMFLAGFGFQF*PAGGW/WGSNPFFAKRYTRSKPYYTGDNGYV\AGWVAGYNFMGLGSFKFTLTNWNEYEFDRDATYAADFLPLYDVDCQDNGNLEYDTYSQPEWKHNLFDHYLAVLYRFKDESGKEQFSGAVVKTREATPGKEIEAITRRMLDFS PRLKKLA
17905	48273	A	18011	228	430	YPROHRQRADGSDRHR**/CWSA*IWANPTSNLPPCRFALTKRKRPILCAPPSSRQSYAAWCRWEIRIA
17906	48274	A	18012	296	1178	
17907	48275	A	18013	I	1395	MPSDISLASCRLRATSRSLFTIDHRQSDCMTAINRIPIVDDEDNVRFETHCANNVRTALHFLFADIHPDVVLMDIRMPMDGIKALKEMRSHETRTPVILMTAYAEVETAVEALRCGAFDYVIKPFDLDELNLIQRALQLQSMKKEIRHLHQALSTSWQWGHILTNSPAMMDICKDTAKIALQSASVLSIGESGTGKELIARAIHYNSSRAKGAFIKVNC AALRESLLESELFGHEKGLFERANEGLLLDEIGRM/PLVLQAILRILQEREFERIG/GHQTIK/VDIASLLAPTRLQAMVKEGTFREDLFYRLNVIIHLILPPLRDRREDISLLANHFLQKFSSENQRDIIIDPMA MSLLTAWSWPGNIRELSNVIERAVVMNSGPPIFSEDLPFQIQRQPV CNAGEVKTAPVGERNLKEEIKRVEKRIIMEVLEQQEGNRTRTIALMLGISRRALMYKLQEYGI PAD
17908	48276	A	18014	I	771	
17909	48277	A	18015	I	2154	
17910	48278	A	18016	859	1014	IKTGETHPGIGPSVM*RHSKADLTHRHCGGIPEPQSFGSSQH GGGQFPL

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met cod	SEQ ID NO: in USNN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, v=possible nucleotide insertion)
17911	48279	A	18017	1224	1520	SPLVNQ*GA*KFFSRGNLFPQG ETH*KTKGVPCWTRYPDLKRS DSAEIIFKTPANASGRTGSGSLGC AAQLEKVADGRDLDEKLAEAG IGGSNKTTSVWQG
17912	48280	B	18018	182	2392	
17913	48281	A	18019	72	266	
17914	48282	A	18020	600	914	PYRGSPRNGHQLCDHCSHRLSE DPFVRYSNHCQSISNYRCDKPP VRPLSPLHQKTDRKHHQRPDPR FQWSAAPAHGRWRSGDS*ETP LHYAQPAGKLRWLWVNY
17915	48283	A	18021	1102	1171	LLGYGQQPPASNLLSEG*RSVV L*ISALRM*ALPPQKSSDAPNG WLPNRWPISSTHMIR
17916	48284	A	18022	1	1279	
17917	48285	A	18023	1329	1403	
17918	48286	A	18024	442	918	
17919	48287	A	18025	3	1345	
17920	48288	B	18026	436	988	
17921	48289	A	18027	637	1086	
17922	48290	A	18028	1	321	
17923	48291	A	18029	1	845	
17924	48292	A	18030	298	581	GARAEARAGSGQQGAGLGVSSP VRWRGWSDKGAERPGGPLSPL REVSRAAGPSG/HAARGQQGPGRP RFPPPGPRPPRRRCPTARPGG AAGGGPCL
17925	48293	C	18031	450	604	
17926	48294	A	18032	1279	2253	

SEQ ID NO: NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, ^=possible nucleotide insertion)
17927	48295	A	18033	1	1957	MAQFHVSHPPAEWPRHVLLM ADSKNELQNMNTGQTCGTRQT LKSKLQGWNPQGSPGSQG HPRCLKTFPVLVAQSSTQERNHV MEKAVLKSNQWAIIEEFITKIG WFPDYSGKVVKYLSSPKSSCTTV LQVTHFSLFFHPNPDELVSKIKV WSKHRLYQNNSEAFLEVQIPEP KCEVYSMRTMGRRQPGTAMD LNAGGSICNVPRTLHLTGESTF RDRQRVGAYLDIRGWYILV VDKEKLGLPGQKQNSSLKLFGE KLKQWVYVKNHAKESITQEAM GIWVGQQRKRQPLGYEERKLT NRKDIHIKNPSVCHHHQRPKV KTTKMGGKQSRKTGNSKNQST SPTLKESSSSPATEQSWTENDFD ELREEGFRRSDYSELQEEVQNN GKEVKNFGKKLDEWITRITNAK KSLKDLMELEKTKARELCDERTS LSSQCNQLEERVSVMEDEMNEI KQEEKFREKRIKRNEQSLQEIW DYMKRPNLRLIGVPESDGENT KLENLQDIIQENFPNLARQANI QIQEIQRTPOYSLRRAUTPRHIV RFTKVEMKEKMLRVAREKGRV THKGKPVRLTADLLAETLQAR RQDTHRLKIKDGGRTFKQMEM RKRQGLQS*SQIKQNLNQQRSK ETKKAIT*W*RDQFNKKS
17928	48296	A	18034	1	2838	
17929	48297	A	18035	1	897	
17930	48298	A	18036	26	308	
17931	48299	A	18037	749	1020	
17932	48300	A	18038	1	1773	
17933	48301	A	18039	1	1890	
17934	48302	A	18040	1	756	
17935	48303	A	18041	399	660	CPPEAVMPRRHEPVWEMTGF LPDVLLSDSDTSEGFRLLHLET WAPFLCRLCLSLRLIS*HHHQTT GNSSPPVVSASQHQSVDRDSL
17936	48304	A	18042	909	2005	
17937	48305	A	18043	1	490	
17938	48306	A	18044	104	775	
17939	48307	A	18045	170	451	
17940	48308	A	18046	1	207	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met/hd	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, !=possible nucleotide insertion)
17941	48309	A	18047	146	678	LGFLRLSEMPRKQGDIYRTRIW KFEDGLSNVLVQLNKLIIICVM CLVRDCDVLKTYFHR*SGLLPI KDTs/RPFTRVTQWGKKNDQ TFQGLLDTGSELTLPEDPKRHC GPPVKVGAYGGQVLHSKWPi YHFLSSHNCNGFCYISIANLPKK FGQNIKECLTNRIVPFNCVQD
17942	48310	A	18048	270	1444	
17943	48311	A	18049	700	1062	
17944	48312	A	18050	3	1096	
17945	48313	A	18051	1	1500	
17946	48314	A	18052	1	6215	MEDNLISINKIKILLAVSDGEIDE TFSLKQLMFNSPVVNQEDGSFN FEGVKAERPRPGTTQYEIKGME DSSSEVTVNREVTTDNPYTISVT NKTLSAIRKMFMPRGVRIESN GDKNNGVRVEYEVQQAVDGGSF ETVLTDVIEGKTMMSGYDRSRRV NLPNFNNQVFRVVVRKTPDSND SNVVDAIQVRSYAEVIDAKFRY PLTGLLFVEFDSKMFPNQLPTIS IRKRWKIVNVPSNYDPESRTYN GNWDGTFKKA
17947	48315	A	18053	1325	1417	
17948	48316	A	18054	1	4971	
17949	48317	A	18055	251	1091	
17950	48318	A	18056	1	2277	
17951	48319	A	18057	2	448	KNDKGDIIVTTKSGGRRGTSTVS FKLLKPEK1/GSKFSQKLEMLF HGMRAFDTSENFSAAWYLIEN HSNTSFQQLKMA/VTNLKRQAN KKSEGSLAYVKGGLSTFFEAQD ALSAIHQKLEADGTEKVEGSM QKLENVLNRASNTADTVYE
17952	48320	A	18058	124	984	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met/Asp	SEQ ID NO: in USNN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, !=possible nucleotide insertion)
17953	48321	A	18059	142	1393	DKKPGMVPPPGEEQSTVILPP GWQSYLSPQGRYYVNTTNE TTWERPSSSPGIPASPGSHRSSLP PTVNGYHASGTPAHPPETAHM SGRKSTGIDSQNLGSSPSKKQS KENTITINCVTFPHPDTMPPEQQL LKPTFEWSYCDYFWADKKDPQG NGTVAGFELLLQKQLKGKQMQ KEMSEFIRERIKIEEDYAKNLAK LSQNSLASQEEGSLGEWAQV KKSLADEAEVHLKFSAKLHSEV EKPLMNFRENFKDDMKKCDHH IADLRKQLASRYASVEKARKAL TERQRDLEMKTQQLEIKLSNKT EEDIKKARRKSTQAGDDLMRC VDLYNQAQSKWFEEVMVTTLE LERLEVERVEREMIRQHLCQYQL RHETDMFNQSTVEPVDQLRK VDPAKDRELWVREHKTGNIRP VDMEI
17954	48322	A	18060	1	435	
17955	48323	A	18061	3	926	
17956	48324	A	18062	3	693	RPPLAYLRDGDARAGLNLQL AVLAMLSSRKMFCCKSGQSYS PSRVLITENDVKEGLQRSHIILYD RAGEEHYNCISALHKSMRGSD QNASLYWLARMLEGGEDPLYV ARRLVRFASEDIGLADPSALTQ AVAAYQCHFICMPECELLA QCVVYFARAPKSIEVVSAYNN VKACLRLNHQGPLPPVPLHLRN APTRLMKDLGYGKGYKYNPM YSEPVDQEYLPEELRGVD
17957	48325	B	18063	1	2020	
17958	48326	A	18064	19	404	
17959	48327	A	18065	1	407	FATITSAKMGAYKYIQLELWR KKQADVMRFLLRVRCWQYRQ LYALHRAPRPTRADKARRLGY NDKQGYVIYRIRVRRGGRKRPD PKGATYKGPKVHHGDNQLKIA SLQSDAEEPAGRHCAGLREQSS Y*VGEHST
17960	48328	A	18066	53	431	AKKGAYNYIQLWRKKRADV MRFLLRVRCWQYRQLSALHRA PRPTRPDKARRLGYKAKQGYVI YKIRVRRGGRKRPVPKGATYG KPVHHGANQLKSAQLQTGVQ ERPGHP*YAMRVLKAYRARPD
17961	48329	A	18067	5	328	

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17962	48330	A	18068	93	836	AKMGA^YKYLHELWRRKKQSDV MRFLLRARCWQYPALHRAGTE WQLSALHRAPRPTRPDKARRL GYKQAKQGYVYIRIVRYYI*D SCSPPWNLTAQFPKGCGNFTGK PVHSWVFNQLKSASKAFQFR WQEGGEAWDGTGGILLEEFLN FFNWVWV/GKISI*QNFFEGIL I/VIPFKS*SEENPDTQWDQPN QSHKHREMRGILTSARPEKSRG L/GKKGHKFHHTIGG/SLRRAT WRRRNLTQAPPLPLI
17963	48331	A	18069	1495	2055	
17964	48332	B	18070	125	2530	
17965	48333	A	18071	345	800	RWRLQNLNSFCSSCSGSGSEGAT CFARGR*RPPGNSLNVSRMGTR SSYSCCRHHSPAFLSWGKGRCHL CNKAHLLAGA*HYSFLSGSAPY *N*VNGQI**R*TAHRSTPDAPT GH*NCCS*L*CHSY*QRA*PGY RHD*CRMCC*CADCSHAC
17966	48334	A	18072	181	1687	
17967	48335	A	18074	205	1734	
17968	48336	A	18075	1	705	
17969	48337	A	18076	590	685	
17970	48338	B	18077	1	881	
17971	48339	A	18078	1043	1248	ITLGIMAIFTVLLP1HEHGMVFH LFVSSFISLSSGL*FSLKRSFTSL VSWIPKYFILFEAVVNNGSSL
17972	48340	B	18079	1	1977	
17973	48341	A	18080	805	1153	AWKVLPPFVSCFCFLSSGL*FSL KRSFTSLVSWIPRYFILFEAIVN GSSLMWILSVCLLVLVYKNACDF CTLILVYPETLLKLISLRRFELLF LSMFSASFRSSCKAGL1VVAESL
17974	48342	A	18081	471	1442	IWSFHIVPYFLEALFV*GVRKGS SFSFLHMAQQFSQHLLSRESF PHCLFFSGLSKTR
17975	48343	A	18082	188	355	
17976	48344	B	18083	I	1677	
17977	48345	C	18084	35	1816	
17978	48346	A	18085	557	724	
17979	48347	A	18086	179	346	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met/Asp	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, ^=possible nucleotide insertion)
17980	48348	A	18087	135	1461	INRIYILLSTTSHLFQNP*PHSWK* STPQQM*KNRNYNKLSLRPQC NQTRTQDEETHSKSLSNYMETE QPAPE*LLGT*QNEGRNKDVIL* NQRFQRHNIPESLGHIV*SNC*QD **RRKERRIK*MQ*KC*RCNKN AKGVITTDPTEIQTTRIYEHKKL YANKLENLEDTDKFLDTYTLPR LNQEEVESLNRPITGSEIEAIINS LPTKRPGPDPGFTAEEFYQRYKE EQRIKYLGQLTRDVKDLFKRN YKPLLNEIKEDTNKWKNPICSW IGRINIMKMAILPKVIYGFNAIPI KLPRTRFFTELEKITLKFIRNQKR ARIAKTILSKKNIAGGIMLPDFK LYYKATVTKTAWYWFQNQRDID QWNRTEASEITPHIYNHLIFDKP EKNKKW/GKDSLFLNKWCWENW LAICRKLLKLDPLIPIYTKINSRW IKDNLNVRPKTISLEENLGIPFR
17981	48349	B	18088	1	2016	
17982	48350	A	18089	659	826	
17983	48351	A	18090	3531	3878	
17984	48352	C	18091	1	2793	
17985	48353	A	18092	1607	1774	
17986	48354	B	18093	1	1666	
17987	48355	A	18094	1	1068	
17988	48356	B	18095	1	1549	
17989	48357	A	18096	557	623	KKWINYWTHTPSQD*TRKKLN P
17990	48358	B	18097	1	1231	
17991	48359	A	18098	263	1461	GGSSCYPWEATIRTAKMVTLR KIRTLKVLTFVLVLFPLTSFLNY SHTMVATTWFPKQMVLELSEN LKRLIKHRPCTCTHCIGQRKLS AWFDERFNQTMQPLLTAQNAL LEDDTYRWWLLESVMFSVTM GFCLQRPFPGDKQGTTQPVYINQ TGRDLTQQQRLQREKPKNNLN DTIKEFLRVVPGNVDPMLEKRS VGCRCAVVGNNSNLRESFYG PEIDSHDFVLRMNMKAPTAGFEA DVGTKTTHHLVYPESFRELGDN VSMILVVPFKTIDLEWWVSAITG TISHTYIPVPAKIRVKQDKLILYH PAFIKYVFDNWLQGHGRYPST GILSVIFSMHVCDEVDLYGFQA DSKGWNWHHYWENNPSAGAFR KTGVHDADFESVTATLASINK IRIFKGR
17992	48360	B	18099	1	4855	

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17993	48361	A	18100	571	4189	FSLKRSSTSLSWIPRYFILFEAVNGSSLMIWLSSV*AKILVQRA*VLAFHPS*LRFVKDQVVVDMWYHF
17994	48362	A	18101	7449	7626	SFRSRLFSFHVVELF*VSFLILSSSLIALWSERQSVIISVLLYFLRS AFLPTMWSILE
17995	48363	A	18102	63	329	SGQRKEVPSPTLPAPPFILKKREWPDPPRSFFSGGGHWAQSSCPS DCSSQLMAC*/CKNAHKQKDNSCLI/STHMKGNSERK*NSGYQGLG
17996	48364	A	18103	2	618	GAFLLEVATAAGLSAGLTRLGSQVGGAMRRSKADVERYIASVQGSTPSTLQKSMKGFYFAKLYYEKEYDLAKKVICTYINVQERDPKAHRLFGLLYELEENTEKEAVECYRRSVELNPTQKDLVLIKAIKLLCKNDVTDGRAKYWVERAAKLFPGSPAIIYKLKN/DGWVRGOMVPKPDEGVQVGRGRSGRPDAGWRLNRSSVGGSAW
17997	48365	A	18104	1	995	
17998	48366	A	18105	1	513	
17999	48367	A	18106	62	521	
18000	48368	A	18107	1	375	
18001	48369	A	18108	76	480	LVKVCHCTYHHFLTVVSLPRDGGKGAPCWGRARSPKSALLPYLAPRG*VGTYEVQN/PNGTS PVQSPATDVGRSPALGNQEP/GT*SPGPOIGRGVTGTAHPHTGVSRDSWRRPPSFILNAVANIPKGNAPIPK
18002	48370	A	18109	445	1128	
18003	48371	A	18110	784	1189	IPLGKLLLKPVGAPQIERFPFQIPVPLCSLSFPSPSSSSARS*VRQES*LGTPGSAPITGSP/TSHHPSSASPPHPSSAKAFLSFVCFLCS*PPSSCHPCGLGPGPDPQSQKMMICTVAHLNQSLIFTVVKVHLL
18004	48372	A	18111	1	2088	
18005	48373	C	18112	169	213	
18006	48374	A	18113	1145	1229	
18007	48375	A	18114	1	975	
18008	48376	A	18115	1	750	
18009	48377	A	18116	288	368	
18010	48378	A	18117	34	168	
18011	48379	A	18118	479	1579	
18012	48380	A	18119	2279	2398	SDCSCPGL*GPPGRWHKRRKSGSPHLSTPEGTPALTSQA
18013	48381	A	18120	21	190	

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18014	48382	A	18121	1	1773 -	
18015	48383	A	18122	18	290	VAGTWPNFLKKVGIVGKYGTR YGASLRKMKVKKIEISQHAKYTC SFCGITKMKRRAVGIWHCGSC MKTVAAGGAWTYK*V*FLVVF SVWTT
18016	48384	C	18123	325	486	
18017	48385	A	18124	1	498	
18018	48386	A	18125	3	306	RQEIDSIHQVGVYCLALVPANT LPKTPLGHHIIISQTKQLFEGSL HPCNILMCPHTCVTNLPKPRQK QP/WCRPCFRDGWESCGCWKT STSCWKGSNTNRRE
18019	48387	A	18126	1	1197	
18020	48388	A	18127	1	390	NSRVDDFVAPGLSEAGKLLGLE FPERQLAAAVG/CSPMSGVIS MSAPFFLGKIIDAIYTNTPTVDYS DNLTRCLGLSGVFLCGAAAN AIRVYLMQTSRQRVVKRLRTSL FSSILQEVAFSDKAGTGELE
18021	48389	A	18128	1	695	SGFMDHLEEKADLSELVEKEEL GFFQYYRERCHQKVYHPIKPG GSAKDAAPGGGHHQAGPGQG GDEGIRMMFCVSPN RATFVV VVPLVSIIDVIYGRYRKLTKVT QDSLQAQATQLAEERIGNVKTV RAFGKEMTEIEKYPSKVVDHVM QKARKEAFARAEGVILNEKSFQ GALEFKNVHFAYPARPEVPIFQ DFSLSSIPGSVTALVGPSGSKS TVLSLLRLYDPAS
18022	48390	A	18129	1	2136	
18023	48391	A	18130	1	822	
18024	48392	A	18131	257	388	
18025	48393	A	18132	1	765	MVNALSLAARIHAEVPADESPE MTEGYEGFYHLASMKGTVERA DMHYIIRDFDRKQFEARKRKM MEIAKKVGKGLHPDCYIELVIE DSYYNMREKVVEHPHILDIAQQ AMRDCDIEPELKPIRGGTGDAQ LSFMGLCPNLFTGGYNYHA/P SPKFSAVSAMLLASASSAGRCG ESIFSPLAYTSSPIESDSCGPAL* RFLRH* E FLTQPVF/SENEAID IWN SPTASVSPLMPSRQNRAVRE LFLLTVRPTGTD

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met/Asp	SEQ ID NO: in USN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, !=possible nucleotide insertion)
18026	48394	A	18133	1	1166	LTHWVYHLYG!QRILIHIPSTSQ PNRVRGDIPPLQR!VVPVTIVQ PRLLIMLLPWTQTVRLVQVMRV LLIKLVAPFII!PAPRRIAVFADE RQRQAPVVAVKMNFSSRRCFV RLHLSGQLLHRQPALRKPRPAF TAHAVCPDFLQPVQQPQHFSR EHHAVAVLT!PFLLERLCQAAPL RFFPLAVLCLDPDERREASRLV YRLDTCGVSLHRRQPVSVAIS LALPMIAILVVQT!FMALY!AIF VTWRMMGKNYDAAVLAAGH CGFGLGATPTAIANMQAITERF GPSHMAFLVVPVMGAFFIDVN ALVIKLYLMLPIFAG*PMKRR* K/SPPQRQMPDTLRLSSVPSA SSVLSG!LLPVGVNVREYGVPGA ELPGSSPDRAVNPL
18027	48395	A	18134	48	314	LVPMTWVIEASYSI!MRKKVGE HPHFLDIAHQAMRDCDIEPELN PIRGGT!DGAQLSF!MGLPCPNLF TGGYN!IMVSMSL*!LWKVWKK RCR
18028	48396	B	18135	83	3044	
18029	48397	A	18136	1	1080	
18030	48398	A	18137	3	979	DAWADAWSKKADVKVENV!D TKEK!PEAKK!V!DAGGKVKKG NLKA!KKPKKGK!PCHS!RNPCP CKEIGRNSRSRGMSRK!AMYK RKYSAAKS!V!EKKK!KEKVLA TVTKPVG!GDKNRR*PGVVKLP QKCPRYYP/SLEDV!PRKACLSH GKKTPVQHVEKNCASIYPRG PF*FILT!VRHRGK!RVGFP!ESSL AKLAYLLC*LGPLVLKSEVPL!R RTHQKFCHLP!PLSTK!N!S!N!VK! PKH!LTGCLLSRRKKLRK!PR!HQ EGE!F!DTEKEKY!E!TEQRK!DQ KAVD!S!Q!LPK!K!A!P!Q!LQ!G!Y!L!RS VFALTN!G!Y!PH!K!L!V!V!N!C!L!K!N!P!
18031	48399	A	18138	858	1418	
18032	48400	A	18139	97	516	
18033	48401	A	18140	1	219	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met/Asp	SEQ ID NO: in USNN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, ^=possible nucleotide insertion)
18034	48402	A	18141	110	768	NLFSGCVESTFRKQPAHQRRSR ARAETMQRRLVQQWSVAVFLL SYAVPSCGRSVEGLSRR/LKPK MRPKNVHPTKVTTYKRAVSE HQLLHDKGKSIQDLRFFFFLHH LIAEIHTAEIRATSEVSPNSKPSP NTKINHPVRFGSDEGRYLTQE TNKVETYKEQPLKTPGKKKG KPGKRKEQEKKRRTSAWLD SGVTGSGLEGDHLSDTSTSLE
18035	48403	A	18142	338	661	
18036	48404	A	18143	443	661	
18037	48405	A	18144	474	531	
18038	48406	A	18145	208	317	
18039	48407	A	18146	1	807	
18040	48408	A	18147	1	1122	
18041	48409	A	18148	283	2204	ASPMAPTSCLCVPTLLPSLNQTSS SSTAPTGKASWGWPMLRPGL TTPWLSLTLW*SRPTFPTSSPC SFVVLASPSTSLKCWPLSEGA
18042	48410	A	18149	208	1212	
18043	48411	A	18150	202	1677	
18044	48412	A	18151	1	3285	
18045	48413	A	18152	3	2206	
18046	48414	A	18153	1	1041	
18047	48415	A	18154	2	1460	
18048	48416	A	18155	1	792	
18049	48417	A	18156	51	362	AHGAAWPSHRKDRESADLGSD GQNGQQLDWGGGCRRC*RC DVLCWGAPHTFRHSYAMHML YAGIPLKVLQSLLLGQAPCRCG LGQNVGTALPLVSGGPMFLP
18050	48418	A	18157	609	690	
18051	48419	A	18158	1	2055	
18052	48420	A	18159	3	2236	
18053	48421	B	18160	406	454	
18054	48422	A	18161	1	2151	
18055	48423	B	18162	1	1215	
18056	48424	A	18163	1	594	
18057	48425	B	18164	1	1380	
18058	48426	A	18165	441	692	

SEQ ID NO: NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion,  =possible nucleotide insertion)
18059	48427	A	18166	2	1311	QHVRSTVTELWTGNFVNLSIQTAFAGIGWLITFCSKGGDCLTSQTRLRLSGMLFLNSLDAKEIYLEVIHNLPDFELLSANTLEDRLAHHRWLFFHGKNENSNPDELKKLKTLKNDHIQVDRFGCSSAPDICSNLVVFQPSLAVFKGQGTKEYEIHGKKILYDILAFAKESVNSHVTITLGPNQFANDKEPWLVDFFAPWCPCPCCRALLPELRRASNLLYGGQLKFGTLDCTVHEGLCNMYNIQAYPTTUVFNQNSNIHEYEGHHSAAEQILEFKDLMNPSSGSLTPTTFLVLTQRKHTEVR/I/*FHCPEGWPPWPRLWPMACKPRNLLP*SSRPLNT*SSLFCSSNQPDLLRGPLLHRPLSLPRRYRGAQVNPNDFGHYSVSPSLIHLHQCSHLFSHSPPPRVLRPPLTTSTGLPSSPRRSATDVHTAYPPTAD
18060	48428	A	18167	1	924	
18061	48429	A	18168	10	1254	
18062	48430	A	18169	1	618	
18063	48431	A	18170	1	460	MAAPMTPAARPEDYEAALNAA LADVPELARLLEIDPYLKPYAVDFQRRMFWMFPLPFTLAFSPSVLVRFHAA DKDIPETGQFTKGRGLLDLQFQVAEDASQS WQKLYL LPNCGGQPHQKLVPTAQKFYIT VEWTGTFSVPGQVVGSEGSMQ SVTVEGSEEE SEDDKMYMTCSS ALLDSFALC**RHT*DWA IYKR KRFIGLTVP/MWLRMPPRNHGRSCISCL LIALANHTKNWFPQR RSFI SQWNGVLF SQCLAKLWAI KEV RCQ
18064	48432	A	18171	1	582	
18065	48433	A	18172	1	1578	
18066	48434	A	18173	1	1293	

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18067	48435	A	18174	344	1358	EAQSVTNHKRNSDCTFKEDNSL PVRKPSFLITNPGSNQGPRFAGS PLGHEFTSLVLA LLWTGGHIPS K EAQSLLEQIRHIDGDFEFETYYS LSCHNCPDVQNALNMSVLNP RIKHTAIDGGTFQNEITDRNV M GVPAVFVN GKEFQGRM TLTE VAKIDTGAEKRAAEESARKGIR TGLMGERFGQQILD TVD IEN YIS VP KTEGQKL A GALKVHV D EYD VDVIDSTGTRSS *AISGFFHTYDS NSPTARCA PT *QNCAPSPSGEY APGEKAMRRTI LVW RHCDY /PL CNAGNFVSMIS RATSNTIATMII *GVCTDNTRLCLYALNCSGDIL SRTSCD
18068	48436	A	18175	1	1561	
18069	48437	A	18176	884	1171	P R R L N N E D H K R L M S W L H C L V P H H A K W L Q R W Q W Q S A K V V * F A * I R A V N F V T A Y R A I I Y Q Q S R K Q H R Y L R S A C H G R S I I T V I T Q S P T K S S A T K M P E N
18070	48438	A	18177	274	416	Q A D D O A D N Q S G D T D A A F G A L I Y / C E S D D L C * L P L P A L K P L C V M W Y Q T M
18071	48439	C	18178	24	509	
18072	48440	A	18179	1	1932	
18073	48441	A	18180	1	2583	
18074	48442	A	18181	1	495	
18075	48443	A	18182	36	798	K Q R H S C F W S C W F S R A G * L G E L V * N P E I A * R P P R P Q Q V T V S G N G A W S G K A P R R R H S W H Y / Y T I S F Q K L P L V E C T N A G P I F * V A K A G R K C S I K P P L T S R S V I T D * P V S L S R S Q L T G R / A G N F V T G W / Q Q L D E E I R Y T M R T T V N A Q T R D R R K G V Q P P T T W I F N D T K D Q L E R R I A R L E T G M A W A E E P S R T R H L I S N C Q I S E T D I P N V F A V R V N Y L L Y R A Q K E R D E T F Y V G T R F D K V R R L E D D T G A S W N G N R T G S A G I S I T
18076	48444	A	18183	114	724	A R T R V P H F G H E T A G G A A H P H L S L L G Q D P G N Q T Q L P G G R G G I P G G R G G G R G G G G G G D D G R R R A L R R Q Q V P V L C V Q R A G P A M D A A A P R H I S P D R E R P K D Q E V L H R L P G H A S H S P H L G R H A G Q P A G P A G L W Q A P G L R H H L H A G I Q P P E / V T N T L T A L T * T R R C P A F S S G T V K P L I F W N L A A G P P L L R K G A A S I W I C S C S I F Q R

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18077	48445	A	18184	1	2130	
18078	48446	A	18185	2	433	EMTLDSRVAAGDLFVAVVGH QADGRRYIPQAJAQGVAAIIAE AKDEATDGEIREMHGVPIYLS QLNERLALSAGRFYHEPSDNLR LGVVTGNGKTTTQLAQWS QLI/GRNQRGNGHWRW^RPAGES DPDKR YNRFGSRSRA
18079	48447	A	18186	114	586	SYITALGQFSRSRGIQLLDRLGNF GTGWPNFDRKRGSTMTRTV GQTR/GPPQRRPAADNLDF**H QRPAAGANRPSGNNGHGLGRRA AVTHPSLNQQLPDKRNHRPKRI CCAGKLSALSGTKRSAMKHSM LERVSTKFAVWKMITGACWN GISSWIKR
18080	48448	B	18187	1	3577	
18081	48449	A	18188	2	861	YHSINAASACSAHHPVAFLLT CRTCSSSLVATTSTMRLPNTLP DLIISPVESILSTSFCAVPAFIREE PVTTSAPTIGVMANSAVVELAL PGLQEIPTVRQPSWRAVYSSPAIT YGVRLAAMP/SHHILCR*INIF QIINTAFPAIFRAFHRLVNGIFSA SNQTNHQTRFHAVCGRRTFGDV GWVAKSQYQVAEERGSITEHQV QGHQSDDTEHFHGGEIERQQQ HYHRQRGDPVGEIGEPELSISRD RHHVCHTGYNPAEPVSPAGEIS NGTANGNKLNMSVCIEAP
18082	48450	A	18189	560	2021	
18083	48451	A	18190	525	804	GG*CRNWCDHYANGCRDTSGT LYDKLAEELGPQQLSPR*NNWQ TARRNQSSGRNSCHLRREVE* RLDKALRRIQFSAPDEGAKCP WPGIIICSNHFARLRCQYGRFL EVTSAGDEKPYPLYDHHVGLV VEQLRCIITAKVTRHFYVVLK SIHPAVAGLPALRDCGELFNSV YCRKPATGPELOADVMVVVAY GLILRKQCWRRCRVLAVSTFMFT AATLARCTTNPTLTRAGDAET GVTIMQMDVEIPVVRCTTSWQ SLAHKA YHHVETI GRRHGETR VQDETLYTAEKLSKEERVLTG HFRQHSLNAALRFQSMANELA
18084	48452	A	18191	1	266	SQYPLVAGHEVIGRVVALGSA AQDKGQLQVGQRVGIGWTARSC G/QLRLY^R*SDQLRARGAD DYESRWLCREVACGLAMGDST ARKY

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18085	48453	A	18192	5	385	
18086	48454	A	18193	330	598	VMRFAIVVTGPAYGTQQASSAF QFAQALIADGHELSSVFFYREG VYNANQLTSPASDEFDLVRVA/S ATTECATWCGAEYLRSGSITPW RC
18087	48455	A	18194	1	2652	
18088	48456	A	18195	1171	2091	
18089	48457	A	18196	486	837	
18090	48458	A	18197	1	2943	MAIYKQSQHMTEVVRRCPHHE RCSDSDGLAPPQHLIRVEGNLRL VEYLDNRNTFRHSVVVPYEPPE VGSDCTTIHYNMNCNSCMGG MNRRPILTIITLEDSSGNLLGRN SFEVRVCACPGDRRTEEEENLR KKGEPIIHELPPGSTKRALPNNT SSSPQPKKKPLDGEYFTLQIRGR ERFEMFRELNEALELKDQAQAG KEPGGSRAHSSHLKSKKGQSRL GTRFLCQPAVTIPVKIVRVTG DTVIRPHAEAGAVRQLRVGQA VTCRVCIGRDADIQRCGGVNA GQPAGGAAVATPGGLARAADAD EFAVVVPGQPFGGGQAVRYTA VRQLPLRVGRMSGLMLAKTCFR LQVMHRLTLTVFSQVKVFTESIE VVEALKVNLMRVFLRRMDLRQ HRKMINIDNYIATGSMNMVD PRYFLRDALPHCPNPNTGPTFA VLEKLGYPHTFVSTDFTNVALD VKTGIKANDDKAKLKLALGEIA HACVDAIIYCKSPTVAGLVAR ELIKLGHGTPTENPHVYWSPLE TVLACILARYRGHCNSTLATS MLENCACFSAPRSLKESTL NTVVIVYDNRDGTRSIDKFNRFCI HAFPKIIRNAIYEVEQHT*RACR YQ*DVGWFIYQPGISLAASKH CSTSSR*RWI*LDW/CASASLL DEATAAAEAMAMAKRVSKLK NANRFFVASDVHPQTIDLMST
18091	48459	A	18198	643	776	
18092	48460	A	18199	1	1257	
18093	48461	A	18200	3	346	
18094	48462	A	18201	1120	1335	
18095	48463	A	18202	312	1108	
18096	48464	A	18203	1	744	

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18097	48465	A	18204	381	1112	GVEPSPPTNPPPATAIPRATCVA AARAASPSPS*SHQPHPPPLAYD RCST*PTPTTTAGQDHGDRH WRSAPAPRSDHLSMDMLQE/RSM SLLPLILSSTRSGNSNPLRSTFLSR SRSISKNCSAEV*SNNSAVGVTI STS/RSTYDINRADTQVRAVNV NYDIIVMSNSFNGQSEHQVWIG GQF/ILHQICPLTQFQYGAEPDR KE*COAPASKWALLHK*HRPPF QDRKAGECLLHEYEDLQYPSVIH
18098	48466	A	18205	2	307	HPARHKFVKGSSEHRKSPVKPP PIPSP*PP*PENTNPMPRLAPTD VTNLRSLSMTGRQRFTPYNNVS RSDPSTTARSSSADRVAEYPT TSSEETSGRSSR
18099	48467	B	18206	I	723	
18100	48468	C	18207	I27	1410	
18101	48469	A	18208	I	1773	MGKKQSRKTGNNSKNQASAPP KERSSSPAMEQSWTDNDFDEL REEGFRRSNYSSY*EEIRT*WQ TSLKALKRNM*MMMIILASPSR TPISGPNPDAGPKFVKAAATT GKARQRFHPTTTFHGRTPPAPP LAHPAPTVPSTPASTQHPARRHQ VARPDRSSTPLPARIALRVCFCPT PSTAPPEHPQRQNPNPAPOTDSA LPGADDVVRVSTTDPPERHPPHT NTTTPGPGVRVLRKELNPRRPR HHRRRRFHVQRAWQLPVPHRH HHLDHTSHTRRLRMLTDVRLD RPQPQRPPRITITVGGDQQLRL DRSYQPESPCDGDLRQLQMA RAPCSPSLMSMLVLEKCDNLKTC TSHGSPVMAETAVINHKKRKNS PRIVQSNDLTEAAYSLSRDQKR MLYLFDQIRKSDGTLQEHDGI CEIHVAKYAEIFGLTSAEASKDI RQALKSFAGKEVVFYRPEEDA GDEKQNAKNEIJGTTSSLPTQFK TDHMESEQKDHLHKEATNLKVP HLVQESQDKDHJKEATNLKVP HPHPGKPQGPPPQEGNKPKRPP PPGRPQGPPPQGGNPQQLPAAA GKPQGPPPPQGGRPHRPPQQQ

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USNN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion,  =possible nucleotide insertion)
18102	48470	A	18209	944	1577	RLCCLIEISSTGYPKSSISSSKYPQ IPRAGAQCSQAV*SGSNPLRSTF LSRSRSISKNCSEAV*SNNSAGV GTISTS/GSTYDINRADTQVRRA VNYYDIVMCNSFNGQSEHQV WIGGGQF/ILHQICPLTQFQYGAE PDRKE*CQAPASKWALLHK*H RPPFPQDRKAGECLLHEYEVDLVP IRDFTLRLFPGGRYLPRAKHVAP SEPDPTHAYD
18103	48471	A	18210	3	634	DRVFDGSKWRSEQDWAAK AVGQCESNGDWRCGNGRYP ARGPAPVA*PSLCLHHPR*RCT CCMPVYR
18104	48472	A	18211	3	255	
18105	48473	A	18212	101	547	TSVELMDLCPIRLCRTFSGIPAY SMCIA*EWRNVCGVTGTEVENT PSAAAAATASPIQVLTIVLTSVT S QIRAFSVLPVRLRRSMSLSRIN TCRTEYPRCAVVCLWKDAVS CLSTTFCARLCGQNTWLPRPCR HVNRAASDASVSLSTVT
18106	48474	B	18213	1	1113	
18107	48475	B	18214	220	1173	
18108	48476	A	18215	1	509	MPNHKAIIKFKKTEIIPITLLDH STIKIENIJKKIAQNHTITWKLN NLLNNYFWPLTVSLCEMKDFYS LGIEFSRFPLQELQNKDCALEK/ HSHWAQMWP*YPCPAKHWW S CRREHVLVNV/DCSTS*NSYWH FSD*LRAMKRRNEQCKR*AIRS LSRSLPARQDLKLSS
18109	48477	A	18216	3	281	
18110	48478	A	18217	878	1135	
18111	48479	C	18218	1	1602	
18112	48480	A	18219	33	608	VDSLRFQSPCSVYSTDTR*ISE T**NKL*PPKPVIACPKMWIQV GQKFRQKAAATP*KAR*SPRPPIP SH*QP*PKIQTRCGPQPPQQRSP T QKPHDRQTALSHRTTTFHGPTP APPLAHFAPTVSTPASTQHPAR RHQVARPDRSSTPLPARIALR VF CPTPSTAPPEHPRQNPNPAPQTD SALPGAVRG

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18113	48481	A	18220	3	893	NPRKRTEQQKAQNKVQWWLT RTPVMVQKRPTIVSLKSSPDSPLETYSMFLFLGMWVGVGVEM/CSVKLEEQVNNTYHYQRILLGISS DNAILLEESEEGRPMHISTIKE PSPDSPILYLTLNKLTTSLILFH YGESWNLRLRADQRLIAFKASWP RASRYQQGHQDLFILRSSDLPSQ VFI RDKL MERRNRRTGRT EKAR IWEVTDRTVRTWIGEAVAAA ADGVTFSVPVTPTHFRHSYAM HMLYAGIPLKVLQSLSMGHKHSIS STEVYTKVFA LDVAARHRVQF AMPESDAVAMLKQLS
18114	48482	A	18221	1	327	LISLRQRQQRTPGKPGKGPRPIP SPWP**PENTNPMRPPSPTRSGH QPRSLMTGRQRHFITAQQRFTV RPQHHSRLIQRPPCQRQVPNQI QRGDIRSLVQIGHQRCRLRG
18115	48483	B	18222	1	1419	
18116	48484	A	18223	1	2784	
18117	48485	A	18224	936	1157	RTSTGLSGCIRCG/CASEGGQAV FV/WPRGPETPCSRCPAEGSP G*SPPREDPSSGSPGKRQTCTQSARSPS
18118	48486	B	18225	67	1314	
18119	48487	A	18226	302	1423	CRWRRFIMPFVMASMSAECL MNYNSTAMSGKTGLQNDTTI ARPWVKPYLGLEMIRIVGN*PH LTWCFCPTMYIPLFSQLLCCPVSF GQCGAFRNPGHPPSPNPEFFLG PRRCNPSLGHKALVQEASDTP GKS/PGKSPPGPIPPIP*PGK HKPDAAPSPHRSGSPNPEAS*PE DSAFTPHNNVFTVRPQHHRSLI QRRPCQRQRPVNQIQRGDIRSLRF GCFARHHPRHHRNIIHDRTTRP RRLTRHSRGLFEDDVVRVSTTDP ERRHPIHPTTTTPGPGVRVLRKE LNRPRPIHLRRRRFHVQRAWQ LPVPHRHJHLDHTSHTRRLR MTDVRLDRQPQPRARITAV GGDQRLRLDRITKPRARPN
18120	48488	A	18227	1731	2392	
18121	48489	B	18228	1	1422	
18122	48490	B	18229	298	1464	
18123	48491	B	18230	1	1800	

SEQ ID NO: NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion,  =possible nucleotide insertion)
18124	48492	A	18231	745	1250	HTQNQSGRSQNDF*RRRKNIS ERSAVYR*RQLYIRRQPYAERP SLR*RQRP*IPC1RSQHGNRKRIP RRRFI*QSVLRRRHELLP*RKPE ASAERHKTRC*VSERRPRYHRV KYDYH*KSIYSR*AHGAA*PSH RKDRESADLGSQDGQNQGQDLC RGGCOPLLLTV
18125	48493	A	18232	1	1661	MAETAVINHKKRKNNSPRIVQSN DLTEAAYSLSRDQKMLYLF DQIRKSDGTLQEHDGICEIHVA KYAEIFLGTLTSAEASKD1RQALKS YAAKEVVLYRPEEDAGDEEGY ESFPWF1KRAHSPSRGLYVHIN PYLIPFFIGLQNRFQFR1SETKE ITNPYAMRLYESLCOYRKPDGS GIVSLKIDWI1ERYQLPQSYQRM PDFRRFLQCNAGHEMTKAIAI AQFNDDSPPEAKITRRWRIGEA ADLGVGVSQAIRDAEKAGRPH PDMEIRGRVEQRVGYTIEQINH MRDVFGTTRLRAEDVFPV1IGV AAHKGGVYKTSVSVH1AQDLA LKGLRVLLVEGNDPQGTASMY HGWPVDLHIHAEDTLLPFYLG KDDVTYAIKPTCWPGD1IP5CL ALHRIETELM1KFDEGKLPTDP HLMLRLAIETVAHDYDV1VIDS APNLIGITINVCAADLV1VPTP AELFDYT5ALQFFDMLRDLLKN VDLKGFEPDV1F1RDKLMERRNR RTGRTEKARIWEVTDR1TVRTWI GEAVAAAAADGVTFSVPVTPH TFRHSYAMHMLYAG1PLKVLQ SLMG*YVHCKALWMDCAHV** TKEKIHSLLHRRHPLQGDKEPL PSPRN55MPAVPYWLPQRSIRI FQHI
18126	48494	A	18233	162	446	
18127	48495	B	18234	144	2537	
18128	48496	C	18235	1	873	
18129	48497	A	18236	700	1198	PFFGTDFFPWARWC1QLRHKFW SKGKQRTTKAPVKPPGPSPAI DHP*PGKHKPDAAPSPHRSGHQ PKTSMTGRQRFHTAQQPFHGPT PAPPLAHAPTPVSTPASTQHPA RRHQVARPDRSSTPLPARIALR VFCPTPSTAPPEHPRQNPNPAPQ TDSALPGAVRG

SEQ ID NO: NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion,  =possible nucleotide insertion)
18130	48498	A	18237	363	940	LQTVLQGYSNENSFMVKQKGS PPGKPGKKPKCFWGPAGPKNGAD IPSQSWRPSGNPGTTTPLLPKPPSF FPGAPRMGQSQAWGHKGFWF KKGKPTEPGPKKARVKKPPGG QSPKAIGPTRGPKGKPKPDMDRA PKPPTDSGHQTQKPS*PADSAFT PHINVSRSDPRTTARSSSADRVN ASEVPTSEETSGRSSR
18131	48499	A	18238	861	1517	SLRPHLSGFYQARTL*DQRSS*A DHE/DISKNCASEV*SNSNAGV GTISTS/RSTYDINRADTQVRRRA VNYYDIIIVMSNSFNGQSEHQV WIGGOF/LHQICPLTQFQYGAE PDRKE*CQAPASKWALLHK*H RPFQDRKAGECLLIEYEDLVP IRDTRLFPGGGRYLPRAKHVAP SEPDPEQDEQKLRFCRKRLHYGG QPRSPVIEIRLQHVAIAYQTHHA
18132	48500	B	18239	1014	2337	
18133	48501	A	18240	1495	1947	IVTLCFSYCLHCEAGP/LPCGH PWLWLC*VLGSPG*TQRTGSW AMPGVQASKPACG*KVAPAAR RVPHPLHMLPHSGHSAAASGGA SCPLCRG*ATGSDQVLKHAFRK GRSSNCASNGTPPPNADFLGQD VHPARHKLQRQKSASEPRKKAR
18134	48502	B	18241	1	2055	
18135	48503	A	18242	1	909	
18136	48504	B	18243	184	395	
18137	48505	A	18244	447	667	HRPRRRFQIKPQSQVPEHAPPL PTASDPP/AHSPRCPSERSLSPGG QRLGFPSSVLNCSKCSWQLAAC MGFSF
18138	48506	A	18245	265	890	
18139	48507	B	18246	1	551	
18140	48508	A	18247	407	636	RIMVHATGLMKHASSPGCWDL NRRTRRCGVRRVTE*QRAS*KR */ERDYISIMPKPDGLTAAKNLA EAFEHYNECIRI
18141	48509	A	18248	1	1448	
18142	48510	A	18249	817	930	
18143	48511	B	18250	303	461	
18144	48512	A	18251	612	3359	
18145	48513	A	18252	1	462	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met/Asp	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, !=possible nucleotide deletion, !=possible nucleotide insertion)
18146	48514	A	18253	268	749	RGGIEYLLLVVFILTRTRF1QAV EHRRNGRRVAEK1VPELITHFM AEIRDLLQRTGVAL/W/*HQSAA YLPG*QICALA**IHPGVAAGEY QRRSIQENGKVQESGQTAS* <sup>M</sup> RG*MSVESRSGIAARCPESDAQ SGVVRHRSRWNLQSLPARFGAGR DYREAS
18147	48515	A	18254	1793	2193	TQRIPAAQKQGSRCIVDSSAEA LSAALAIIGNIELVKPSRTMS/DK AAQEIVNSGKAKRVRVVSLSGPQ GALGVDSENCIQVVPVVKSQS TVGAGDSMVGAMTLKLAENA SLEEMVRFGVAAAGSAATLNQG TRLCSH
18148	48516	B	18255	1	1557	
18149	48517	A	18256	606	1123	QRDNPSGTDGGRNRAFGAGNI HTRGAAQAAVERLVDSFPQEK DPGESTGRTDSDLPSRPQKVAY PVHNRDERR/LWFAAPSPSN ATWGNAEWTLNFSSSDSVTGA SSER*NLFLRLATVRCTLPSSVS ADGAIVAALATHIGEAELTLS QCGAWRATFSSTCSSLPLNPN
18150	48518	A	18257	110	318	TALKLPLPMSTKVTRCLSNLLK PKFNLLPLVQPPKKMLPRHLSR *APNTKTSRVLKKN*PIPIPTRR KT
18151	48519	A	18258	2	3062	
18152	48520	A	18259	4435	4954	
18153	48521	A	18260	1	1959	
18154	48522	A	18261	2	715	
18155	48523	A	18262	1	756	MIRRVSVASGNAYPMRPAASYIR TAPTVYPSSPAGTWFAGNAPA SSCGFRDRYLIVCSHQTPHVPG KREENVYETGIYWLRYHYGYTD YSRNAKQRLQRNNNLA1PILFTTT VPLGGRQYNNNSQHLPQROSLE RIRHHTQAFALT1PHGAAGQGC GSGDLHLYSLEDVAVSSKATPD GSGVTRKASANLRVTIQIGGFQ LRTCGFPSCRGCHPALQISRAL AVAAHQQAADNNMFEFANYGP FELLQARQLIES
18156	48524	A	18263	1	799	
18157	48525	A	18264	1	270	
18158	48526	A	18265	2	188	LGFFFQRLGFGQELSKL*EQVL LAPEEVGHLGEHLLFRHASEWP APRVQLLLLVVRVQDLQE

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18159	48527	A	18266	2791	3274	SKIFPRHDDLLLWRSHRNGDDLRAGMNAFKQRLTLGFKITILTANDYLFADGQ/RSVKKYPOAQVSRVAGADLWEELMARAGKE/GTPVFLVGGEPVLAQTEAKLVRSSATSAIWA <sup>P</sup> LIPCAISSWIRSTAFCCCSWVSEGKPADRS <sup>P</sup> APSRTWLRC
18160	48528	A	18267	202	627	
18161	48529	A	18268	1	2390	
18162	48530	A	18269	1081	1911	
18163	48531	A	18270	86	272	
18164	48532	A	18271	674	2808	FILKLRTRRR*RHRLIRPWLFWQTARNAEV <sup>P</sup> VMKA/LVRHLWLEVKGVDLGRFPERRYGSDKPDLRNPMELTDVADLLKSVEFAVFAFGPANDPKGRVAALRVPGGASLTRKQIDEYGNFVKIYGA <sup>K</sup> GLAYIKVNERAKGLEGINSPVAKFLNAEIIEDILDR <sup>T</sup> AAQDGMIFGADNNKKIVADAMGALRLKVKGKDLGLTD <sup>E</sup> SKWAPLWV <sup>V</sup> IDFPMFEDDGEGGLTAMHH <sup>P</sup> FTSKDMTAAELKAPENAVATLGDPLESPDDGLHNRISTHGCFYVLCGISTNIGVESTARNAWE <sup>L</sup> GFNLVIAEDACSAASAEQHNNNSINHYPRIARRGRDPQRVM <sup>I</sup> YIGLPQWSHPKWVRLGITSL <sup>E</sup> EYARHFNCV <sup>E</sup> GNTTLYALPKPEVVLRWREQTTDDFRFCFKPATISHQ <sup>A</sup> ALRH <sup>C</sup> DDLVT <sup>E</sup> FLTRMSPLAPRIGQYWLQ <sup>L</sup> PATFGPRELPALWHFLDSLPGFNYGV <sup>E</sup> VRHPQFFAKGEEEQ <sup>T</sup> LN <sup>R</sup> GLH <sup>Q</sup> RGVNVRV <sup>I</sup> LDSHPV <sup>H</sup> A <sup>A</sup> ARPHRK <sup>L</sup> GGTA <sup>V</sup> WEWEPEGAHWVGDEPGWFSSGDL <sup>S</sup> KA <sup>E</sup> YWAQKAADSGDADACALLAQIKITNPVSLDYPQAKVLA <sup>E</sup> KA <sup>A</sup> QAGSKEGEVTLA <sup>H</sup> ILVNTQAGKPD <sup>P</sup> Y <sup>K</sup> KAISLLENASEDLENSAVD <sup>D</sup> AQMLLGLIYANGV <sup>G</sup> IKIADDKATWYFKRSSAISRTGYSEYWA <sup>W</sup> A <sup>G</sup> MMFLNGEEGFIEKNKQKALH
18165	48533	A	18272	532	2103	
18166	48534	B	18273	1	4401	
18167	48535	A	18274	343	765	
18168	48536	A	18275	447	709	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met/Asp	SEQ ID NO: in USNN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, ^=possible nucleotide insertion)
18169	48537	A	18276	1	1571	MIEVKHLKTLQALRNCGSLLAAATLHQTSALSHQFSDEQR LGFRILFVRKSPQLRFTPQGEILLQLANQVLPQISQALQACNEPQQ TRLRIATECHSCIQWLTALENFHKNWPQYSVIFKSGVTFDPHFF FQQGELDPERAFDDFGIKPMAS ASIAQVVISARFNSNGHEVVIVK VRAETLPVIAKDLKLIYRLARW DAAFAAGWSPSPAAANLSCAGST KIHRLMNRTCCRNLPTPSFGA KPGLYLVEAMVGGYRATTVVF VSDTVALKSVGIELLWVGAG KKQGEANAGSEILWTIDGLGVMT RGVTTDSGTLQLQHISPERSYI LGTLAMVQLREDMAKRQAAGI IAPRSRMRMHRTQHKPPMTTE MGPRAVLREDTIPFLEALKASG KQRILLTNAHPHNLAVKLEHTG LDAHLDLLLSTHTFGYPKEDQR LWHAVAEATGLKAERTLFIIDDS EGDAMKEKPAVEVRLDKWLW AAR/SL*NPRAGP*ND*RR*GAL QRAAHEAEQNRRAECHAHSAP
18170	48538	A	18277	2080	2274	RFQVYYFDHEKPSLRHF*FALE EYTGTRN*GCVNLLDR*KPFPF KFMERWLAFSPPPGLTLESSRG
18171	48539	B	18278	1	3126	
18172	48540	A	18279	1	341	MLDRLESEiLADRVSSEESRRWL ASCGLTVEQMQNQMDPVYTPA RKIHLYHCDHGRGLPLALISKEG TTEWCAEYD/GMGQPAE*REPA SAAAAYPPAGAAV**GVRPVQL QPPPLL
18173	48541	A	18280	945	1484	
18174	48542	A	18281	965	1403	
18175	48543	A	18282	703	1149	
18176	48544	A	18283	161	476	LLPWRSCLRSDPLAAHPVI/LV P*ACIFIARNCYPRPSCDSACKL RRESCG*FG*TRMVSQAQATFSIQ ITSA/LPFCEHLPKGKRSQGFDTG EDNALSGQRPEFRHG
18177	48545	A	18284	1	443	MLSEPALRELATAIAGVRKGENDIAVENIGANIFIIVVLGLPALI TPGEIDPLAYSRDYSVMLLQAG KEVLAIERECLAELDQYINQNFTLACEKMFWCKGKVVVVMGMGKS/RAILGEKWPVRNVCQHRIAHENRDSIRKICCYHR
18178	48546	A	18285	3	550	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met/hod	SEQ ID NO: in USN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, !=possible nucleotide insertion)
18179	48547	A	18286	2157	2504	LVSLAGAA <sup>Y</sup> RSPQDPV <sup>P</sup> YMPISPG <sup>L</sup> DWVRQIVCCV <sup>M</sup> ASAD**R <sup>V</sup> PRQNALLP <sup>V</sup> CTSG <sup>P</sup> YHALAT <sup>G</sup> CGFRRGQMLKTTV <sup>L</sup> PRHYK <sup>L</sup> YLGASSG <sup>M</sup> RY <sup>S</sup> T <sup>T</sup> PAT <sup>A</sup> LMPLPLPHLAER
18180	48548	A	18287	I	621	
18181	48549	A	18288	I	423	
18182	48550	B	18289	I	1551	
18183	48551	A	18290	1171	2757	
18184	48552	A	18291	347	690	
18185	48553	B	18292	I	528	
18186	48554	A	18293	I	1417	
18187	48555	A	18294	292	699	
18188	48556	A	18295	859	1377	
18189	48557	A	18296	I	3036	
18190	48558	A	18297	I	942	
18191	48559	A	18298	I	2124	
18192	48560	A	18299	1955	2797	GGISIDRSGDH*GRGA <sup>V</sup> HVG <sup>R</sup> *NAGR <sup>T</sup> A <sup>E</sup> LYFASRPTCG/RW <sup>L</sup> VAA <sup>V</sup> QGA <sup>A</sup> TARISTIEMSVW <sup>A</sup> QL* <sup>Q</sup> MCRGKIRAT/ISLPEATA <sup>Q</sup> VISSGSGATKVEDGLGDLNKP <sup>V</sup> SNQNL <sup>V</sup> TGIDTPVYNAPSAGS <sup>A</sup> PFGV <sup>L</sup> ADNMRY <sup>P</sup> ILHKLKD <sup>R</sup> <sup>L</sup> NQTWYQIRIGDRLAY <sup>I</sup> SA <sup>L</sup> DA <sup>Q</sup> PDNGL <sup>S</sup> VLTY <sup>H</sup> HILR <sup>D</sup> EEN <sup>T</sup> R <sup>F</sup> RHTST <sup>T</sup> ITS <sup>V</sup> R <sup>A</sup> FNNQ <sup>M</sup> AWLR <sup>D</sup> RGYAT <sup>L</sup> SMVQ <sup>L</sup> EGY <sup>V</sup> V <sup>K</sup> N <sup>K</sup> IN <sup>L</sup> PARAVVITFDDGL <sup>K</sup> S <sup>V</sup> R <sup>Y</sup> AY <sup>P</sup> V <sup>L</sup> KQYGMKATAF <sup>I</sup> V <sup>T</sup> TRIK <sup>R</sup>
18193	48561	A	18300	I	1191	
18194	48562	A	18301	I	298	MPVVFTVFFLWFPSGLVLYYIV <sup>S</sup> NLPRY <sup>A</sup> EYLTVKDADGSVLD <sup>Q</sup> GI <sup>A</sup> W <sup>F</sup> P <sup>G</sup> PN <sup>S</sup> FTGEDV <sup>L</sup> E <sup>L</sup> Q <sup>G</sup> HGGPVILD <sup>L</sup> LLL <sup>I</sup> R <sup>L</sup> TV <sup>C</sup> G <sup>L</sup> R <sup>I</sup> ARPACSPRS <sup>L</sup>
18195	48563	A	18302	I	1011	
18196	48564	A	18303	I	1845	
18197	48565	A	18304	I	755	MSPVIDKMYVDAYOPFSEEKIS <sup>M</sup> QE <sup>A</sup> LEK <sup>G</sup> A <sup>Q</sup> PLREFMLRQ <sup>T</sup> RE <sup>A</sup> DLGL <sup>F</sup> ARL <sup>A</sup> NTG <sup>P</sup> LQ <sup>G</sup> PE <sup>A</sup> V <sup>P</sup> MR <sup>I</sup> LL <sup>P</sup> AY <sup>V</sup> T <sup>S</sup> EL <sup>K</sup> T <sup>A</sup> FQ <sup>I</sup> G <sup>F</sup> T <sup>I</sup> F <sup>I</sup> FL <sup>I</sup> DL <sup>V</sup> I <sup>A</sup> S <sup>V</sup> LM <sup>A</sup> LG <sup>MM</sup> <sup>V</sup> PP <sup>A</sup> T <sup>I</sup> AL <sup>P</sup> FKLMLF <sup>V</sup> L <sup>V</sup> D <sup>G</sup> W <sup>Q</sup> <sup>L</sup> L <sup>V</sup> AL <sup>V</sup> T <sup>G</sup> L <sup>I</sup> I <sup>S</sup> IQ <sup>A</sup> T <sup>Q</sup> IN <sup>E</sup> MTLS <sup>F</sup> PK <sup>I</sup> I <sup>A</sup> V <sup>F</sup> I <sup>A</sup> I <sup>I</sup> AG <sup>P</sup> W <sup>M</sup> L <sup>N</sup> <sup>L</sup> LD <sup>V</sup> VRT <sup>L</sup> FT <sup>N</sup> LP <sup>Y</sup> I <sup>G</sup> RT <sup>M</sup> L <sup>Q</sup> <sup>V</sup> T <sup>S</sup> EQ <sup>C</sup> A <sup>I</sup> L <sup>V</sup> K <sup>P</sup> V <sup>L</sup> L <sup>A</sup> V <sup>T</sup> A <sup>R</sup> A <sup>G</sup> AD <sup>L</sup> H <sup>R</sup> AD <sup>S</sup> ERT <sup>Q</sup> R <sup>T</sup> K <sup>T</sup> GG <sup>G</sup> F <sup>CRY</sup> W <sup>A</sup> G

SEQ ID NO: NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, !=possible nucleotide deletion, !=possible nucleotide insertion)
18198	48566	A	18305	I	1977	
18199	48567	A	18306	I	630	
18200	48568	A	18307	1715	1996	LFRLLKLTGRRKRSNKSITT CRGFWGTCAGWSRP*VVQK CRIYTMWR*WQHAQR*VSPAT LNGLMLITISRKNPHTRGAGK HCPFSGPS
18201	48569	A	18308	517	675	
18202	48570	A	18309	480	626	
18203	48571	A	18310	757	1146	
18204	48572	A	18311	318	724	
18205	48573	A	18312	I	1743	
18206	48574	A	18313	I	1197	
18207	48575	A	18314	161	613	LLRQGFIVVISAGGKRVEQOKLV FPAKFEAGFRHGVIANLRLYPF PEEKIGEMATAPLSTSGDCRT* YALIGIQ/PTDGDARGSPRYKPA LALLPACVGSAKSTPHGRTPIPA IVVPSSPT*FRALASDVSVAQT*Y CRPASQTRRASPASRL
18208	48576	A	18315	177	425	SRYFSATSTWPLVMSIPVTCFPS PASWLST*QSLPLPLPRSKIQQQF CRCSGITRPOPYYPDPKSSSFVD AQGSPDHSHNILGLLRRVHFAR LPECAWGPAWLW
18209	48577	A	18316	1	576	ADSSKKIADIISVIDGIAFQTNIL ALNAAVEAARAGEQGRGFAVV AGEVRNLASRSAQAAKEIKALI EDSVSRVDTGSQLVESAGETM NNIVNAVTRVTDIMGEIASASD EQSRGIDQVALAVSEMDRVTQ QNASLVQESAAAAAALEEQAS RLTQA VPRSVWQPAHSPINRK HHPVLPATGALMPGCGS
18210	48578	A	18317	121	1819	
18211	48579	A	18318	I	2151	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met/Asn	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion,  =possible nucleotide insertion)
18212	48580	A	18319	3	1127	GTPYASQPVIRPVEGSKPLIKQVL LDIGAHGTDKTIQKLRVAR MHFAQRRLAATVFCASQNA IALMEIAAANFSYEMIRLTECIL GFTWNRLYQGINVHNAERVHQ LAHDGHELVYVPCHRSHMDYL LLSYYVLYHQGLVPPHIAAGINL NFWPAGPIFRRLGAFIRITFKG NKLYSTVFRYLGELFSRGYSV EYFVEGGRSR/TGRLLDPKTGM LRRGGTRPITLPIYIGYEHVMEV GTYAKELRGATKEKESLPQML RGLSKLRLNLGQGYVNFGEPMP LMTYLNQHVPDWRSIDPIEAV RPAWLTPTVNNIAADLMVRIN NAGAANAMNLCTALLASQR SLTREQLTEQLNCYLLDLMRNVP
18213	48581	A	18320	1	2470	MFQPSDSGKSFIFNMSVGYNLE GIKQPPMCMQFIDNMMMDASDHP KFAQYRDTLNKLLQDDAFLAR HGLQEKRQSLQALPARITPSMV HGVTLSTMHGCPPHEIAICRY MLEEKGLNTFVKLNPTLLGYA RVREILDVCGFGYIGLKEESFD HDLKLITQALEMLERLMLALAKE KSLGFGVKLTNTLGTINNKGAL PGDSTSGVLRTYERLLTAWML TCPCADEHQRGESVKLATA WWLRLGSQNRDEITKDGFSQNH AGGILGGISSLQQQIAHMALKPT SSIDVPGRTINRFGEEVEMITKG RHDPGCVGIRAVPIAEAMLAIVL MDHLLRQRAQNAADVKTDPICRC AQSIGFSNNGCIVGADTLPIQSE HYQVMRTDQRRYFGHPDLVM FIQRLLSSQVSNLGMGTVLIGDM GMPAGGRFNGGHASHQTGLDV DIFLQLPKTRWTSALQLRQAL DLVSRDGKHVVSTLWKPEIFSL IKLAAQDKDVTIFVNPAIKQQ LCLDACTIATGCAKCDPGVSIG AYAYLLTLRAQCLAHDLDPDLE PLEIDGTLPRYVFHGGPRVFT YYTPKEESIKLFHDYLDLHGRSN PNLDVQMVPVSVMFGRAPGRE KGEVNPPLRMLNGVQKFFAVL WLGRDSFVRFSPSVSLRRMADE HGTDKTIQKLVARVARMLHFA RQRLLAAVGPRPLPARQDFNKL
18214	48582	B	18321	1	1460	
18215	48583	A	18322	2	234	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met/Asp	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /'=possible nucleotide deletion, ^'=possible nucleotide insertion)
18216	48584	A	18323	282	422	
18217	48585	A	18324	1	1974	
18218	48586	A	18325	154	1944	
18219	48587	A	18326	18	386	KACEAVF*DQGLPLGPVKVQQW WDWFPGPGLRHQQSAHQA GGFRSLWGYSGVSGQCRRHS *SRPGREARRRRSVAAG**SHAL HRQTALFGARSIDALPAAAPR YLLYRGLSAAHFRPQAG
18220	48588	A	18327	181	655	KARSPEDQGFRPRVHIDGGVW HLDVGSSHPGAEVGPKGMAVR HLKWyASWV*NVVRQGPYLV WALEN/WRGAAPSTRGHGVC/G ITVFGKSDGTT/SHDQY*TAPYG SPHPPGRWSLRHRYPAAHLTSSA LAFLSDARRNAARQPRRNPLS GYSQVICLPAW
18221	48589	A	18328	1	658	MDDGTSIAPDGDWLWAFIGDELK MGIPENDRIREQKQYLRNKSY LHDVTLRAEPYMYWIAGQVKK RNMPMELVLLPIVESAFDPHAT SGANAAGIWIWQ!!PSTGRNYGLK QTRNYDARRDVVASTTAALNM MQRLNKMFDGDWLLTVAA SGEGRVMKAIKTNKARGKSTD FWSLPLPQETKQYVPKMLAIS DILKNSKRYGVRLPTTDESRAL ARVHLISPVKCARFSRFVFCPA VCRDSSGGADERRTDSDCGQYA GGVKPE SVMGA E1VEGFHSIV TSAWSRGDNSPAPMAFSRLWL TVFMSIVFKRETVRSLSAVGA GELRGAAPSTRGPEWTHHWC GCHANGTARSAVVPDPMPNS EVKRRSADGSVGSP*RLITA VGS*RQLKRTKRVGNPRTSGRY RCRRKRSSSTCLKWCWV*VIFSKT ASVMAYVCQRPMLKAVLWRVC
18222	48590	A	18329	642	1343	LCLHPLPLTRFPRQL*EEGGPV QPAAMPQWRTLPGPGPGRPALPL PRLRGSSLRARPGRRLRGPRLR* RRHVGCGRRRAPLRLRAGLRRP RLPRARGPVRRAPLCSRPLL PLLPRPLRLRSRLHGSVA*VPSA PRRRKRLARGPAGPQARGPSAL PFASGSGTARGRGRRLCALA GPRAPPWPLPGCWVSLAGWD GAVSPRTPGCTQQPKDAGGFR GWSEAGVHDAQTV
18223	48591	A	18330	1	810	

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18224	48592	A	18331	236	717	ALPVGAFFSSTTGFSGFGAGG ASTFGLGGSTGFGGGATGAGS GSNSVLLAIVAGSSDGAASP ARTSSAAPSGGC/DQERRIVDFK RNKDGIPAVVERLEYDPNRSAN IALVLYKDGERRYILAPKGLKA GDQIQSVDAAIKPGNTRLSYG QHREAWR
18225	48593	A	18332	49	291	
18226	48594	A	18333	75	839	
18227	48595	A	18334	1	579	
18228	48596	A	18335	223	563	
18229	48597	A	18336	1	1219	
18230	48598	A	18337	157	864	RGNRQLQQFPRHWRSNRLDGL LLQIQLQILGGHTVERHLVVQI ALVVNVNGHPGHADGMWILCIRV LLSLQQNGFRRVPSIGHWTGH* AATDQARLMLGHHINAQFAGI QRLEDLGTQQLLHTTNGLVEVE ARRQILQLGLPLFLLLNQTDVVW AIPGVHVLRFDVVGRDPS/EVLI DPRQNAGLLWKVFAFTRPEPTR PAVCCPRGGQSGDDRAGCAC NHVELVARHRRSCPWHSDRH
18231	48599	A	18338	1	219	
18232	48600	A	18339	1	2226	
18233	48601	A	18340	46	228	
18234	48602	A	18341	382	1431	
18235	48603	B	18342	1	2400	
18236	48604	B	18343	1	912	
18237	48605	A	18344	2267	2539	
18238	48606	B	18345	1797	3411	
18239	48607	A	18346	1842	2560	
18240	48608	A	18347	1	1284	
18241	48609	A	18348	1	792	
18242	48610	A	18349	1	978	
18243	48611	A	18350	757	1011	LFGRFSNGFLIVVCQRLRQAVV NEQFLPETATLTHRCELLFHSP A*LPGVFRYLAQM*RHAVIDQVF RATGVPEPERCRQRRPHER
18244	48612	A	18351	148	679	RMSDDKFDIAIVGAGVAGSVA ALVMARAGLVDLVIERGDSAG CKNMTGGRLYAHTEAIIPGFA VSAPVERKVTRKEFISLTEESAV TLDFHREQPDVPQHASYTFVLRN RLDPWLMQEQAQAGAOFIPGV RVDALVREGNKVTGVQAGDDI LEANVVLADGVNSMLGRSLG MVPAS
18245	48613	A	18352	1168	2241	
18246	48614	A	18353	1	1344	

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18247	48615	A	18354	440	886	
18248	48616	A	18355	1	2876	MAGVPGFEPGNAGIKNRLCTA WRYPIRTTLSGEWCGRRLNSQ EATLQQPLLQAIIDLKKHYPVKK GMFAPERLVKALDGVSFNLER GKTLAVVGESGCGVLAETLFA WNKNYFVLLFGVFLSSFGSTA NPQMFALAREHADKTGREAV MFSSFLRAQVSLAWVIGPPLAY ALAMGFSFTVMYLSAAVAFIV CGVMVWLFLPSMRKELPLATG TIEAPRRNRRDTLLLGVICTLM WGSNSLYIINMPLFIINELH
18249	48617	A	18356	606	726	
18250	48618	A	18357	1271	1726	
18251	48619	B	18358	1	1633	
18252	48620	A	18359	1	407	
18253	48621	A	18360	427	2307	
18254	48622	A	18361	120	694	
18255	48623	A	18362	804	1087	KRQHILCTHSGAIRLRIAGVGSW KG/GRPNWRKMAVRWRVPASA VVSGWLRRWHCWPVAMPSAE SPRIRCGAGCCICRLPLFRCGCC TPARLTISH
18256	48624	A	18363	216	436	
18257	48625	A	18364	476	577	FRRWYWGCCSTTRLSHCLTR* M*CMRWSLAVCC
18258	48626	A	18365	1159	3744	
18259	48627	B	18366	169	743	
18260	48628	A	18367	2811	3513	SLPRGWFQPEYGNLEIMEKTYN PQDIEQPLYIEHILGFPRVGLRRE LKKAAQESYWAGNSTREELLA GRELRARHWDQQKQAGIDLLP VGDFAWYDHVLTTSLLGNVP ARHQNKDGSDVIDTFLFRIGRGR APTGEAAAAEMTKWFNTNYH YMVPEFVKGQQFKLTWTQLLD EVDEALALGHKVKPVLAGPGT WLWLKGKVSEQFYRLSLLNDI LAGYQQGLAETGVGPDDIVTA

SEQ ID NO: NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion,  =possible nucleotide insertion)
18261	48629	A	18368	1	2810	MKQTVIYIASPESQQIHVVNLN HIEGALTTLTQVVDPGVQVPMV VSPDKRVLVGVVRPERFVLAY RIAPDDGALTFAAESALPGSPT HISTDHQQFVFVGSYAGNVS VTRLEDGLPVGVVHVVDGLDR LARQLIKNLATLKAGNARVVN SNAMSFLAQKGTPHNIVFVDP FRRRLLEETINILEDNGWLAD ALIYVESEVENGLPTVANWSL HREKVAFAAGAEPYHYNLHTL GFPVRGLRRELKKAQDSYW
18262	48630	A	18369	2279	2563	MNFGASLNSPTPRSYLSLGGK KAPVWEHTLGVPSSRPAAGKL KKAPERYWGGEHPVKKWL G*ARKCRPRPWETL*KSHLRRR PSLGPWAGGL
18263	48631	A	18370	481	1020	
18264	48632	A	18371	1	998	MNENFGTQICVNRRSLFTDCSG YVTRYDHDRFGQVTAHVREEG LSQYRAYDSRGQLIAVKDTQG HETRYEYNAAGDLTTVIAPDGS RNGTQYDAWGKAICTTQGGLT RSMEYDAAGRVIRLSENGSHT TFRYDVLDRLIQETGFDGRTQR YHHDLTGKLIRSEDEGLVTHW HYDEADRLTHRVTNGETAERW QYDERGWLTIDHISERHRVTV HYGYDSKGRLASEHLTVHHHQ TNELLWQHETRLAYKRTGLAN RCIPDTCPVNAYLGTCACQHE ICDTPWLSYRDPFTGKSWLSGR YELHKRIVGITAKERKDVDFW HPDVRFFELYDENNELRGSFYL DLYARENKGGAWMDDCVGQ MRKAIDGSLQKPVAYLTCNFNR PVNGKPALFTHDEVITLFHEFG HGLHIMLTRIETAGVSGISGV WDAVELPSQFMENWCWEPEA LAFISGHYETGEPLPKELLDKM LAAKNYQAALFILRQLEFGLF FRLHAEFRPDQGAKILETLAEIK KLVAVVPSPSWGRPHAFSHIF AGGYAAAGYYSYLWADVLAAD AFSRFEEEGIFNRETGQSFLDNI LSRGGSSEPMDFKFRGRREPQ L*HTVVELPRPFHREILAFRPL*I TQAYLRHHR*RA*RC*CLASGC

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met in USSN 09/540,217	location of first codon for peptide sequence	location of last codon for last amino acid of peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, =possible nucleotide insertion)
18265	48633	A	18372	409	533	TGNADAPVPAQSAQYRYLQ*SVRNFCRLSFRGLINLSSLPPYHIVDDVPLMAEGKILPYLDIPLQHASPRLKLMKRPG
18266	48634	A	18373	222	659	SAGSVKTQRSQGANKQRRTRSRLASF/ETLSSVSPFWRKISFLIPVGLPISNNYVCSLNPVWCAMRLNMPMPSKICWQKHWKSTVSRWITTRISFVQLTISTACWRSPVTQSSWRSTFACSTGGLSHAPP LPIRHCTNITNVWY
18267	48635	B	18374	1	1527	
18268	48636	A	18375	1	1005	
18269	48637	A	18376	2	314	WVSYCSGSGTTL/LLRALQECQRQQGPWASAGDPGEAGERERLPOQALASPLQVKPARQ/RDPGLRTPDPGDTASPALNGHIIALPA GTAGDCFPRPPRGRKNNSGT
18270	48638	A	18377	3	576	
18271	48639	A	18378	189	563	QGRGSSRPAGCGHLDPGGEELWPQRPGHQHLCPSAYILIFAGVLVMVTGFLGFAGAILWERKGCLS TTGDRFWKDRQPWTCR/WQTSHRNQSGAGGQWDRFRSHQGRDHEGRTSN/WGSGFPREVA
18272	48640	A	18379	1	531	
18273	48641	A	18380	1385	1673	AASTDRAAETG**KTR/HRWFLSVKLRTSTPTAVSPKK*KRLAWTRCMTPPSKR**KKRVTITPSSPTSLTSTLPGATVATSPVMPRVNWCSTAVCRS
18274	48642	A	18381	1	921	
18275	48643	A	18382	1	2115	
18276	48644	A	18383	2	149	ARRNESRRGGR*HPCRPIT*TGTVNQRPAGFRRFAGPFYRGKPGRERL
18277	48645	A	18384	482	1655	
18278	48646	A	18385	1	776	MENACVLLMGVLSTFLVSWLGKDAMAGVGLADNFNMVIMAFFAAIDLGTTVPGAFSLCKRDRRQARVATRQLSVIMTFLPVLLAPLIHFGEQIIIDFVAGDATTEVKAALTYLELTVLSYPAAAITLIGSGALRGAGNTKIPLLNGQVAMLMQAPYYFQEAQIEAAIAMDVAPEYADIRQVESSTAVLYLFSERFMTYKGAYGLCEWFEGSRLSIAHIPVTNDNETQYHFFRQSCQHC/DRCSVHRLPDGGVVA

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met/ Iod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, !=possible nucleotide insertion)
18279	48647	A	18386	1017	9228	FGRCAGVVCQ*RG RDGQRRDEA GDGRLRRL*ALYQTITHDLR YRHKNLYRRKLA SQRVTEHV RAGL RYSYQYEKDCITITDSLA HNKV LHTQGEAGLKR VVKKK HADG SVTQS QFD AVG RLA QT DAAG RTTE YSP DV VGL ITR PDGR ASAF YNNH NQL TSATG PDGLE LRRE YDEL GRL I QET DGDIT RY RYD NPH S DLP CATED ATG SRK TMT W S RY QG LLS T CSGY VTRY DHD RFG QM TAV
18280	48648	B	18387	1	1431	
18281	48649	A	18388	575	835	RQKPERYL TAF I SITPLR RWMT LVR VMR PIV TCR SRS ILRSIS HLCK W RV VSTKSPV ILW TLISN* RL FWK SWR* NGL QSKY QDG
18282	48650	A	18389	1207	2465	ASTAQ QHQQLL SPAKEE TT GW FHPS DPW ALGRS QGGAGL IQPP EVQ KG SVR YRAR F ALLG PAMV AHR HTGR PEIR YRYD S DGR VTE QLNPAGL S YTYQYEKDR II ITD SLDR REV LHTQGEAGL KR VVK KEHVA DGS V TQS QFD AVG RLA QTDAAGR TT EYSP DV VGL ITR ITTPDGR ASAF YNNH NQL TSATG TGP DGLE LRRE YDEL GRL I QET APDGDIT RY RYD NPH S DLP CATED TEDA TGS RKT MT W S RY QG LLS FTDCSGY VTRY DHD RFG QM TAV VHREEGLS QYRAY DSR GOLIGV KDTQ GHETR FEY NIAG DLD GGI APEG G/RNG/TQYDA/WGR RRTT /QGG DADRS SAG GTR ARK RGHT SFRS VGD RTV SRH GY PGR NLR RMVR SS VPL YRL TASI APV PQE YRFP PHQ SEE VY
18283	48651	B	18390	1	2604	
18284	48652	A	18391	1	2640	
18285	48653	A	18392	1	549	
18286	48654	A	18393	290	389	HLCGP RTAR*AR FWHL*RAYG L*SGEC R RAG SV
18287	48655	A	18394	1095	1268	HLCGP RTAR*AR FWHL*RAYG L*SGEC R RAG SV AEN ARSAC RC RRSA HAG RFL QTAS
18288	48656	A	18395	1056	2178	
18289	48657	A	18396	1	669	
18290	48658	A	18397	1628	1856	
18291	48659	A	18398	227	668	
18292	48660	A	18399	1	3186	
18293	48661	A	18400	291	631	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met	SEQ ID NO: in USNN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, =possible nucleotide insertion)
18294	48662	A	18401	1	1437	
18295	48663	A	18402	345	727	
18296	48664	A	18403	870	1043	
18297	48665	A	18404	1	2175	
18298	48666	A	18405	1	1332	
18299	48667	A	18406	1	1566	
18300	48668	B	18407	1	921	
18301	48669	B	18408	1	2487	
18302	48670	B	18409	1	2919	
18303	48671	B	18410	1	2214	
18304	48672	A	18411	1714	1979	RLAWRLAGRWWAGSWRTSTIP PAAACSLRLCSPPSKFCSAWCR WCSTRACSSCCRSTSSPMPAWR PSAGS=LSTARRRAPPSSALVRLI
18305	48673	A	18412	1201	2118	PSRQADKENRPHPGRGRYPARM MSGLTGTTTVSTGWCCTTRGHN MKSRSWVKVAIFTTWRGVRRVAK RVWRRERDLTGWMSSLRKPKQV TWYGDGDRLTTIQNDRTRIQ TIYQPGSFTPPLIRIPVLLGGDDTT MDCLRTSIRLNAASVTCAYRRD QISMPCSRKEVVNAREEGVEFQ FNFQPQYIACDEDGRLLAVGLI RTAMGEPGPDGRRRPPPVAGSE FELPADVLIMAFGFQAHAMPW LQGSGIKLDKWGLIQTGDVGY LPTQTHLKKVFAGGDAVHGAD LUVVTAMAAGRQAARDMLTLF DTK*PGTAGTATG*POYRITEP ASRRFISRGASRHSSSEGS/SVLG GGDTT/MGLFADFHPQQCRQRD LAPYRRDQISMPCSRKEVVNAR EEGVFQFNFOQPYIACDEDGR LTAVGILRTAMGEPGPDGRRRP PPVAGSEFELPADVLIMAFGFQ AHAMPWLQGSGIKLDKWGLQ TGDVGYLPTQTHLKKVFAGGD AVHGADLVTAMAAGRQAARD MLTLFDTKAS
18306	48674	B	18413	1615	1656	
18307	48675	A	18414	1287	5056	
18308	48676	A	18415	1	271	
18309	48677	A	18416	1	588	
18310	48678	A	18417	2150	2332	
18311	48679	A	18418	1	238	LEELGVIGAVLVGFSL*VLWAP LQLPKAGGRVKVAGIQQLGEVEF WKVSVKSCSSPDPPPGVMAAKIS ISQALQQPQSTR
18312	48680	B	18419	1	2721	

SEQ ID NO: NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, ==possible nucleotide insertion)
18313	48681	A	18420	712	1031	PVMRQRGVFRSVLILKIRSARCC QMIQPRVISHAMYSLSPFFALR RSTKSPKRFSMNNS*ASRSSGST SRDTSAIS*ARRSISSRTSRLLIRS LISLISSLLVNVV
18314	48682	A	18421	1	1779	
18315	48683	A	18422	693	921	
18316	48684	A	18423	758	1183	ALTAASRSECAVIMMTGRTSCC DIVEKWIPIARCCQMIQPRVISH AMYSLSPFFALRRSTKSPKRFS MNNS*ASRSSGSTSRTDSAIS*A RRSISSRTSRLLIGWRSLWYTILI NSIPPTNRAKSMKPEPSPNACSK VKRCC
18317	48685	B	18424	1	708	
18318	48686	A	18425	1	2436	
18319	48687	A	18426	1382	1813	
18320	48688	A	18427	900	1028	AGYAAPGRTDRRSSPSG*GYR SGCYQICRQPGRGLGSRKSPV
18321	48689	A	18428	1	881	MTPSRFAKKNGSLVKRCPMGI DAEVMTIKPIAARPVKVSHSKVR SYMIRLSVSFSREPITQPFSAVEI QTRIRYGVSGFFLRRVDTEHHP DRHAARALQYHITGSNRCDAIN AVQFDAAGGECTNRRMAEDHG RNVAVIQMLIRLVIKQAFREV SELWTRNQKACCPFLDFDCGENS AIAANNYDWFGGNMNVLTFRLD IGKHFSVNQMINKEAVKQRLN REDQGISFTFSYNNLQQGYDFA CLNKQYGVVLQIGGSQDWGNI TSGIDLNPSSASESGVVWPDRSA DH*SRWHQIW
18322	48690	A	18429	1	3270	
18323	48691	A	18430	1	374	MKTCWQILEIESTTQIDIIRQAY LARLPLCHPETDQPFKALRQA YEEALRLAVNPVEEADDEEKD AAAEHEILRAFRT/FTGFRK*SFS AFRLAEIYSAIKYLEHGGCRSIT LAAVCNRHRSAI

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met/Asp	SEQ ID NO: in USN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, ^=possible nucleotide insertion)
18324	48692	A	18431	63	1272	LRRSCNAVYCW*CVATCP\$IGE EDGIVLIDQDKCRGWRMCITGC PYKKIYFNWKSGKSEKICFICYP RIEAGQPTVCSETCVGRIRYLG VLLYDADAIERAATENEKDLY QRQLDVFLDPNDPKVIEQAQIKD GIPLSVIEAAQQSPVYKMAAME WKLALPLHPEYRTLPMVWYVP PLSPLQSADAGELGSGNGLPDV ESLRIPVQYLANLLTAGDTKPV LRALKRMLAMRHYQRAETVD GKVDTRALEEVGLTEAQAQEM YRYLAIANYEDRFPVPPSSHREL AREAFPEKNGCGFTFDGDCHGGS DTKFNLFSNRRIDAIDHQQEMF EAIAASKNLPKDEADHALGIFLR DLTTMDPLDAQAQYSELFDRG RATSLLLFEHVHGESRDRGQA MVDLLAQYEQHGLQ
18325	48693	A	18432	2	859	WPLRSPYSIINGSGKSAASGSV MQVAQFNSHYQYDPKPFRGM LYEHRRCFNNIUDYCNSLCYH AWLVAHKDDIERNYRGPLVQV VGWCDAIFGAELGIRSAQFDQ FLRMMQGGAQFGGGYQQQTG GGGRPGGHFFEKRRLRVMVDR LNARFTGGVLVFSFKGPLLEGFG PWQGLSPWVIGPDLGLPG/CLG AWGAWSVCHCPWPVCKTGSFWR WVPHRRFHPPG*KFPENWMG FCSSRTCSGLFSHPHSPTMFKN FELGHGTPPRGTRNRPTMSSNT YRPHRFQ
18326	48694	A	18433	479	601	CWRPLPAEKRWYLAANWW RLAARFVFPMLCVRQ*PSSMIW TTPDADIAIGTWRSCCAVLRGR KMPVSSITMRRRCY*CWRPLPA EKRWWYLAANWWRLAARFVF PMLCVRQAAPYTK
18327	48695	A	18434	69	194	ATYENMLANPRN^KHDANRH PPGLSCSLTVVSSRNRSARV
18328	48696	A	18435	173	298	ATYENMLANPRN^KHDANRH PPGLSCSLTVVSSRNRSARV
18329	48697	A	18436	1	1734	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met/Asp	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, ^=possible nucleotide insertion)
18330	48698	A	18437	851	2202	RQKRLIFCCVKGKNWPP*WRWLNEKLPCLMMLPPTLPPSVLGIQLQNQLQRQFVRQGGVWMPGD EVKKVTCNGVNEIWTRNHA DIPLRPRFAVLASGSFFSGGLVAERNGIREPILGLDVLTQATRGEWYKGDFAAPOPWQQEGVTTDE TYARHRQGKPLKTCPLPSVRCWADLIPS PRDAAAVFVPSVLYMPLNRLPNAQEANNE
18331	48699	B	18438	1	5301	
18332	48700	A	18439	710	889	
18333	48701	A	18440	1622	2615	
18334	48702	A	18441	1	1309	
18335	48703	A	18442	1	266	PRQCGFMKKRLENGDDYFAVNPRGRCLHCCWMTVLC*RKRSDDYAVSCRQRPRPPVLA PVNSISRSVSPYTPPEEYKPTVRAQLEKNCNM
18336	48704	A	18443	267	395	
18337	48705	A	18444	1	3807	
18338	48706	A	18445	1	2193	
18339	48707	A	18446	1278	1846	SCRSPRNRHQIPGTYRSRLPRHTTPPGYDHNRKNPNNLYISTRQKRD AFFAVQVHSLLYYRQTLPPNDHNQSVDR*FVFRLL*QNQGYNSGRHLWYRWHSYNAWL*LCHRHPVYYRLYYIFLQPVQMQMPQCPSPLMPECSSFSFLILINA/SNIQRESPVENRKVFNLRLKKIYRLIIIFLKGCGNLLNL
18340	48708	A	18447	1	2106	
18341	48709	A	18448	881	1401	
18342	48710	A	18449	1	233	MMGFDGTVQYMASLGAPMPMLAA/MYCGSYGSARRDINRAWLFHPSAGGAVYFLHAGYGGDWSPLLGYDRRCGWAKYD
18343	48711	A	18450	1	1960	
18344	48712	A	18451	563	928	FSAIKSSPKAQALWHVHLHY*AVN*TNIKFTEKPIFNRGKRRPPTP TRQLRECWIVWGSASCQLTKQAVVARWTIILMRRKGWHGRAII LMPGGPRLKQVPRQFCKPPAACARLSKSMGRC
18345	48713	A	18452	1	828	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met/Asp	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=-possible nucleotide deletion, !=-possible nucleotide insertion)
18346	48714	A	18453	1	1327	MMQKPATVDEEESPRETHRYS VRRRGELIVEAGGRAENTVVT GAGWLKVATGGIAKCTQYGN NGTLSVSDGAIATDIVQSEGGA ISLTLATVNGRHPGEFSDKG YACGLLLENGGNLRVLEGHRA EKIIIDQEGGGLVNQTTSAVV DEGGELLVYPGGEASNCINEQG GVFMLAGKASDTLLAGGTMN NLGGEDSDTIVENGSIYRLGTD GLQLYSSGKTQNLSVNVGGR EVHAGEVTDIHEVITDASRQT LCNALKLQPDEGGSSRVIPTCK ASRLRIDANFKRKFVDEEVLPGT GLDAAAFAWRNFDEIVHDLAPE NRQLLAERDRIQALDEWHR NPGPVKDKAAKYSFLRELGYL VPQPERVTETTGIDSEITSQAG PQLVVPAMNARYALNAANAR WGSLYDALYGSDIIPQEGAMV SGYDPQREAMECP
18347	48715	B	18454	71	4995	
18348	48716	A	18455	1	3572	MARKRKSRNNNSKIGHGAISRIG RPNNPFEPCCRNRYAQKYLTAL MGGAAFFVLKGCSDDSVNDND GDGTFYATVQDCIDDGNNNADI CARGWNNAKTAFYADVPKNM TQQNCQSKYENCYDNEVQS WIPVVSFGFLSRVIRKDRDEPFV YNSGGSSFASRPVVWVPSIVIMS YGLASYVIAVAFLERDRIQAL DEWHRSNPGPVKDKAAKYSFL RELGYLVPQPERVTETTGIDS EITSQAGPQLVVPAMNAR
18349	48717	A	18456	485	1999	
18350	48718	A	18457	44	270	
18351	48719	A	18458	1	2223	
18352	48720	A	18459	290	756	
18353	48721	A	18460	8	314	
18354	48722	A	18461	2	686	
18355	48723	A	18462	1	732	
18356	48724	A	18463	1	780	
18357	48725	A	18464	101	435	
18358	48726	A	18465	805	993	
18359	48727	A	18466	452	2180	
18360	48728	A	18467	691	1443	
18361	48729	A	18468	1	320	DPRDCRLKVGKEMFTLFGPQF VRELQQRGFDIFLDLKHFHDIPNT AAHAVA AAAADLGVWMVN VH ASGGARMMTAAREALVPFRPD APLLIAVPV*RSIKASDLDVPL

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18362	48730	A	18469	632	796	
18363	48731	A	18470	129	425	TDIITRQNGTGANIDAEIIATKA STGLFVYQPRFARCPRVMSGY HTATRGSSGTRTVARVCHTA AGVYGSKSKTQF*NRFCQRKCR RYPDGCRRA
18364	48732	A	18471	1	1062	
18365	48733	A	18472	1	996	
18366	48734	A	18473	1	1004	MLRVYHSNRLDVLEALMEFIV ERERLDDPFEPPEMILVQVSTGMA QWLQMTLSQSKFGIAANIDFPLP ASFIFWDMFVRLPEIPKESAFN KQSMSWKLMTLLPQLLEREDF TLLRHYLTDSDKRKLQLLSSK AADLFDHVSGASVSSKVEQLR AQLNERILVLDGGMGTIQSY RLNEADFRGERFADWPCDLKG NNDLLVLSKPEVIAIHNAYFE AGADIEETNTNSTTIAMADYQ MESLSAEINFAAKLARACADE WTARTPEKPRYIVAGVLGPTNR TASISPDVNDPAFRNITFDGLVA AYRESTKALVAGIVLMPAIPAL WEAEPGGCA
18367	48735	A	18474	606	846	
18368	48736	A	18475	3042	3933	GPHPPAPGGPA CHYDVHQPYL RQRTEDRRTRHYLAQSFQAYSL RQWAFHFLLDNITPDIQQVIAH TRRTGGFTITASEAAIEMLLCFK RDFVALQHLFNQIDAPARAQVQF IAQKLIGWACCEAARKNQLPH NTTKRSLLMSILYEERLDGALP DVDRTSVLMLREIIVPGLEILP TDEEIIPYQCDGLSAYTRPPLV VLPKQMEQVTAIALAVCHRLRV PVMVFPGLRLSREAFLTAEFG TQELRRAQQLRQLVYRLLSTAG RHHPAQNSPIRVLEVDidLLGG TQELWGKETH
18369	48737	A	18476	869	1639	ICSRCKSRTSPTRCRKAIVIL VCFVIRELLVVAPELIIIGIPEG NWITVSKGMLAKSPVDSNSTQ LKEAEEERLKAQYGLQLVES QNELQNQLDKCRNEMMTMT MQLRNKRRRELGNLIIKRFRSG AESLPDAVVLTEEGGIFWCNG LAQQILGLRWPEDNGQNLINLL RYP/EVVAISENA*FFSPAQSGA QHRAASGNRSHALYPTQTVADG GA*CHANASTGRGAA*LFCQRE P*VTYAIIDRVTVGLPGDDE

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, -=possible nucleotide deletion,  =possible nucleotide insertion)
18370	48738	A	18477	388	2356	
18371	48739	A	18478	137	318	GGQLSSWAMDFCHL/PAFWNS MTWHLQRLWGACGYFWHAQ WERLLTTFEGNEWLIFIGGIL
18372	48740	A	18479	923	1149	
18373	48741	A	18480	I	373	
18374	48742	A	18481	168	360	
18375	48743	A	18482	I	147	
18376	48744	A	18483	161	440	
18377	48745	A	18484	277	2172	
18378	48746	A	18485	164	406	LFRREGSYDRYLLMDDYCRRK DDSYFDRYRDSFDGRGPPGES QSRAKGKVAETVSY**NTL QKREETNNQYPHLKKG
18379	48747	A	18486	405	999	
18380	48748	A	18487	64	288	
18381	48749	A	18488	159	550	CAVCHISFQDTPVLVSSNVTMQ FGSKPLFENISVKFGGNRYGL IGANGSGKSTFMKILGGDLEPT LGNGSLDPNERIGKLRLQDQFAF EEFVTLDTIVMGHKELWEVKQ ERDIYALPEMSEEDGYKVAD
18382	48750	A	18489	3	481	
18383	48751	A	18490	2	233	
18384	48752	A	18491	2	3026	SVPTIFFFFLPVLRFWRPGIQQA KKCHLFATGTQSRRNTRQRT AKGIPQQRMATAKREEISIGILHV TPQQRRECRGDNRFTARRRTP WRLLGHCVSAAVTVGLPVAVG SPLAYSDTDEFYPVAGGTMSPQ HLPLVAAQPGIWAEMAKLSELP\$ AWSVAHYVELTGEVDSPLLAR AVVAGLAQADTLLRMFRTEDNG EVWQWWVDDALTFLPEIIDLRT NIDPHGTAQALMQADLPQDLR VDSGEPLVFHQTTLGF
18385	48753	A	18492	2714	3079	RLIGLRLMVRFVGLIRRASVAS GSWHCCRMRKKRLIRPKPSILQ SMLWSPSTRRMFFTLVPIFSIEE LPFTFRSLMMVTLSPSASRLPLA SLTISSSLSCAGSASFHS*AHSG QMYMPPLSS
18386	48754	A	18493	I	888	
18387	48755	A	18494	1778	2025	
18388	48756	A	18495	I	1425	
18389	48757	A	18496	3	96	FVGRIRRLRRIRRY*FTPLTD*LS CAHQVP
18390	48758	A	18497	420	955	

SEQ ID NO: NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USNN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, ^=possible nucleotide insertion)
18391	48759	A	18498	533	1006	RPSIFACVSP*RINHSRIMPQTN AKNAKPNPAQVMRGVISRRR AMLFNSNAITRTPTTSTPMAITS ASSSPPAVKVVSICPHGINTPTNIC NTTSCFLIPHPMTPKPLPLYSE SGPSCSSCASAARSNGSLPISIKV ANAQAQSASTSGMLWLQSGQ
18392	48760	A	18499	3	418	EWHYLSDARRQCAFQGVSRKT ATVCHHPDYYAGSLYRLYFT DRLRARLAGHAAES/GTPASHA VFQLVLE*L*SPLFSPVSTSGGR TANSTVLMKSCMSGAVERQPT NWQAILMFLIFVVFTLQITYWA SNAYVLAG
18393	48761	C	18500	63	500	
18394	48762	A	18501	1	1107	
18395	48763	A	18502	1	153	
18396	48764	A	18503	88	510	
18397	48765	A	18504	204	654	
18398	48766	A	18505	241	771	
18399	48767	A	18506	1655	1909	
18400	48768	A	18507	2	48	
18401	48769	A	18508	1	585	
18402	48770	A	18509	1	723	LQPPGRRWAAPAVISGLSRQV RCFSTSVRPFA/KLVLGVP/SVQV SVIEGRYATAL/YYAASRQNKL EQVEKG/LLRLVAQILEGTPKWA ASVLESPLMLKAFPLKVKKPKM TITAKVGGSLPLTYQTLINFA ENGSD*GNYPRESFSGLFLTM GVFHRSRERVP/CTV/TSQIFL*EG RPQFSEFKNCSSRGFLRSRAKFL KLGAK/TDPSNLGGMIVRIGE/K YVDMMSVTKTIIQKLGVRAMREI
18403	48771	A	18510	400	894	
18404	48772	A	18511	1	1023	
18405	48773	A	18512	73	424	RPGMWSTRSPNSTAWPLSLEPD PGMASACTTMHTTTIAEPPDG MSGWPDRGMETSSPTIMDIVVI *CAIAAEAIIVLVSLLFVMLRYM YRHMGTYHTNEAKGTGVADS ADACPAGDPA
18406	48774	A	18513	141	563	RPGMWSTRSPNSTAWPLSLEPD PGMASASTTMHTTTIAEPPDG VSGLPUDGRMETPTPPIP/LTMV VIAGVIACLWPFPVLSLPSFVM VALTLLTGHKGARTTPNEAKG/ TEFAES/ADAALQGIDPAL/QDA GDSSRK/KEYFI

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met/Asp	SEQ ID NO: in USNN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, + =possible nucleotide insertion)
18407	48775	A	18514	182	935	QAFELHCPCKRKPFSTLPLSPAWPP RHTDLRKGRRTAQ*YAGNES HPPSLPRYLRRSRH/SMRQAPSS TCSYSHTSLQCSAPQNH/AQHP *PALEELACG/SPSVSSPYLVLSS CQEQQPHCCPPSTPRPSW/CPSS GDAICYSPGQ/CPRSRCPGLP\EDS SDSPPAEQVLPSSGSHNTLYLR CKRFSAFILNCEPPSKV\*KPGHHR CRS\AGILTLLPPG/ERGP/GDGP CSTGRQSASKTPPPPSHPTGHSLWSEEK
18408	48776	A	18515	48	676	KARLTWQQTREESLCRETTPYK TIRSRETYSLSPREQHKGDKLPP\*F NYLPPSPSHNTICPG\*QDQGRFT Q\PLYLCKRFSAFILNCEPPSKV\*C\*KPGHRCRS\*AGILTLLPPGGE AQHFVKVHPSIPL/REGGEVGIK PKKTSPTGTELLMQP/CHQPSRPT CQAPRKSNSRPL/GCLCPLMKHSL TLGYLLWLQKATWLKGFGTSG W\*M\*GRFH
18409	48777	A	18516	86	92	TANAALHQPSPRTCQAPRKSNSR RPQAA\*ALNC
18410	48778	B	18517	1	2031	
18411	48779	A	18518	98	367	DLFLYLSWQHCHPYSHCHPNQ KPGRFLMKLSS\*ETVTIELKNGT TRSHGTVIHQVWDVQ\*MNTHL KAVKMTLKNREPVQ\*AETLSIR GNNIRV\*FILPD/SVYPLDTLLVD VDPKVKSKKREAVAGRGRRG RG/TRDVARGR\*RGNNIR
18412	48780	A	18519	1	310	
18413	48781	A	18520	37	136	RRRPSSSWALPPSRGPSS\*AER GAQHQQPVPA
18414	48782	A	18521	3	305	FFTLCIQLWGLFSCESPCSGVGR YWA\*VCLCFLQIEAIELPMDPK LNKRRGFV\*FITKEEEPVKKVL EKKFHTVSGSKVRCSQLCLASC AAGELALRGMG
18415	48783	B	18522	249	367	
18416	48784	A	18523	1	1008	
18417	48785	B	18524	17	835	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, ~=possible nucleotide deletion, ^=possible nucleotide insertion)
18418	48786	A	18525	2	1188	SLIKLNSPPPRGGGTARYGAWL LVGGFPCGGGGGGDVTGAAP WADWGEASAAAASFVLAEC ARLSSLRVGDEAGSRGVWRA SPPRRLGLALSEAG^E\QPMETT GASENGHEAVP^VASRGRGCW TPLRRGLEAPRRPRAIGTAPR D/QRINASKNEEDAGKMFVGGL SWDTSKDLKDYFTKFGEV\W DCTIKMDPNTGRSRGFGFLFK DASSV^KVLDQKEHRLDGRV D\PKKAMA\MKKAPVKKIFVGG LNPEPSTEKEIKRESFGE\GIEIAI ELPMDPKLNKRRGFVITFKEE EPVKVKLEKKFHTVSG\SKCEIK VAQPKEVYQQQQYGGGGGRN RNRGNRGQ/GGGGGG*GQGS TNYGKQTQRRGGHQ\NNYKPII EAGRQERPT
18419	48787	A	18526	3	784	
18420	48788	A	18527	3	1990	PAMNGLSLSELCLCLFCPPCPG RJAAKLAFPLPEATYSLVPEPEP GPGGAGAAPLGLTRASSGAPG RWKLHLTERADFQYSQRE\RST IEVFPTKSARGNRVSCMYVRCV PGARYTVLFSHGNAVDLGQMS SFYIGLGSRLHCHNIFTYDSSGYG ASSGRPSERNLYADIDATWQAL RTR*GRPLVGRVRAWRPRLTL LRRRQVRHQPGQHPSTCTGRSIG HGAHRTWPRATSVPRWCCTR RSTSGMRVAFFDTQERPTASTP FPYIRERCPRLTSPRAHHPTGTK DEVIDFLEAGWRSTRCHQGG GAAVGGGGPGHNDIELYSQYL ERLASLSFSQELPSQRA
18421	48789	A	18528	82	406	

SEQ ID NO: NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
18422	48790	A	18529	2	1474	ARASGSGSSSGQKGMQGS\QRG GHGSGGGKKDDKKKKYEP VPTRVGKKKKTKGPDAASKL PLVTPHTQCRLKLLKLERIKDY LLMEEEFIRNQEOMPKPLEEKQ EEE\RSKVVDLKGGLPRLSVGNL GKRFINDDNHA\IVSTPVGSEHY\ VSILASFVDKDLLEPGCSVLLNH KVHAVIGVLMGD\DPPLVTVM KVEKAQETYADIGGGLDNQI\Q EIKESVELPLTHPEYYEEMGIKP PKGVVILVPPG\TGKTFPLKAV ANQTSATFLRGGGSELIQKNLG DGPKT\LSRELFIRVSEELAPSRL FIDRILPPLGTKRY\DSNSGGE\R EFQRTMLELLNNQLIDGFDSRG DVVKVIMPTNR\ETLDPALIRPR PAFDRKYEFP/LCPDEK\TKKRIF QISHKS\RM\TLADVGTPTWTTLI MAIKDDLSGA*PSKA\CTEAGL MAL\RENRRMKVVPN\EDFKKS KENVLYKKQEGTPEGVVSLMN PWLVIRKVMVGRFLNP
18423	48791	A	18530	2	274	WQDLICRMAASVKEQSTKPIPL PQSTPG\ESHSLSTSGKSEVRDL FVAERQFAKEQ\HTDGT\KEVG EDYQIAIPDSHLPVSEERWALD ALRN
18424	48792	A	18531	3	844	

SEQ ID NO: NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
18425	48793	A	18532	261	2814	VRFRNLIRIYCNIKICAVSHC KVFKLSLFFLHRFDSVAFGES QSEDEQFENDLETDPNWQQL VSREVLLGLKPCIEIKRQEVINEL FYTERAHVRTLKVLDQVFYQR VSREGILSPSELRKIFSNSLEDILQ LHIGLNEQMKAVRKRNETSVID QIGEDLLTWFGPGEEKLKHA ATFCNSNQPFALEMIKSRQK KDSRFQTFVQDAESNPLCRR LQKLDIPTQMQR LTKYPLLLDNI AKYTFEWPT TEREKVK KAADHCRQ JLN FVNQAV KEAEN KQRL/E EDYQ RRLDT SSL\K LSEY PNVE RLRN MDL TRK KMI HEGP LWV KVN R DKT IDLY TLL LEDIL VLL LQK D R L V L R C H S K I L A S T A D S K H T F S P V I K L S T V L V R Q V A T D N K A L F V I S M S D N A Q I Y E L V A Q T V S E K V R R A L D A L R N L G L L K Q L L V H Q L G L T E K S A L E N W Q H P R Y R T A F Q G P Q T D S V I Q N S E N I K A Y H S G E G H M P F R T G T G D I A T C Y S P R T S E F A P R D S V G L A P Q D S Q A S N I L V M D H M I M T P E M P T M E P E G G L D D S G E H F F D A R E A H S D E N P S E G D G A V N K E E
18426	48794	A	18533	90	383	IQLHSSGPCLLWL*LSFRSLST TAVICQCCRPAADFHPSGSSRVS AVLIIQ/HRRPLPLPIGLKACYFS AASLDKV
18427	48795	A	18534	1	456	
18428	48796	A	18535	830	1092	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met/Asp	SEQ ID NO: in USNN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, !=possible nucleotide deletion, !=possible nucleotide insertion)
18429	48797	A	18536	391	1824	GSGADASGFISDAGLIFKKASSK GPKRLEKFSDERAAYFRCYHKL FLLFSSLCYGTYHVVWPLTLKP REDEDWISLCLRHCLMQKDTH SMLGECGERREGKKQKTGALG SSLSLEDAKHLLPFIPALPFSWN ALPQDLCNFKLWWDYRIRVDP PSPIAGTLIRRDTDPQGESHVKT GRHWSDTICKSQRQCQGLRQPPDR PIPILLMVKGQHVWPQLDKAQ IQEVTELNNVKNVARLPKSTKK HAIGIYFNDDTSKTFACEDSDEA DEWCKVLQMCEVGTRINDISL G!EPDLLAATGVEERQSERFNV YLMTSP*LRMLHG!ECALQV!T Y!EYICLWGRPTPQEFLISWP LSALRYYGRGTPWFNYQAGR MCOTGEGLFFIFQTRDGEAIYQK VHSAAAI.AIAEQHERRLILQSVKN SMLQMKMSERAASLSTMVPLP RSAYWQHITRQHSTGQLYRLQ DVSSPLKLHRTETFPSLQDS
18430	48798	C	18537	22	620	
18431	48799	A	18538	48	413	EDSKSKTISHPWRDCGDYCHH QGLERCRRGGDSHHTPVQLS*LA CAEDINKSWRMT!G!IVSLTKC* LQMQLLYQMWFHCLSKLTLLL GISTLQLCVTILFRE!ITFPLHKI SHWSITLMTLR
18432	48800	A	18539	23	124	QWVIIISLTWK*!LQLQLLYQMW FHCLSKLTLLRP
18433	48801	A	18540	I	1860	
18434	48802	A	18541	209	3816	QGRPTFRRKYREHHKDTPREE QLQDT*SSDSPKLL*KKC*GQ PERKVKLPTKGSPSD*KRISRQ/ KTLQARRQSWFKEKINKIDRPQ ARLIKKKREKNQIDTIKNDKGD ITTDPTE!QITIREYYKHLANK LENLEEMDKFLDTYTLPLRNQE EVESVNRPTGSEIEAITSLPTK KSPGPDGFTAEFYQRYKEELVP FLLKLFLQPIEKEGILPNFSYEAII LIPKGPRDTTKGNFRPISLMNI DAKIL
18435	48803	A	18542	I	1521	
18436	48804	B	18543	I	2265	
18437	48805	B	18544	I	1716	
18438	48806	A	18545	I	1704	
18439	48807	A	18546	I	3618	
18440	48808	A	18547	I	3087	

SEQ ID NO: NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion,  =possible nucleotide insertion)
18441	48809	A	18548	277	350	SPVEKELKLWKNRHKLLSC*W LTC
18442	48810	A	18549	197	422	IVNKVVLPOGGPASPSSLKGFVW YKLAQVWKLIEGP*FPIFIQQISL LSI*PRSLFLFV*IK*ECSFLPLSFTS SGR
18443	48811	A	18550	I	3171	MVKGSIQQEELTILNIYAPNTG APRFIKQVLSDLQRDLDHTLI MGDFNTPLSTLDRSTRQKVNK DTQELNSALHQADLIDIIYRTLH PKSTEYTFFSAPHHTYSKIDHIL GSKALLSKCKRIEIIITNYLSDHS AIKLELRKNLTSQRSTTWKLN NLLLNNDYWVHNEMTEIKMF ETNENKDITTYQNLWDAFKAVC RGKFIALNAYKREERSKIDTL TSQLKELEKQEQRHSKPSRRQE ITKMRALKEIETQ
18444	48812	A	18551	209	2432	QGRPTFRFRKYREHHKDTPREE QLQDT*SSDSPKLK*KKC*GQ PERKVKLPTKGSPSD*KRISRQ/ KTLQARRQSWFFEKINKIDRPQ ARLIKKKREKNQIDTIKNDKGD ITTDPTEIQTIREYYKHYANK LENLEEMDKFLDTYTLPLRNQE EVESVNRPITGSEIEATNSLPTK KSPGPDGFTAEFYQRYKEELVP FLLKLFQPIKEGILPNSFYEASII LIPKPGRDTTKKGPNFRPISLMNI DAKILNKILANQIQQHIIKLIH DQVGFIPGMQGWLEVЛАRA/IR QEKEIKIGIQLGKEEVVKLSLFAD DMIVYLENPTVSAQNLLKLISN FSKVSGYKINVQKSQAFLYTN RQTESQIMSELPPFTIASKRKYL GIQLTRDVKDLFKENYKPLLNE IKEDTNKWKNIPCS WIGRINIVK MAILPKVIYTFNAIPIKLPMTFFI ELEKTTLKFIWQKQRSHIAKSIL SQKNKAGDITLPDFKLHYKATV TKTAWYWWYQNRDIDQWNITTE PSEIIMLHIYNHILIFDKPDKNKQ WGNDSLFNKWCWENWLAICR KLKLDPFLTSYTKINSRWKDL NVRPKTIKTLNEENLGNTIQDIDG MGKDFMSKTPKAVATKAKIDK WDVIKLKSCTAKETTIRVNRQ PTEWEKIFATYSSDKGLISRIYN ELKQIYKKKTNPIKKWAKDM NRHFSKEDIYAAKRHMKKCSSS
18445	48813	A	18552	I	3255	

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18446	48814	A	18553	I	3139	
18447	48815	A	18554	I	3210	MVKGSIQQEELTILNIYAPNTG ALRFIKQVLRDLQRDLDHSHTIIM GDFHTPLSTLDRSTRQVKVNKDI QELNSALHQEDLIDIIYRTLHPKST TEYTFFSAPHHTYSKIDHIVGSK ALLSKCIRTEIITNCLSDHSAAIK LELRKNLQTQNRSTTWKLNNLL LNDYWVHINEMKA EIKM FETN ENKDTTYQLNLDITFKAVCRGK FIALNAHKRKQERSKIDT TSQL KELEKQEQTSHSKASRRQEITKIR AELKEIETQ
18448	48816	A	18555	I	3345	
18449	48817	B	18556	I	3127	
18450	48818	A	18557	I	3325	
18451	48819	A	18558	I	3145	
18452	48820	A	18559	I	548	
18453	48821	A	18560	I	3229	
18454	48822	A	18561	I	3352	
18455	48823	A	18562	I	1965	MGDFNTPLSTDRLSTRQVKNK DTQEMNSALHQADLIDIIYRTRH PKSTEYTFLSAPHHTYSKTDHIL GSKALLSKCKRTEMITNYLSDH SAIKLELRKKLTQNCSSTTWKL NNILLNDYWVHNEMKAERKM FFETIENKDTTYQLNLDWDAFKAV CRGKFIALNAHKRKQERSKIDT LTSQLOKELEKQEKTHSKTIRRQ EITKIRAELEKEIETQKTLQKINES RSWFPERINKIDRTRLARLIKKKR EKNQIDRIKNDKGDTTDPDTQIQ TTIREYYKHLYANKPENLEMED KFLDITYTLPLRLNQEEVESLRNP SGSEIVAIINSLPIKKSPGPFDGT AEFYQSYKKELVPLLLKLFQSQIE KEGILPNSFYEASIILLPKGRDT TKKENFRPISLMNIDAKILNKIL AKRIQZHKKLIHHHDQVGFIG MQIGIKYLG Q LTRDMKDLLKE NYKQLLNEIKEDETNWKWNIPCS WVGRINIVKMAILP/KELEKTTL KFIWNQKRACIAKSILSQKKKA GGITLPDFKLYYKATVTKTARL YTKHGTSCCGSFGEELLPMQKA KRELAHHMAKAGARVKQGLG HVTQHQLGSIEWFNKYSLSSTYY TVDTKPKQFSHPTKDNKTTGLTCR NRTITVGVDLQAKGNLTVVKHLS SLQHCYEFICHI

SEQ ID NO: NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *-Stop codon, !=possible nucleotide deletion, !=possible nucleotide insertion)
18456	48824	A	18563	1	3099	MGELITPLSTLDRSTRQKVNKD TQELNSALHQGDLIDYRTLHP KSTEYTFPSAPHHTYSKIDHILG SKALLSKCKRTEIIITNYLSDHSA IKLELRINKNLTQRNSTTWKLNN LLLNDYWIHNEMKAEIKMFFET NENKDTTYQNLWDAFKAVCR GKFIALNAHKRKQERSKIDTLT SQLKELEKQEQTHSKASRRQE ITKIRAEELKEIETQKTLQKINESR SWFFERINKIDRPLARLIKKKRE KNQIDTIKNDK
18457	48825	A	18564	1	3253	MGDFNTPPLSTLDRSTRQV р DTQELNSALHQGDLIDYRTLH PKSTEYTFPSAPHHTYSKIDHIV GSKALLSKWKRTIEIIITNYLSDH SAIKLELRINKNLTQRNSTTWKLNN NLLNDYWVHNEMKAEIKMFFET ETNENKDTTYQNLWDAFKAVCR RGKFIALNAHKRKQERSKIDTLT TSQLKELEKQEQTHSKASRRQE ITKIRAEELKEIETQKTLQKINESR SWFFERINKIDRPLARLIKKKRE KNQIDTIKNDK
18458	48826	A	18565	1	3095	
18459	48827	A	18566	2	2678	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USNN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
18460	48828	A	18567	1	2478	MKAEIKMLFETKENKDTTYQN LWDALKAVCRGKFIALNAHKR KQERSKIDTLLSQLKELEKSEQQ TLSKASRRQEIJKIRAELEIET QKTLQKINESRSWFFERINKIDR PLARLIKKKREKNQIDAIAKNDK GDITTDPTEQTTTIREYKHYLA NKLENLEEMDKFLDTYTLPRLN QEEVESLNRPITGA\EVIAINSLP TKKSPGPDGFTA\EFYQ\RYKEEL VPFLLKLQFQSIKEFGILPNSFYE ASIIILPKPGDRDTTKKENFRPISL MNIDAKILNKILANRIQQHIIKKL IHHIDQVGFIPGMQGWFNIRKSI NVIQHINRAKDKNHMIISIDAEC AFDKIQQPFMLKTLKKLAEIKYL GIQLTKDVKDFFKENYKPLLKE IKEDTNWKNI\PCSWVGRNIV KMAILP\KELEKTTLKFIWNQK RACIAKAILSQKNKAGGILPDF KLYYKATVTKTAWYYWYQNRD IDQWNRTETSEITPHINYNPID KPEKNKQWKGKDSLNFNWKCWE NWLAICRKLKLDPLTPYTKIN SRWIKDLNVRPKT\KTIKLEENLG TIRDIGMGKDFMSKTSTAMAT KAKIDKWDLILKLSFCTAKETT IRVNQRPTKWEKIFATYSSDKG LISRIYNEELKQIYKKKTNPIKK WAKDMNRHFSKEDIVYAAKKH MKKCSSSLAIREM\QIKTTMRYH LTPVRM\AIKKSGNNRPTP\RIQ
18461	48829	B	18568	1	3403	
18462	48830	A	18569	2	2976	APRFIKQVLSDLQRDLDHSHTIIM GDFNTP\PLSTLD\RSR\T\ROQVHKDT QELNSALHQADLID\IYRTLHPK STEYTCFSAPHHTY\SKIDHIVGS KALLSKCKRSE\I\TNCLSDHSAI KLELRKKLTQNRSTT\WKLNNL LLNDY\WVHNEMKAEIRMFET NENKD\TTYQNLW\DT\PKAVCRG KFIALNAHKRKQERSKIDT\TLS QLKELEKQEQ\THSKASRRQEI KIRAELEIETQKTL\QKINE\SR SWFFERINK
18463	48831	A	18570	472	829	AIASESASPKAWQLPCGAAQOF AALPGLGNYKFPLTLITGYGSN KSPP\GYLVFQTYSSLPLRLPP GHFGFLPLSQR\LRRELCQWL G\LTQ\T\KMKSVYH\STT\EV\RK MHG\I\QEIH

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18464	48832	B	18571	1	2293	
18465	48833	A	18572	1	3810	
18466	48834	B	18573	1	4107	
18467	48835	B	18574	87	3161	
18468	48836	A	18575	1	3192	
18469	48837	A	18576	1	1983	
18470	48838	A	18577	1	3156	
18471	48839	B	18578	1	3471	
18472	48840	B	18579	1	2337	
18473	48841	A	18580	1	3852	
18474	48842	A	18581	1	3057	
18475	48843	A	18582	1202	2004	SGIYMIGFEQVLKAQPPPLSSPMPMNKVATVVGMEVMHGLSNMDFHSSRLTWLRLPLGFTGPG/YQGVKVEVAPLTITPSDPLAKFLLLISATSTSLEVTVPEGEMLPPRDTTKIAATFGTQTGFLALQLADGLLWDLVIIPGKGKPSRDLVESPSPYSTYEGIDGWPDEPAPTAKPPVMPAPALPPDTRSGSKAPTPVTPYPQMEHHHQVQLASNNSNTAALGHILSPQSSWVQTPGQNSGP AIPNHLGKDMISPPQMAPAGVKWESQKY
18476	48844	A	18583	1	2832	
18477	48845	A	18584	1	3702	MQKKHDKIRNSFMKTLKKLRT EGIYLNLTIKATYKKPITNIILNGENQKAFALRSGTRFWILACQM SRLRKLTNYLSDHSIAIKLELRINKPTQSRPTTWKLNNLLNDYV VHNEMAEIKMFETENKDTTYQNLWDFAKAVCRGKLIALNAHKRKQERSKIDTLTSQLEKE KQEQTHSKASRRQEITKIRAELEKETETQKTLQKINESRSWFFERINKIDRPLARLIKKKREKNQIDT KNDKGDITTDPT
18478	48846	A	18585	1	3139	
18479	48847	A	18586	2	2918	
18480	48848	B	18587	1	3242	
18481	48849	A	18588	1	3640	
18482	48850	A	18589	371	522	
18483	48851	B	18590	1	3918	
18484	48852	A	18591	1	3057	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met/Asp	SEQ ID NO: in USNN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, !=possible nucleotide insertion)
18485	48853	A	18592	1	3233	MGKKQSRKTANSKKQSTSPPP KEHSSSPATEQSWTENDFDEL EEGFRRSNYSSELREDIQTKGKE VENFEKNLEECITTNTTEKCLK ELMELKAKAQAELRECRSLSR CNQLEERVSAMEDEMNEMKRE GKFKREKRIKRNQESLQEIWDYV KRPNLRLTGVPESDGENGTKLE NTLQDIIQENFPNLARQANIQIQ EIQRMPQRYSSRATPRHIIVRF TKVEMKEKMI.RAAREKDRSTR QKVNKNTQELNSA
18486	48854	A	18593	965	4165	TWKGTTSRCKIMPKYRSTRQ KVNKDTQELNSALHQADLIDIV RTLHTKSTEV/TFFSAPHHTYSK IDHIVGSKALLSKCKRTEIIITNY LSDHSAIKLELRINKLNQSRSTT WKLNNLLNDYVVHNEMKAE IKMFFETNENKDPTYQNLWDA FKAVCRGKFIALNAHKRKQERS KIDTLTSQLKELEKQEQTHSKA SRRQEITKIRAELEKIEJETQKTLQ KINESRSWFFERINKIDRPLARLI KKKREENQID
18487	48855	A	18594	1	5093	MEGENNEMKREGFKREKRIKR NEQSLQEIWWDYVKRPNRLRIGV PESDGENGTKLENTLQDIIQENF PNLARQANVQIQEIQRTPQRYS SRRATPRHIIVRFTKVEMKEKM LRAAREKDSTRQKVNKDTQE LNSALHQADLIDIVRTLHLKSTE YTFFSAPHHTYSKIDHILGSKAL LSKCKRTEIIITNYLSDHSAIKLE LRIKNLTQNRSTTWKLNNLLN DYWVHNKMKAIEKMFETNEN KDTTYQNLWDTF
18488	48856	A	18595	1	131	
18489	48857	A	18596	5382	9269	RAKSPANIIITGSNSHITLTN VNGLNSPIKRHLASWIKSQDP SVCCIQETHLMCRDTHRLKIG WRKIYQANGKQKKVAGVAILVS DKTDFKPTKIKRDEGHCKVVK GSIQQEELTILNIYAPNTGAPRFI KQVLSLDRDLSHTLIMQDFN TPLSTLDRSTRQKVNTDTQELN SALHQADLIDIVRTLHPKSTEYT FFSAPHHTYSKIDHIVGSKALLS KCKRTEIIITNHLSDHSAIKLELR KNLNTQS
18490	48858	A	18597	1	312	

SEQ ID NO: NO:	SEQ ID NO: of peptide sequence	Met / cod	SEQ ID NO: in USN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, !=possible nucleotide deletion, !=possible nucleotide insertion)
18491	48859	A	18598	142	876	RKKGILPPKESLKELEEEAEEEQ RILQQSVVKTYEDMTLEELEDH EDEFNEEDECAIEMCRQRQLAE WKATKLKNKFGEVLEISGKDY VQEVTKA/ERRALWVILHLYK QGIPLCALVNQHLSWTLPGSFP DVKFIAISTTCIPNYTDRNLPT ILVYPGRRYQGLSLLVWLCLAG MNPDQEWSWEWKLLSEGAIMT DLEENPKKPIEDVLLVLSAALW SS*RGSDSDSEGDLRATASITCRT
18492	48860	A	18599	1	2310	
18493	48861	A	18600	3	1124	LYNRRRRRRCSHCRHRCRRLSS GLRKEEVISLGASLGRVFPVPCSP PTVSAARGPTGAPGGPNKSPKLS GCCDDGFNLGRQQWGNPLPFC SKTISSSLHWTWSQVNVLVEILP AIFSSFLNLQHVNLWFLAAM KAVTQQGHELSNEERNLLSVA YKNVVGARRSSWRVISSIEQKT ERNEKKQQMGKEYREKIEAEL QDICNDVLRVGQCFCEQWF NSINLMLYKCRSLNYFRLSEVA SGDNKQSK*YL*KEIRPVMEPV FFHRDFTLIRLGLALNFSVFY YEILNSPEKACSLAKTVRKTLC D1*PQNSACVINFILFLNLRDN LTVSTTSTGFIVSFLFTYLIHCY LQEIGCTIKCSFKLLNLL
18494	48862	A	18601	340	1323	AARPKRHNHHSSLTGTSHIH WKRGRVQNIADVLQFCLYLLT VLFPVCSPTGTMMDKSELVQ KAKLAEQAERYDDMACSSERH VTEQQGHELSNEEKKSCSLVAY KINWVGARRFLPGRVISSI*A*K QRRNEKKAADGQKSTREKIEG RTCRTFCN*CFWELLGQISLFPN ATQPRKVVKFYFEK*KGDYF.R YLF*KWQS*RQQTQPTCVGTSP ARAYPGSNLKI*LRKKMQP*TH PNSVLVLAQPKFPQSFYYEILNSP NEKGLVSLGKNGHFD*SNLLNL DTLEWKSLLKDSTSWSWQLR DNLTLWDIRKTRGDEGGDAGEG
18495	48863	A	18602	33	89	
18496	48864	B	18603	167	232	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met/Asp	SEQ ID NO: in USN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, -=possible nucleotide deletion, !=possible nucleotide insertion)
18497	48865	A	18604	14	600	MAELAPASPSDIKASVNSGDTTLLCSRQSCGMNEVRQVSLTYPGSPAPSHSLPLQPRSGGSLCPSRAW/PDPHQFLFDDTSSAQSRGYGAQRAPGGLSYPAASPTPHAAFLADPVSNMAMAYGSSLAAQGKELVDKVNNSGRGWWEGWDARGHRASDLSSASPDWRFIPITKLKYFVAVDTMYVGRLGLLFFPYL
18498	48866	B	18605	1	1230	
18499	48867	B	18606	41	931	
18500	48868	A	18607	3	166	PRPFPKSRLPPIIGGEYD\QRPN PILP\GRGGPNDRFPF\PRSGRP\TDGRLSFM
18501	48869	A	18608	212	1881	CLRVLLLKRTWPVEVTPETGARP/TGGILRSW\LRQSLLLCT\WGYSSNTRFTITLNKYKDPLTGDEETLASYGIVGSDLICLILQDDDIPAPNIPSSTDSEHS\SLQNNEQP\SLATSSNQTSMDQEQPSDSFQGQAQSGVWNDDSMMLG\PSQNFEAESIQDNAHMAEGTGFYPSRTPCSW*LNPVEQQPVHSLETLYQLADCS\ANDALIVL\I\HLLMLESGYIPQGTEAKALSMPEKWKLSGVYK\QYMHPLCEGSSVT\LTCPVPLG\NLIVVNATL\KINNEVRKC*KGCSLLPESF\ICKEKLGENVANIYKDLQKLSRLFKDQLAHPLLA\FRTRQALNLPDVFGLVVLP\PLEKLRI\FRLLDVRSLVLS\AVCRDLFTA\SNPPLLW\RVFYICVNRDNTV\RVQD\TDWERTV\QGRRAHTKE\KESPKGRV\WMLLAIRQTHATIPFYSQPLW\HPRGHFPKLP\AFPPG\YSGGW\NMDQ\RP\PTF\VVY\GRTQSSSLNSW\VLGETPKPSFLPLR\RFDPVWPHFPGP*PPSL\PARAGPNDQISPF\RPQQGSQQL\GRLSIH
18502	48870	A	18609	1	1065	
18503	48871	A	18610	1	1513	
18504	48872	A	18611	1	2247	
18505	48873	A	18612	3	421	
18506	48874	A	18613	1	103	
18507	48875	A	18614	3	435	
18508	48876	A	18615	268	501	QLECIPGTWELKEE\QERAMA\GGGLKKIISATEKKL\ARM\LLAP\SA\SWCCSGP*VFHG\ST*WGKPG\PVS\SLLQGV\LGK

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18509	48877	A	18616	3	296	EAMEAVILTCOPATPAASYYQWWMNGQSLPMTHRLQLSKTNRTLFIFGVTKYIAGPYCEIRNPS*VPAASDPVTLESPPLLNFNGLATTETLRKRGNP
18510	48878	A	18617	3	1464	GAVRTWGRGFQTEKQCASLLNFWNPPTAQVTIEAEPTKVSKGKDVLVLLVHNLPQNLAGYIWKGQMKDLYHYITSVVDGQIIYGPAYSGRETVYSNASLLIQNVTREDAGSYTLHIVKRGDGTRGETGHFTFTLVLIPWTLLYL*RSLAQVSHYETPGKTAPPCGSTA**L*N*PPDLTLFSPVLFLLKYPVPGQAFQYPKGLKTIGSSITHL*DVLKGKSCRENIPIRAAK*D*N*EDSSTACSK*GPQVETPKPSISSLNLYPREDMEA VSLTCDPETPDASYLWWMNGQSLPMTHSLQLSKNKRTLFLFGVTKYTAGPYCEIRNPVSASRSDPVTLNLLPKLPKPYITINNLNPRENKDVLAFTCEPKSENYYTIWWLNGQSLPGSVPVRVKRPINERVLIFTPCSRGIETGIPY\QCEIRDRYGGHPQLPSHPPGMSIITTKHSGLYACSVRNSATGMESSKSMTVKVSAPSGTGHLPLG
18511	48879	A	18618	79	1516	
18512	48880	B	18619	96	1730	
18513	48881	A	18620	9854	11033	ESLCFPKTEQEASQSLSP*IIHLSCTDCTSYWLSRTHVG*QVGDNSE*RMPVEESKVPHRTIFCYPHS\KLPMPYITINNLNPREKKDVL AFTCEPKSRNYTYIW\WLNQSLPVSPVVKRPINRLLILPSVTRNETGPyQCEIRDRYGGIIRSNPVTLNVLCEYPLFLCGPGHQLNSKRPEARPLSLPVQV*TLULLDIRPGHDSLPEIILGRHSLNQEYKGRGALVMGH*GPTACNERNRGIPOAWA**T*MGFGCHLRLCLGSEGHCVPLRDQEHPPLPDDITCGFILFPPDGPDLPRIYPSFTYRSGENLDLSCFA\DSNPPA\ESWTNGKFDLQGQKLFIPIQ\ITNHSGLYACSVRNSATGKEISKS\IVKVSGKWIPASLAIGF

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18514	48882	A	18621	3	1350	GRTAQLTAVLRKLLDPRLISTEENTQAAETMGPLSAPPCTHLITWKGVLLTASLLNFWNPPPTAQVTIEAQPPKVSEGKDVLVLLVHNLPQLLAGIYWKGOMTYVYH YITSYVVDGQRIY GPAYSGRERVYSNASLIIQNVTQEDAGSYTLHIIKRRDGTGGVTGHFTITLHL ETPKPSISSNNLPREAMEAVILTCDPATPAASYQWWMNGQSLPMTHRLQLSKTNRTL FIVGVTKYIA GPYCEIRNPVSA RSRDPVTLNLLPKLSKPYITINNNLPRENKDVLTFTCEPKSEN YTYIWWLNGQSLPVSPRIVKRP IENRILP PNVTRNETGPYCEIRDRYGGIRSDPVTLNVLYGPDLPSIYPSFTYYRSGENLYLSCFAESNPRAQY VSWTINGKFQLSGQKL SIP ITTKHSGLYACSVRNSATGKESSKSITVK
18515	48883	A	18622	273	2271	CGSWLMTQFSMDKRQGRSRSVTTITNTA VTSLEWVPFHAFAPRSTLVSQGQATSH TDNTQEMD SPGQEPGFAKEVEVEPGFQQLPQM TLLVPA MC LLHGACSAKGFC AAPHFLLASPMGKGQVPLNPFS FTLSEEDL LPQSLKRNPKGCIAR RAKPILAAERHKRLI LHTSTKEN TLLDNRVIECLTMEA VAKFN IMKERE GPHSQPAL SPPKARWHIL WOKL MFATSL TFWE PTTAR VTEAMPFN ATEEEEEEEFFLLA HNL PQNLT TRATIY W GQMRH LYHY ITSYVV DGEIIY GPAYS G RETA YSNA SLIIQN V TRED AG SYTL HIIK R GDGTGGV TGR FT TLYLETPKPSI SSNNFNP RE ATE AVILTC DP ETPD ASYL WW MNG Q SLPMTHSLQLSKANR TLYL F G V TNY TAG PY ECE IRNPV SAS RS DP VT LN L P KLP KPY IT NN L K P R E E * G CL R P F C E K E * G T T PY I W V W V K R F R S L P V S P G V K R P H L K N R I L P T P V F R K W K Q G P Y S MW N Y G D R Y G G I R S L P S P W N V L L W V Q D P R I L P F H T Y Y R S G R K S S Y L C S G G T L N P P A Q Y S W D N * W K S F Q L T R G Q K L F Y S G H T T K H S G L Y V C S V R N S A T G R E S K S M T V E V S D W D I L N S T S N S F
18516	48884	A	18623	1	1131	

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18517	48885	A	18624	1	603	MDIADPFSGFPGMGGMGFTNNM FGRSRPAQEPRTRKKQDPPVTHD LRVSLLEIYSGCTKMMYQEDIKI SHKRLNPDGKSIRNEDKILTEIV KKGISLPEALCG/TTVNPVTLDG RTIPVVFKDAIRPGMRKVRGE GLPLPKTPEKRGDLIIELEVIFPE RIPQTSRTILEQILSSYSLYSSP GLTRDLSRAQGFGLDLSTSCGP
18518	48886	A	18625	3	1228	WSAAEPVVDGDSGSAGRRRGWPW PKTTYHPWAARGASEKEIKR AYRRQALRSHPDKNKEPGAAE KFKEIAEAYEVLRDPRKRKREIFD HYREEAALKSGSGPSGGVSGGGAN ATSFSYTFHGEPLAMFAEFGGG RNPFDTFFGQIRNGEEGMDIDD PFSGFPMSG/LWGGFTNVNF\GRS RSAQEPRKKI\QDSPVTHDLRV SLEGDLTA\AVP\PRCTKKMKISH KRL\NTPDGKSIRNGDKILTRSE RRGWKEGTQITFP\KEGDQTSN N\VPADIVFV\KLDPH\NIFKRDG SDV\YI\PARISLREA/LCVGCTV NC\PHSGTGR\TIPVVFKECYQGL GMRRKSSWENG\PLP\Q\N\TREN VGDLI*GFEV\IF\PERI\PQ\TSRT VLEAGSFQYSYLEV\POGLTRGP FPELKDFWDLFLPVVGP
18519	48887	A	18626	321	1121	GDAVPSA\PRRPSRRRTPGCGSRG ALQPGPPR\A\PPPEP\PPRGAAA AAP\PGPAAPAA\ARQPPRPPA\Q PRSCP\RRVRP\TPA\WSP\PGRRGP RRSRRRPPGGP\GPA\PLRLSRA HSPPAPP\GSPYR\PHGAG\GTSVAP WTRP\PA\RGTEADP\GRC\VP\SA\P GTAPQ\QMRGRGSAT\QRLR\GH STAPGAGGR\GCR\GRRPGG\SG\GP AGAGP\PRSTA\APPR\CR\RR\SP\TG PRSPR\GPR\SA\PAR\G\SV\GG\PRG TPGKQ\QPG\PR\RA*TSG\PE\PR\CCG HARG
18520	48888	A	18628	191	653	KLE\QRL\LRM\TTECIR\HTKQKK FGSPG\I\Q\PLP\G\N\KA\RS\RAD\STA LP\ALPA\Q\KET\KQ\Q\EG\ESS*E PGGSSPSR\MER\AE\AA\PA\QS\PA GGTGTGQ\Q\W\GA\PH\LG\PA\L\ARR VTGPPQ\HG\SPG\PR\TR\PT\Py\PAR C\PSR\PI\VF\PA\IV\WS\RL\APP\GLP
18521	48889	A	18629	141	319	

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18522	48890	A	18630	178	722	PLGNVSCSHRSFQATARVDYSLI YVLAWGQKKEVWELRNWQTH ALMKLKNKLREPRTSVNKD/SP KSLLYSCSYSFDEPVELRSSSF SSWDDSSDSEYETHLLHHLKLV* PNLAVFNCRPTARRKPDYEPVE NTDEAQNSFCKTAHNLSLTFP FPCLL*YETRARLESWSLSCLR YEHISSG
18523	48891	A	18631	2	367	
18524	48892	A	18632	1	381	QRYSSRRATPRH   VRFTKVERK ETMLRAAREKGRVTHKGKPIR LTV DLLAETLQARREWGPFI N LNEKNFQPRISYPAKLWSLFI SEGEI  NPQMLR/DFVTRPTLRLDLLK ALNMERNNNRYLPGRPL
18525	48893	B	18633	1	846	
18526	48894	A	18634	3	1170	VGSMTGEASGNLQSQRKAKRK EARLTCLPVEEPGSHTPPMC YLAPPMWKQCQKPETGKIEGDR DHNSLPAREENQTENESDELTE AGFRRWVITNSSRLKEHVVTQCK EAKNFEKSLKELLTRITSLEDN INYLMEPRNTAREHREAYSSIN SQIDQAEEKIPEI EDQHNEIKRE DKIREKRMKRNKQSLQEIWDY VKRPNLSSLAGVPESDEENGIKL KNTLQDIIQENFPNLAKQANIQI QEI QRTPORYSLRRA TPRHII VR FTKVEMKEK MLRAAREKGRV THKGKPIRLTVADLSAETLQAR/ RTEWP F PNILKEKNFQPRISYP AKILSFISEGEIKYFTDKQMLRD FVTTTR PALKRAPGKEGT*TLE RDNRYQPLQKHAKL

SEQ ID NO: NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
18527	48895	A	18635	73	1504	QDLRLFYLKDTMFSKLAHLQR FAVLSRGVHSSVASATSVATKK TVQQPPTSDDIFEREYKYGAAHN YHPLPVAL\ERGKGILLMGM*E GRKYF\DFL\SSYSALSNSNQ\WC HPKIVKCSGRVWKWDKIDL\HLE AFYNNGTLVNMREYYY*TFST YHKVLP\MTNGVEAGETAICKL ARKWGL/YTVKGIQKYKAVKIV FAAGGNFWGRTLSAISSTSDPTS YDGFGPFYARDFIDIPY**SCPH MEQCSFKDPKCGLAFIGH*EPIQ G\EAEGV\VVVPDPG\YLMGSAESS GTRDQVLFICLMEIQTGLARTW *DGLA\VDYENVRPDIVLLGKAL SGGLYPVSAVLCDDDIMLTIKP GEHGSTYGGNPLGCRVIAAL\ EVLEEENLAENA\DKLGIILRNE LMKLTLP\SMLV\TARKKEGIY LNAHLAIKGNGQI\WDA\WGKV CLRLQDNGLLPKPTS\ATLSRF APP\LV\KEDELRESIEINKTILS
18528	48896	A	18636	2	348	
18529	48897	A	18637	588	801	RTAYFCQYHTASVYSERAMPP GCPEPSQA*ELQETGHRQVALR RSGRPKCAERPGA\ADTGACHT STDGRL
18530	48898	A	18638	175	510	NSESPGPLWWLSCDNPAKDRY STEADGLGLPDQS\VFVHRAQL* CVAG*LGTHSRFQEWAV*D*SD LLKAQLHFKVGR\CVWEAGGL EWVLLGGRCR\CRV\VPQPLETLIQ WGPW
18531	48899	A	18640	1	1431	
18532	48900	A	18641	202	994	RWQGQRLLLDNSIRLWV\LP\IR YSFTFFR\ALIRIHYV\SI\LLAERQ RSFTQGNKYLDSSSPNFEGRV\IR FRGKLGNYIPKQS\FFG\RRKLF FPNPEDGIFS\KKL\KREV\PPSPM TDPTMLTDMMKG\NV\TNVLP\I LIGGW\INMT\FSGFVTTK\VP\FPL \T\LRF*^A*WLQQGNR\SYSPRCI PG*WFCIPGYFPQ\CLGFR\SI\YT LWISGGKDNGRN\W\NQSRMM\DR SRMTGASHGP\WPADSGR\RFPN KRWEAL\ELTDHQ\WALDAAGE DAA
18533	48901	A	18642	97	224	LPTKSTWVAGKK*KKRSNIKD Y\STPLTSYRS\IRSHAFKIVAS

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18534	48902	A	18643	117	457	IWGDVEKGK\KVFPYL*RCSQCH TV*/ERGGKHKTGPKSP*VSFGR RTGQAPWDTLYTAANK\NKGII WG\EDTLM\EYLENPKVHPLD TKMIFVRHLRKREERADIALS SKKLLN
18535	48903	A	18644	411	1054	VTGAQRLVTCRMGKQNSK\LA PIEVMED\LVKSTEFNEHLKQ WYKGFLKDCPSGRLNLEEFQQ LYVK\FPVGRRLPS\FAQHAF\PN LSTRM\GDGT\UDREFIC\LSITS RGISFEQKL\NW\A\N\MMY\GPGW VMGK\ITR\VEML\EI\H\RL\SYQN G*GTVIMMMKMNEDGLT\T\PE\QRV GQDF\SA\W\VRN\KDDQIYT\GID FKGSCQRADPFIV*LL\QCDIHK
18536	48904	A	18645	3	475	GAEGARGGGSSYSEMAETVAD TRRLITKPQNLND\AYGPPSNL EIDTNLPIFKLKESTVRRRYSDF EWLRSELEREKS\VV\PP\PGKA FLRQLP\PRGDDG\IF\DDN\IEGKK TRG\WEQFINK\VS\LG\HPL\AQNE PLFFHML\QDE\IDKS\YTP\SKIR
18537	48905	A	18646	1	695	LRARS\LRDCARAPCPHGGQQ RRRRRLNAE\GAEGARGGGSSY SEMAETVADTRRLITKPQNLND AYGPPSNL\LEIDVSNP\QTV\VG\G RGRFTTYEIRV\KTN\LP\CFQS\*KN LIVRR\YRSD\FEWLAK\WNLERE SKVVV\PP\PG\KAFL\RQLP\VG DDGNILMDNFI\*EERKIRGWSS FLNKVA\GH\PL\AQN\ER\CL\HM VFYQDE\I\DK\LL\LP\SK\N\KAMP WKFGPRKGAK\NV\DY
18538	48906	C	18647	3	474	

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18539	48907	A	18648	156	1254	RPLHTILEVLRRMTKRLVTKAA ASAARAQPAEPRDRKYDKHLS YLATWGRSAAGRASPRGAGR ELARAPVSLPAGVPGRGSAA HSSEARTGPNKGKMGSSREPGT EKVPCPRLSPTREVGHQVHGT LGAGPNELHPSPGAGARCRPGR REAKLGDAARSEAQSAAHKFHII DSLSLPWNPTAMEMLMPKKNR IAIYEVLLFKIEGVVMVPPKKDVPI PKHPELAEQKCAPTFHVMKVA MQSLKSPRPT^KEQFAW^RHFY WYLTNEGIQ^YLDRYL^HLPPEI VPAHPPYGRSPSRRLARPCKV WKGEATLRDFTRGEADSFLCH S/DSYRRAAAPP/GAIDKKAEAG GLGQKPNFQFRGGFVGRGQ^P
18540	48908	B	18649	1	1053	
18541	48909	A	18650	1	529	MGRYMEREPLQGNHRRSGLSG ERCSHMGGLVIERRELQTETRK EGVVEWCWLEKEVVLATITKPV RGDKNGGTQVVKHRKMPRYY PTEDVPQKLLSHG/KKKPSQHJM RKL/FLYRRHARNLSSLPPQPELII SDVK/PRHPADA*LEEEQQLSEP E/HSEGTSY^RIPEKVLSSYPAIRP
18542	48910	B	18651	258	363	
18543	48911	A	18652	197	398	ARMSQEKKDFHKVMSALKARTG HLHFFCGGMSVSKVGGQFSLLL *FFSYFRPSGCLPL*ELPEARCP
18544	48912	A	18653	215	932	GTQSCNQKVLSANNLQELGIG PKFQMRKLPQLAPMPPQRGTS LGRSICPCPPVLCMSMRKIIHLRPLQV LRPTSPRNISPILNRVSEVSDH GTPALVLHP^RQVPLFWGRGK YPNPFSLCLYVPSAFLGGKKHP TPSPSP^VASPLF^RSKYVPLVSL CPSPLPFRPDLLSLWPNPFL^RTP TSYISVPQSLISMPRPLISAPQPLI STTQPLSRFSGRSLLQVPEIWPP GQGMPAARDSS
18545	48913	A	18654	1	378	
18546	48914	A	18655	14	380	
18547	48915	C	18656	228	260	
18548	48916	C	18657	99	335	
18549	48917	A	18658	55	474	RQVPLFWGRGKYPNPFSLCLYP FSAFLGGKKHPTPSPS^VASPL F^RSKYVPLVSLCPSPFLPFPD LSLWPNPFL^RTPTSYISVPQSLI SMPRPLISAPQPLISTTQPLSRFS GRSLLQVPEIWPPGQGMPAAR

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18550	48918	A	18659	1	187	AELATGNVKVEASGTPEEKAG SVLG*ACFAGP*ERCCWQNN*D GIISIQSYCLCLNLGCFIQT
18551	48919	C	18660	1	357	
18552	48920	A	18661	3	148	
18553	48921	A	18662	1	312	
18554	48922	A	18663	149	457	
18555	48923	B	18664	1	675	
18556	48924	C	18665	110	928	
18557	48925	A	18666	495	817	LTSPSPRCTIIEKCSSLPLP*DKP QPHLQHTRTSKRLNCSSQVFLQ NLLPEELATSSRNLATGPRNAC SPGFLLSHIPSVWDPGNRTVQ LTWQPLPPEPLELWPKAL
18558	48926	A	18667	228	3021	VFDRTQNVQGRIMEAQNVLYL DEIDFSDDISYSVTSLKTIPELCR RCDTQNEIDRSVSSSSWNCGIST LITNTQKPTGIAADVYSKFRPEKR VLPLKHQPETLENNESDDQKN QIVGEYQKGGESDLGPQPQELG PGDGVGGPPGKSSEPSLGL EHYDLDMDEILDVPYIKSSSQL ASFTKVTSEKRLGLCTTINGLS GKACSTGSSESSSNMAPFCVL SPVKSPHLRKASAVIDHQHKLS TEETEISPL
18559	48927	A	18668	1440	1764	ERSTVNLRSSDQP/RPRNILNTNF KS/VDKGDTFYPWTHNSGASH GLGRVRLPWC*ELATSARNLTP RPTAGSPGFLLSHVPSVWDP ANRTVQVLTWQPLPPEPLELWPK
18560	48928	A	18669	1	3255	MLTLTGAGGESWIIRFGNLLEQ LGAETTLGRRQEPGDEVTAHFL LQGVINMGPVPPGAHSSNMP GSVSPILGHHSVKLFEYYYPVGD PLMGSGRPHTPRKIKIWSDLNA HSDLYLALDWTPLPEQSEPGPG LAAWKPQAEYYTCKCAEGNE NTPFDLRKGTLPCPRNLERARQ AYMHIEEKPFELTEQHICEFQS MCYVILVRVLGACSQSTWLILEP DGVSGPSKGASEAIGQCQSSAA KPRRGSKESVREPWA

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18561	48929	A	18670	1	1442	CSEYEDSSPAPVPATDLSSTLSSVPQPQDTGTSQQLHLDPWELLRAQELQGATNHKGYSYSHAEHEHAGLGVQGGNGAL.AFSNSGHRAVPTIISGGTGRRTTPSSAFGLLNLLHQWFVSGFQAFSDRLKAALSASLLLRFGDSDWLPSSSACKCLMLGLHFVIVGNICATLKEKYSSMLHLDVTMVKNGEKRTLQKRKKGMPPHPA/S*GPKIISCHHSPCQCCPSSAK/SASELQGSWTPFGLLTLTRTRMKFGAKTRDLDQGTSLGRSLPCCPTLCSMRKIHLRPQVLRPTSPRNISPINSNPRQRRQVLSMDPKLRLRHSRTGK/DSLPLVFNHCRDTSLIHPCFKGVPRPRDACLGPSPLAASPAFLEKGQDLINLAFKVYNNRKKLQFLASTVRQTAATSPAHKNFQMPPEPQRPQVPPPEPTGACYMCRKIWLPGQANARSPGFLLSRVPSVRDPTGNRTVQLTWQPLPEALELWPKA
18562	48930	A	18671	140	327	
18563	48931	A	18672	95	115	IIRHLCND*TPREGCLPSP*PAWSDTFETWVNQQASLQ
18564	48932	A	18673	218	674	MPISRPTARFKRIKVYHSPATAWPSKAYKLPLQFPHFTCPKTRQGLQVTSGSAPYQPNCFVYPPRVAKTKYSPILNTSLHNPPLCCSGSQTCFLY/SFLCTFHPSSLSSLQLTLTPIRLSKLRGLYCHKASQTAITSIKPKFLPHLLPISA
18565	48933	A	18674	1	268	
18566	48934	A	18675	1	458	
18567	48935	A	18676	3	461	LLLTQSLFGGLFTRTRMKFGAVTRIGGPPGLGNQSPSSCSLLHEKDPPPTSGPQTDQPKKKHLTNFKSARPTFLGGQQVPLNPFSFTLS/EQVLLS*/ARTPQSLISTPQPLISVPQSLISVPQPLLYFSGGQEPFFFFLLCVSSLFSRLASFTM
18568	48936	C	18677	156	329	
18569	48937	A	18678	449	667	
18570	48938	A	18679	79	311	

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18571	48939	A	18680	1	693	MAPTNCKGSRKCGRPHQEYMPH PYLPLLLTFSDSLRLHGPGEINSR VPHTKPVWWWSLHTDAYEIWYH DSDWGDLPWEINPLSSCSLLHE KDPPTTSGPQTNQPKEHLMNFK SGPHWKSDCPTRQPLGPLELW PKA/HLTDSFPDLLSSLAED*CC LIALEAPWTITDAELWITLTVED SQLYEDTLAGRSVLIKNLTP*TL Q/PLDGLDP*SSIVPQLPSACRI LPTGFTVPE
18572	48940	A	18681	328	865	
18573	48941	A	18682	451	1238	TALLLTQSLFGGLFTQTRMKFG AVTRIGGPPPLGDQSPVLLFVPR ERSTYDLGPQTDQPKKHLTNFK STSFVFSSCIPPP*PSSISLLPPW/T TDHAPLTISL/TT*SPLPCSMPI/S ASHSML*KD*SLLSLACYSMAF *SL*TLLTIPPFYLS*NQRRTG* FRICALSTKLFCCLSTPWCQTHIL SYPQYLPPQSII/LFWISNVLSLLF LCTLHPSLSSLSLGLTLTPFRLS KLPGLYCRKASQTAITPSVKPK FLPYLLPISA
18574	48942	C	18683	870	1037	
18575	48943	A	18684	933	4323	AASHLCGTPLEIGLSNSPGSHSQ SPWNSGPRLSDCFPDLLG*VAE D*HCPIASEASWTVT\ELWVTLT VEVAATALLLEALKITSYAPLT LYSSHNFQNLFLSSHLT/PYTF PQ/GPFSYTHSLLSLPQSPLLA QTSIRPPTLFLIPHLTPMTVSL*S/ ILTFFPPIHSFPVPHDHTWFID GSSTRPNRHTPAKAGYAIIVSST FIIEATLPPSTTSQQAKLIALTQ ALTLAKGLLVNIYTDISKYAFHI
18576	48944	A	18685	849	1944	WQVPLFSGRGRKYPNPNPSPCLYP FSAFPGKRQELATSARNLSDHQ AKECLQPRIPPKPCPPIAFPHWK SDCSTSPQQLPPELELWPKA/H LTDSFPDLLGLAA\ED*HCPIAS EAPETITDAELPVTLTVEGKSI CLIDTGATHSTLPSFQGPVSLAP ITVVGIDGQASKPLKTPPLWCQ LGQHFSMHNSFLVPIPTCPLPLLGR NILTAKLSSASLTIPGVQLHLIAAL LPNPKPPLCPPLTSPQYHPLPQDL

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met/Asp	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, >=possible nucleotide insertion)
18577	48945	A	18686	2	377	KGATIVYALDTLFIMEMKHEFE EAKSWVNEENLDNFVNNAEISVFE VNIRFVGGLLSAYYLSEEEIFRK KAVELGVKLLPAFHTPSGIPWA ILNMQSGIGRNWA WASGGSSI LAEPFGTLHLEFMHL
18578	48946	A	18687	215	1135	PITLRRHLFFSGIGRNWNPWASG GSSILAEFGTLHGMKIV*HFH GNILFSIKVMNIRTVLNKLEKH YLN*KLNHSKIHFFPLFPDHVS GGLGDSFYEYLLKAWLSNLLRR DYKMLKNKCFCSQAEIETHLIRKS SSGLTTYAEWKGGLLHEKMGH LTCFAGGMFALGADAPEGMA QHYPVSTVQENNPSFIPCPLV MKGPEAFRFDGGVEAATRQ NEKYYILRPEVMETYMYMFRL SGSDFFSSFLLLPPQASSCFQTLF DLFKVPSLCSILEFRHSSRQP YSTDQPFIYLVGKRLFCPLT
18579	48947	C	18688	304	400	
18580	48948	A	18689	16	450	
18581	48949	A	18690	1	777	GHSMMDMRVPAQLLGLLLLWLP GARCVIWMTQSPGTLSSLPGER ATLSCRASQRVNSNYLAWYQQ KPGKTPKLLIYGASNLETGVPS RFSGGGSGTDFIFTISSLQSEDIA MYYCQQYNNWPHPSVTFGQGT KLEVIRTVAAPSVVHLPGPSD EQLKIWELPSACVPA*NNFVYPQ SRPKVQWEGGITPLQ*SG*LPQE SVHGRGTRQGTAPYSPQQAPW TVRQSRIETEQSLTACEVTPS GALRFRPVHKGAFNRCESF
18582	48950	A	18691	3	688	HASADA WAANA EEHHRDRPR GTLREYKVVVGRLPTPKICHT PPLLPACEIFAPNHVVAKS/RAF WYFVSQLKKMKVVFQKGKIGL LVGQVF*ESSPLR/V*KNFRGSW LAAMDSRERAPTNMLPGNNRG P*PPAGGCSTQQLTRDNGVAPG TGAPKPHFHFRIERLEGFA QQSCRNP/ALVQSSFHDSKIKP ACPNGVLRROHQKPRF/TTKRP TFFLGAGPSSGVCPK
18583	48951	A	18692	1	784	

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18584	48952	A	18693	1	4713	MQGPyLLWLWLPDSLEEGKEGLYLGNCIHTCLTVTPEDAFFPHFLTQHSGTTHLPSSSDIPSIFHMNNSTGRLAQRLGTSTEAFLSPEVMVFVHARNATVRTAMSILERAKNCGHIPFFFPTQGHDYVLAEKQVQRSRNKQVRELFPDGFSIHA GMLRQDRNLVENLFSNGHIVKLVCTATLAWGVNLPAHAVI\KG TQIYAKRGSFVDLGLDVMQI FGRAGRQPQFDKFGEGI\IIITHDKLSHYLTLLTQRNPI
18585	48953	A	18694	313	489	SSCFKLHFFQLFKNCNTQMRN QIGFLRF*NNLVMLLSSSSVTNQ LELQKKIILLTCKMQ
18586	48954	A	18695	1	851	ACGWALAQRPARRAMVAGIDAGRSILGVLSVVCLLHCFGFISCFSQQYQGVVYGNVTFHVPNSNVP LKEVLWKKQKDVAELENSEFRAFSSFKNRVYLDTVSR*PSLT T*TSSR*KMKYEMESAKIVTDT MKFLPYVP*VSFQSPLT\CALTNGSIEVQCMIEPEHYNSHRGLIM YSWADCP\MEQCKRNSTSIYFKMENDLPQKU\QCSLSNP\PLFNTT SSIILTTCIPSSGGHSRHYALIPIP LAVIPTCIVLYMEWVF\KCARN PDRTQLQLIGNRRMKTTC
18587	48955	C	18696	35	181	
18588	48956	A	18697	75	344	PQVLRPTSPRNISPLNVRVSDHA GTPALVLH*RQVPLFWGRGK YPNPLYLCAPIPYFR\HNLISLR PNPLCPHPDLVSLCPDPFALE
18589	48957	A	18698	1	268	
18590	48958	A	18699	39	376	QYISELQFLASTVRQTPATSPA KNFQTPPEPQQPGIPPEPPPPGAC YKCWKSGHQAKECLOPGIPRK PRPISGSHSQSPLELWPKA\HLD SFPDPLLGLAAED*HCPIASEAL
18591	48959	A	18700	2	295	CQTTQGRLLTAGTPL*SFTHVS RVSDHAGTPALVLHP*RQVPLF WGRGNHHSIGTQELPNT*TAV\V QAF\LPEPPPTG\CLLHVPEIWPL GQGMPAGQDSS
18592	48960	A	18701	81	402	VKFGP\EIWCRDSDQGRGGVGT SLGRSPICPPALCSVRIYLRPL VLRPTSPRNISPLNRDPTVQLT WQPLPEPLELWPKA\HLDTSFP DLLGLAAEDRCCPIASEAP

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18593	48961	A	18702	165	439	PPRQAKM(QNLAAPGSQSHSQSPW/TLRPKAL*LTPSQIFSA*RLKTD TARSPrKPPSFQGPVSLASITVV GIDGQASKPLKTPQLWCQLRQ YSFK
18594	48962	A	18703	284	511	IILVVKWANGLRCLTSRHSFTH QSLPSPLCPVQLVPN!SRLSPQS QPQASLSLSNLPFLQTHLTSPL PRLLLARPK
18595	48963	C	18704	414	557	
18596	48964	A	18705	1	1284	MNFEGTETLHCNGHCKVIA MT LGNQE VNQRNFSTGTTGPMEG MWL LSSNSHHSLKYAGALAILS AFQYQERGSQAGH RDSWPETK E THFICGP KTPALVTDWEGSLP LVFNHCRDASLIIHPRFSGVRPR RDACLGP SPLAATPQTIDTEL WVT LTVEVWDIST/LFPGN*SH A/TLPSH*NLITLTPNANI/AIPQ HALKG LKP VITRLLQHGLLKP I NSPYNSPILPVQKLDKSYRLVQ NLRLINKIVSPH PVPNP PAFTS QITQAVS QALG I QWNLH I PYHP QSSGK VERTNGNLLK VHLTKL S QLK KDWTVLLPL ALLRIRACPR DATGYSR FELLYGRT FLLGP NLI PDTSP LDYLPV LQQARQAAN LLLPTPD P QPH E DTLA GRSV L KNL T PQT LQPRWTGPHIIY STP TAVCLQDPH
18597	48965	B	18706	1	933	
18598	48966	A	18707	3	435	TKETGF IHGP KTPAPV TDWE GS LPLV FNHCRD TS LIIHPCFK GVR PRRDACLGP SPLAASPA FLEKG QDLIN LAFK VYNNR KNLQFL AS TVR QTAAT SPAHK N FQM PEPQ RPGV PPEP PPTG /CLLHVPEIWP LGQQGM PAARDSS
18599	48967	A	18708	2	111	
18600	48968	B	18709	1	595	
18601	48969	C	18710	1	1344	
18602	48970	A	18711	227	385	VPILPQPLLLH PAIFLSP PLLTPG PAYS FVP* LALPHLPSNLLK R WLEPKA
18603	48971	C	18712	148	258	
18604	48972	A	18713	215	693	
18605	48973	C	18714	1	816	
18606	48974	B	18715	1	513	
18607	48975	B	18716	1	1452	
18608	48976	A	18717	1137	1303	

SEQ ID NO: NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, !=possible nucleotide deletion, !=possible nucleotide insertion)
18609	48977	A	18718	2	2107	IDMIFTPGPSPTPKHKKSQKGSA FTFPSQQSPRNEPYVARPSTSEI EDQSMMGKFKVKVERQVQDMG KKLDFLVDMHMHQMERLQVQ VTEYYPTKGTSSPAEAEKKEDN RYSDLKTHCNYSETGPPEPPYSF HQVTIDKVSPVYGGFAHDPVNLP RGGPSSGVQATPPSSATTYVE RPTVLPILTLDSRVSCHSQADL QGPVYSDRISPRQRSSITRSDTDP LSLMSVNHEELERSPGFSISQD RDDYVFGPNNGGSSWMREKRYL AEGETDDTDPTPGSMLSST GDG1SDSTVPLFLSSEIQLQKVG QSITSMLGFLSRGPGSMKLCMGL ACVLSLWNTVSGIKGEAKKEK GMTFLPTTDSSKKFFSLLSNTSYS SFAFHKSFSVAVYNNISNLTKTVPD AKFPTRCYCLNNRTNDLSDPT ALLVDIIGNSTSYLTEIFKSTSIL SVNQSNESDCIFICVMTGKSGR NLSDFWEIEEKYPIINYTFTSGL SGVLLALLTTQSLFGGLFTRTRM KFGAVTRIGGPGLNQSPSSCSL LHEKDPPTTSGPQTDQPKKKHLT NFKSAARPTFLGQQGVPLNPF FTLS/EQVLLS*AAARTPQSLISTP QPLISVPQSLISVPQPLLYFSGG QEPPPPPLLCVSSLFSRLASFTM GAFTHGTQTPSTKATAPRYPQ TGDLSAEWPFATAGEEPVLVPRP
18610	48978	A	18719	828	1063	RHSQAAED*HCPIALE/VPQTID AELRVTLTVEGYSLPPGCLRGL MLSVSGFSRSTVQAVSGSTVLG SGGQWFSCASV

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met in USSN 09/540,217	SEQ ID NO: location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, !=possible nucleotide insertion)
18611	48979	A	18720	183	1140	LGSGDLPWEINPLSSCSLLCEKH PPTTSGPQTDPKPKHLTNFKSG ETKEMHIFIRGPKTPVPTWDWEG SILLVFNHCRDGLSDHSATFQG CQT/MAGMPALVLHP*RQVPLF WGRSKLLLRLRS*VPILPQPLLL HPIILLSPPLLTGPAYSFV*P*LS MSIHQVVLRPDEQGPQEQQPP LYVMEPGEINSFIAHTKPVWWS LHTDAHEIWCHDSDRGTSLGRS IPCPPALCSVNRILRQPVLRPITS PRNISPILNQERQRRCILFVDPK LRCQSRTGKAFAWSCLIIAGTA SLIIQPHFKGVRPCRDACLGPSP LAASPAFLGKEQAAPCQAEALGP NSSASAPPYNPFITSPPHTRSG LQFRSVTSPPPAQQFTLKKVA GAKDIVKASLAPALAOQGVPGTP QATASEGASLKSWECLCGVNL ATAQSARVKEACQEACQSLPRF QRMYEKAWVPKQTTAEVELS QRASTRVVLRGNVGLESPRSFRV SIALSSGAVGGVHCPSDHRMIE PAAFNLSMKNPQRQSCLRA
18612	48980	A	18721	372	906	LRSADLPWEINPLSSCSLLEKHD PPTTSGPQTDPKPKHLTNFKSE KKETRFRGPKTPAPVMD*GRQ PSLGV*PLQGCLSDYSPRFQRC QTTQGHLPWFSFTLSSKSHFSGG RGKSLLQVPEIWPPGQGMPAA QDSS*AVVPICAGPRWKSDDCPTH LAATPKAPGTLAQGSLLPSQIFL
18613	48981	A	18722	983	1980	KFGLVQLTLGKPLPEPLELRPK A/HLTDSFPDLLGLAAED*HCPI ASEAA*TITDTELRVLTVEVW DIST/LFPGN*SHA/TLPHS*NLIT LTPLNANI/AIPQHALKGLKPVIT RLLQHGLLKPINSPYNSPILPVQ KLDKSYRLVQNLRLINKIVSPIH PVVPNPPAFTSQITQAVSQLGI QWNLIHIPYHPQSSGKVERTNGL LKVLHLTKLSQLKWDWTVLLP LALLRIRACPRDATGYSRFELL YGRTFLLGPNLIPDTSPGLQYLP VLQQARQAANLLLPTDPQYPHE DTLAGRSVLVKNLTPQTLQPR WTGPHFIYSTPTAVCLQDPH
18614	48982	B	18723	1	271	

SEQ ID NO: NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, !=possible nucleotide deletion, !=possible nucleotide insertion)
18615	48983	A	18724	803	1158	CSWHDRFPDWKAGNLLSAA* D*HCPIASEAP*TITDAELQVTL TVEGGSDLPWEINPPSYTLCE KDPPTTSGPQTNQPKKHSHQFQ IRDKGDTFYPWTHNSGASHGL GRQPSLGV
18616	48984	A	18725	1855	2506	GASPVVWDPTENRITVQLHLGS HSQSPWNTGQRSDLTSPFDLL GLAAED*HCPISEAPLTITDAR AMG*LSTVEGKPVPLNTEAT HATLPSFQGPVSLASITVVGID G!QAFY*TSKLKPNSWCQH*TIRR FKHSFLVIPVTCQVPLLG/EDTLT KLSASLTIPGLQLYLIATLLPNP KPPLCPPVYVPHLNPQV*DISTR SLGDRSCTPYHLIKT
18617	48985	A	18726	2	979	TSTMAVGKNKRLTKG!GKKG KKKVVDPPPRKIDWY*RRKHP MPHIRNIEKDVGSPRTPRDPKL QSDGLKGSVCLVSPAEPE*L KFAFRKFKLITEDVSGVKTCPD LTSHGAWDLYP*QNCCSMVQK MGRPMIEA/HVECSRJTD/GYLL RLFCVGFYLNKRNISDHGRPSY AQPPNRVR!Q!R!KKMMEHDPQ RLQTNVP*KEVNNKLIPASIGK D!NEKACQSIYPL!QNVFVKV KMLKVKPKFELGKLMEHLHGE SSSGKATGDETAKVERADGY GPPVQESVGKFR!P!VG!NRSGH CVKKEKQSSRRDFGVSVHPRJ
18618	48986	A	18727	1	615	ASTAAPRMLLLFQPRYRTLQPO RLLMPKKNR!UAIE!EL!FK!EGV MVPKKIDVPIPKHPELA!DRNV NLHVMKAMQVSQSPRG!YVK!E QFA/WKKISYWLCTN*GYQGV ISSRDYL!HLPP!EIVPA/TPLRRS RPED/SGRPSA*KGLEG*SDLAR LHKNGEAGQRLPYRR!SAVPP!G !ADKKAEAGGLGQKPEF!QFRG GFVRGRGQ!PPQ
18619	48987	A	18728	3	395	SAEVGAAETT!TELRTVQSLEI DLDMSMRNLKASLENSL!GILLHL ESELAQTRAEGQRQAQYEAE LNIKVKEAEIATYRRLLEDGE DFNLGDALESSNSMQTIQKTT RRIVDGKVSETNDTKVLRH

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18620	48988	A	18729	323	1973	PCMWIGFAAVRKGLKDSSASC GCTRRVRGWTWQGLSRVCVA RNEEVRWLWGLCWLGSSPPAGW NNVFYMLISADVLACLEPRAN KEAANELAGAVD LGWMANVR RNPRDMVTSTH LGTHFHLRKTP PRGEKTCELASQQP LIEATTKT KSVAVSHILTYPPTLNGVAAV SSRVHFSFWPPTLQ TGLEQGSM SFTICFTSTNYQLSHISQPHSHS VQFISSTAKVYAVLRLGLGSRTS VSFSTSFWSGWGSGGLAAGMP GIDNARLAADDFRVKYKTELV MCLSVESNVRLHKTDDTNV TRLQLET EMEALKEELLFMKK NQEKEVKGLQALIASSEL TMEV NAPKSQDLSNIMADLPAQYDEL A\RK\N*EELDKY\WQS\QED\IEEHT TVVTNTSLL\EVW\SC*DARLTEL RRTSPGLWRF\LDMS\ARNL\VAS LENSL\IREVEA\PYAL\QMEQL\N GILLHLESQLGQTPRTEAQ\RQA Q\YE\EA\LL\NIKVKL\EA\EA\ATLP GRLLGRMAKD\FN\GDS\ILDER NSFQL\QKTN\TPPGN\VDGKV S\ET\ND\TKVLRH
18621	48989	A	18730	1	897	MGH\HRRQSLSPVLS\YSPDSMS FTTRSTFFTNYQLGSVQAPS\Y GARAVSSAASVYAGAGGSRSI SVSRSTSFRGGMGPGLAAGM AGGLAGMGGI\QNKKT\QMSLN DRLAS\YLD\RVRS\LET\ENR\LES KIREHLENKG\QV\KDW\SHY\CK TIEDLRAQIF\ANT\VDN\ACIVL\H DNR\LAADD\FRV\K\YET\QLAMR QSVENDI\HGLRK\LET\EA\AL\REE LLFMKNH\EEE\VKGLQ\Q\Q\IAS\FR LT\VE\DA\PK\Q\SD\LA\KIM\AD\RA QY\DD\LAG\K\N\REEL\DK\Y\W\P\QQ\EF E\EN\TT\TV\T\Q\SA\EV\GAA
18622	48990	A	18731	3	423	S\SPV\LS\SPD\MS\FT\TR\ST\FT NYR\SL\GS\Q\AP\SY\G\AR\PV\SS\AA SVYAGAGGLATG\IAG\GLAG\MG G\I\Q\NE\K\ET\TM\Q\SL\N\DR\AS\I\LD\R V\RS\LET\ENR\LES\KIRE\HLE\KK G\P\Q\VR\RD\W\SHY\FK\I\ED\LR\A\Q\IF A\NT\W\DN\AR

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met/Asp	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion,  =possible nucleotide insertion)
18623	48991	A	18732	663	2089	AFTTRSTFSTNYRSLG SVQAPS YGAGPGRARAPASYAGAGGSG SRISVSRSTSFRG GMGSGLGQ RELAGGLAG MGGI QNEKETM A/QALNDRLGLFTWDRVRSLG DRRTRKLGRAKFREHFGRKKG PQVVRDWSHYFK I EDL RAQIF RKYLLDNAPHFLQDLTIAPSLL LD *F EFKY*GQSALMRQFLWR ND PLGSAKV DDTQYHTDLQ AWRQRFEEAPQRRELALSMKKE PRRRKLKG LSSPRLPSSWG*PVE VRLPPNFQDLRQRSLADIPGPN MNELGSKKNPRRKLRQSTWSQ QI*GRAPQLVTTTSLEVGSLLK TTL TQKLRRRTSPGPWKIRPWTTS MKKS*KAQLGRNSP*REVGRPP YGPYKMEASFKRGSLLHP*SQS W QTRPG AEGTAPQAPRSYEGP C*NIKRSKLEA*DRPPYPPALLE D GEDF*SLVDPLDSKQLHAKPI QKTTT PPG*VGLGKVVS
18624	48992	A	18733	53	1100	NFRVEAGVRGVQQKETCAFKV LESINGKF GLALAVAGGVNSA LYNVDAGHRAVIFDRFRGVQ \br/>DIVV\GKGTHFLIP WVQETQLS FD CRSPRPN VPSQSTG*AKDL QNVQHITAASLFRACRQPSFPR I FTSIGEDY GWSVCLPS VTEVIL KVSVGSL WMLGELITKRE LVS RQVSSDDL\TERAATFGL L DDV SLTHLTFGK DFT*AVEAKQVA QQEAFKGQ CWLKAEQQKK \br/>AAII SAEGDSKAAELIANSLATA GDGLIELRKL/E*AAEDIAYQLS RSRNITYLPTG QSVLLQLPQLR GPPLPCTSRG LDLG PQPRLNNS SLSFL PTPEINCEIFMIGLK
18625	48993	C	18734	222	458	

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18626	48994	A	18735	2104	2758	QFCPSRQKGCLQKTFRHVFAGH GGDFLFRSPTHAFPFVCPVLFPLP P/TVRPCPPFS*VLSSSPRNSQ NTIPRSPPFLSPGTLSRSPAGSRDP GNPAGPSNTRLGPTAPVSRALP VDIGFRSTDCAWSLQPQVPVNPG SRPAPTNPRSRSTPVDPGSNTRL GPTAPVSRALPVW*ALGPLTAG PYSPR/CPVNPGRSPAPTNPRSR STPVDPGSNTRLGPTAPVSRALA PVDIGFRSTDCAWSLQPQVPVNPG GSRPAPTNPRSRSTPVDPGTRTT PEGL
18627	48995	A	18736	2	280	AMGFIVAPSLGCF/VGSRFVHG EGLRWYAGLQKPSWHPPHWV LGPVWGTLYSAMGYGSYLVW KELGGFTGVSRASEVAPPEPPP GSSVLCFLHA
18628	48996	A	18737	331	972	AAAAAAMAPPWVPAFMGFTLAP SLGCFVGSRFVHGEGLRWYAG LQKPSWHPPHWV/LGPVGWGTLY SAMG*VGVHWPGDKPGPLQGE AWPRTEDTQLALNWAWPPIF FGARQMGGALVNLLLSIGAA GHLLGGGRGASIQWLAARLLYP \YLGIAWPSTTTTQTCVWRD\ NHGWHGRRRLARVSARPTMG LQLHQAGAITLVMWWPSRFHD HWAC
18629	48997	A	18738	1	603	
18630	48998	A	18739	1	1782	
18631	48999	A	18740	237	876	CESFCWHHFFWDIFNLFVTPF LVHVHDYQGFESVAKKYDVMN DMMMSLGIHRVWEGFSCSGKMH PLPGD\QLLDVAGGTGDIARFL NYVQSQHQRKQKRQLRAQQN LSWEETIAKEYQNEEDSLGGSRV VVCDINKEMLKVGKQKALAQG YRAAHKSGVILDCLWFPPILHPI AQQICQLYLQNTSGIWPSLPSYL CYHLLVQATIPSYLDCCNSL

SEQ ID NO: NO:	SEQ ID NO: of peptide sequence	Met /od	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, ^=possible nucleotide insertion)
18632	49000	A	18741	112	995	VLGSLSQEKRAAETHFGFETVS EEEKGKGKVYQVFESVAKKYDV MNDMMSLGIHRVVKLDLLWK MHPLPGTQLLDVAGGTGDIAFR FLNYVSVPAEKTEEAVKGPTK FILGKNLPKSTRMKKIPWAG/TR VVVCDINKEMLKVGKQKALA/\ KDTRAGLAWLL*DAEELPFDD DKFDIYTIAFGIRNVTHIDQALQ GSSFGCLKPG/GRFCLCLGFSQVE QSPILSRLYDLYS^SRVIPVLGEV IAGDWKSYQYLVE^SIRRFPSE ^KFKDWMIEDAGFPQ/V^LTKV^H QGIVAIHSGPKL
18633	49001	A	18742	117	403	
18634	49002	C	18743	62	370	
18635	49003	A	18744	179	527	IQEPPVII*GLHMVHNFTNTIFVSS YFKFESTFAISFLKVFTCFSSI* IKSLDSEQCVVGKISKHWGTLIR EAFTDADNFGIQFPLLDLVKMK AVMKVGICGKNLVKQGNFTMT HSN
18636	49004	A	18745	3	1242	AAPQAGLSPVIAAAIQLLHLS TQCSSPNTCCPRLRTRATIYYSR WSYIIPLGSPVSP^PFQEAES/AL TLPPACSFYGPPLT^FQPKP*GSFP LSQ^MEYTIGLYT^TFHCPGTSR RQIPSSYLNCKDAFLPLL/SNPP QCRPTFTVGLVDVDLTGFETNN KYEIKNSFGQRVYFAAEDTDC TRNCCGSPRPTLRIJDNMGQE VITLERPLRCSSCCCPCCLOEIKS LDEQCVVGKISKYWTGILREAF TDADNFGIQFPLLDLVKMKAV MIGACFLIDRNCSPAMEQSWM ENYFDEMTEIGFRRSVITNFS KEHVLTHCKEANKNLDKMLDE WLTRKNSVEKTLNELMEVK NEKLTIKGKISKYWSGFVNDVFT NADNFGIHVPADLDVTVKAAM IGACFLFAFRLGSELHN
18637	49005	B	18746	277	2415	
18638	49006	A	18747	102	196	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met/Asp	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, ^=possible nucleotide insertion)
18639	49007	A	18748	897	1656	SNAGLRRHVCRTSCQSGRARSCHVGLHTPWVS*VPWHPWGIRWRGDPQKSQRKCCVPGGAP/QKGGDPEPQPSLSVSWNWLGSACA GFRAVLPRKPKQRKVWLFASSAGTAATEPPR**LAWKADSGGDPWQQPQSQSARPHATWTRGDGAPPGRVA/QQRGTAAGGASAGVSSGRSRGSPQTGFQALQSCLEASRRPPVVACNPHPAGALPAACAGNRATLMTGSCLQMPIMYEEAQLRLEELCTKARLNQWFL
18640	49008	A	18749	756	884	CLQRLLPPGFRRQPSKYRRNRGKSGK*RPSPVATWQPDYNI
18641	49009	A	18750	1826	2772	RRVLEAMGPsRAAKVLSVCVR SRIGPLICSQRHPATSKTKPQGR PPGEQGTPRDNPRNNRPARSATPRGA/PQGAPPRGEEPNAPOT IDKGPSPPSRQHTRRLARSQNP PPERHTPAAGGKTRYVRQSVL HRARGGEPVRMPLPRIAEAP APDRVECF*VVQSPAREMHSCQ ADSMCPVW*GRIWRSAAGSC*SR SEKILWIPQSGLQAHACPSEA HKMPGNPRDGGAGICKSSPGG KGERRKVEGGSTTRAQTSRDS VSKRHANTMGEQAQGEKHPREG TV*KTKRRGPKGQTRGKAPPEE ETSRREPPCTGPI
18642	49010	A	18751	196	322	
18643	49011	C	18752	189	650	
18644	49012	A	18753	1	53	
18645	49013	A	18754	31	449	
18646	49014	A	18755	1	389	GMPTSTIASCSQDGRVFIWCD DASSNTWSPKLLHHKFNDVVWH VWSWSITANILA VSGGDNKVTEG QQNEQ*QDRWGLAPHPPAPGL PLPGPTNQTTGKSPQLQQDYFP RRSYRCSHRLIICLNVIGNAL
18647	49015	A	18756	1	1041	
18648	49016	B	18757	15	782	

SEQ ID NO: NO:	SEQ ID NO: of peptide sequence	Met no	SEQ ID NO: in USNN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, ==possible nucleotide insertion)
18649	49017	A	18758	1	1425	EVKKINNAHTIGCNAVSWAPA VVPGLSLIDHPGQQKPNYIKRFA GGCDNLILKLWKEEEDGQWKEE QKLEAHSDWVRDVAWAPSIG/ IWPPTIASCSQDGKRVFVWTL** CPQAITVVPLNCLHKFNDVVLG MLNWGPSQPTSLAVSGGDNKN GNTNTVCPWGWLQDSNTLVHLV TYKMPRSSLGLGFLWCQQLLSPR KYREGTSPVSLWVGEWWFNP DWWGSIRVYHPSPSGSYRTHKP PLNNLSCDTSIARELLKGKKFLL FVSVYPVPSTVLGRKKVSVINT VDTSHEDMIHDAQMDYYGTRL ATCSSDRSVKIFDVRNGGQILIA DLRGWPRASRYQQGHHQDLFIL RSDLPSQVFIRDKLMMERRNRRT GRTEKARIWEVTDRTRVTWIGE AVAAAADGVTFSPVPTPHTF RHYSAMHMLYAGIPLKVLQSL MGHKSISSSTEVTKVFALDVA RHRVQFAMPESDAVAMLKQLS
18650	49018	B	18759	323	1583	
18651	49019	A	18760	3	419	PSASSSPARIPAATRQGRRSPRIP PAPSNEAPRLPADREFLEQQPPIP FPKPTIQASGADRAVDCGILKL QKSPARLARPRWPRRPSKRFW SAAGSVEEQPKPPRRRAKSPEQ SPQLSVLPLVTITPQASGASFEK MKN
18652	49020	A	18761	2	385	WGRGGGRGLLYGRRHFVRRR RGGRSPGESPALTVT*GAV\PSA AFRESAQGPGRSSEAHISTSPKR TDGGRDS*PGLPRSSLTPSLPRP ASFSTSPGRVSAPHRLPRHS/AG PGLSGSS*PQPYSDPT
18653	49021	A	18762	242	422	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met/bud	SEQ ID NO: in USNN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, !=possible nucleotide insertion)
18654	49022	A	18763	2	992	AREKKQKTRRQNKNIPRQINKT QRICC*QSCLTMTQDFFWPLCQ GHSRGAPCLLVPPGLSLTCAPA QPAARPGVSQLCAIACTHIQW FPSSCPSEKNGDTLTVKTPSA SSSPARPIAATRQGRRSPRIPPAP SNEASAPGPRPVPGA!PPRFP KPTIQASGADRAVDCGILKLQK SPARLARPRWPRRPSKRFWSA AGSVEEQPKPPKAP/PAKSPEQS PQLSVLPLATITTPQAYGASFEK MKNLKTRRGGRSRWHPFNVIP QAPS LKWGFQTS DASSAEVFH VDRSLASHKMGPGRRPSPLW APPFCEAAAARRQEPGVICIMVE
18655	49023	A	18764	292	348	
18656	49024	A	18765	2	466	LITVVKLDTMVDTFLQKLVA AGSYQRFTDCYKCFYQLQPAM TQRIFYDKFIAQLQTSIREEISDIK EEGNLEAVLNALDKIVEEGKVR KEPA/WQRDTLRRHVQKQEAЕ NQQLADA VLAGRRQVEELQLQ VQAQQQA WQALHREQRELVA VLREPE
18657	49025	A	18766	2	511	FNMAEASSANLGSCEEKRH GSSSEVPPGTTISRVKLDTMV DTFLQKLVAAGS/YSTPSLGRK CWSVRLPSGGQSVKQAFSWAAC RLPQGRKEEISDIKEEGNLEA NALDKIVEEGKVRKEPAWWRPS GIEPKDLHSVMAPYFLQQQRT RCHVQKQEAENQQLADA
18658	49026	A	18767	224	748	NRPSVGRRAGYHRRGGSYQRFT DCYKCFYQLQPAMTQRIFYD!K FIAQLQTSIREEILFDNQKQEGE PRKLSWNALG*KFVGTKGKVR KEPAWWRPSGIEPKDLHSVMAP YFLQQQRTLRRH!VQKQEAENQ QLADA VLAGRK!QVEELQLQV QAQQQA WQALHREQRELVA LREPE
18659	49027	A	18768	1	421	

SEQ ID NO: NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, >=possible nucleotide insertion)
18660	49028	A	18769	666	1445	AGITTEIAAKRTIQVHLHQAND AQERAERSQREFRERRAREPG LRLK*SFNLNRRIQLVVEEL\DRA QERLGHLPCKKL*RS*KKLADE SERRY*RLFEN\RALKRLKEKIG TSREIPTQKKLKHICRKEAD\RK YEEVARKLGLDHLKEDLEPTEE\E RA\ELAESRC*EIDEQIRLIDQNL QCLSAEDKYSQKEDKW\EEE MK\LTNLKREAETRAEFAERS VAKLKKTIDDLLEDKLKCTKEEH LCTQRMLDQTLLDLNEM
18661	49029	A	18770	2	158	SAAPGAVPPPEADSTSAGMSRR PCSCALRPPIRSCSASPSAVTAA GRPRPSDSCKEEESTLSSVKMKC DFNCNHVHSGLKLKVPPDDIGRL \VSYNIPAYLEGSCKDICKDYER LSCIGSPIVSPRIVOLETESKRLH NKENQHVQQTLNSTNEIEALET SRLYEDSGYSSFSLSQSGLSEHEE GSLLEENFGDSDLQSCLLQIQSPD QYPNPKNLLPVLFKEVVCSTLK KNAKRNPKVDR\EM\LKEIIARG NFRQLQNIIGRKMGLECVDILSEL FRRGLRHVLATILAQLSDMDLI NVSKVTTWKKILEDDKGAFQ LYSKAIQRVTENNNKFS\PHAST REYVMFRTPLASVQKSAAGTSL KKDAQTKLSNQGDQKGSTYSR HNEFSEVAKTLKKNESLKACIR CNSPAKEYDCYLQRATCKREGC GFDYCTKCLCNHYHTKDCSDG KLLKASCK\UGPLPGTKKSKKNL *RLHVGWHEPAPLQLRPTATPL LLQRQPQRSDSRAPSTLG

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18662	49030	A	18771	4	1276	RKAASSYVSRMALPIIVKWWGGQEYSVTTLSEDDTVLVLKQFLKTLTGVLPERQKLLGLKVKGKP AENDVKLGALKLKPNNTKIMMMGTREESELEDVLGPPPDNDDVVNDFDIEDE/R*FEVENREENLLKISR RVKEYKVIEILNPPREKGKKLLVLDVDYTLFDHRSCAETGVELMRPYLHEFLTSAYEDYDIVIWSATNMKWIEAKMKVKPLGLVIWGKFSEFYSSKKNTIMFDDIGRNFLMNPQNGLKIRPFMKAHLNRDKDKEKLKLTQYLKEIAKLDFFLDLNHKYWERPRVRCHIHFHGKEDRYDPCPMGACSCKTVCCTNLA LPALPLGSMKNGQPCRNVIGQKGYALTIVNSGPQQGLFVRILLGLFIRDFPPAGCCGARPFVNNEGLMAYFQRRTLVGVMLVSSSKSFK
18663	49031	C	18772	113	257	
18664	49032	A	18773	143	330	HHGPVPFPGLIS*HSLHCPCTPGGKNVFFFCEYFLKLAGIETTNCSDAKRGKKVCCLI PR
18665	49033	A	18774	3	432	
18666	49034	C	18775	112	192	
18667	49035	A	18776	3	1015	SSRPVRPRPAARLSAMSSTQFNKGPSYGLLSAQVKNRLLSKYDPQKEAELRTWIEGLTGLSIGPD FQKGVLKDGTILCTLMNKLQPGISVPKINRSMQNWHQLENLSNFIKAMVSYGMNPVDLFEANDLFIESGNMTQVQVSLLALGGKRPKTKGAAEGGLDIGVKYSEKQERNFDDATMKAGQCIVGILQMGTNKCASQSGMTAYGTRHLYDPKNHILPPMDHSTISLQMGTNPKCASQVGIMTA/PGTRRHIEYEQAGNPTSCDNFSM/SLQIMGYTQGAQTQSGQVF/PGPRPDI*TPSTCPQGTIADGAPSGTGDCPDPGEVPEYPPYYQEEAGY
18668	49036	A	18777	2	110	
18669	49037	A	18778	74	289	

SEQ ID NO: NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=>Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
18670	49038	A	18779	138	2039	GAAMAAAAGRLPSSWALFSPLL AGVALLGVGPVPARALHNVTA ELFGAEAWGTLAAFGDLNSDK QTDLFV/LAGKK*LNRLFGRPE CTRILNPK*RYLSRITVH**QV* LGAYDGSQMDVLLTYLPKNY AKIMN*ELLSSGDKIKH*LTI*P YSIGL/LQDEPLIMDFNGDLIPDI FGITNESNQPQ\I\LLGGD/CYHGI QH*PLQVKCEFH/PHAFIDLTE DFTADLFGATLNGTTSTFQFEI WENLDGNFSVSTILEPKQNM VVGQSAFADFPGDGHMGMSFTC QGCGR*K/CAKRVPSPYLVRSGM KQWVPVLQDFSNKGTLWGFVP FVDEQOPTEIP\I\PTLHIGDYNM DGYPDALVILKNTSGSNQQAFL LENVPCNNASCEEARRMFKVY WGADRPKSN/SKGAMVATFDFI YEDGILDIVVLSKGY\I\TKNDFAI HTLKNNEADAYFVKIVIVLSQL S\SNDCPRKJTPFGVNQPGTLYH VYNCRKWVSEKWRWPNSAQ SAHLALQLPYNVLGFRVGSANF LDHL\SLGLIPRPSWRKIFYGKQE WTAIIPNSQLI\I\VIPYPHNVPPL GVPNCILYTKLILFWLTAIALIR CLCFQSLAINWHTLGREKKAG WIEEKRTKAHREPPFWMAMW
18671	49039	A	18780	1	966	
18672	49040	A	18781	1	1035	RPPFPVPGVQKCPPLTRGLLHG RWLRDRAGGPPEAQDGTGRRSR SRRRPPALPNSRSPSPVASGREM VVLSPVPAEVTV\I\LLDIE\I\EGTTTP IAFVKKG/DILFPYI\ERKMLK\I\YEL QTHWEEEEE\I\QDVS\I\LFEGNK A\I\EEDAHLDG\I\AVPIPKHLGIG V\I\DDL\I\LQQM\I\QA\I\VV\I\DN\I\VCWQM SLDRKTTA\I\K\I\QLQGH\I\MWRAA FTAGRMK\I\A\I\EFFADV\I\VPA\I\VR\I\K WREAG\I\MKVY\I\YSSGS\I\VEA\I\QKL LFGHSTEGDILEL\I\VDGH\I\FD\I\TKI GHKRRRVK\I\VTRK\I\AD\I\GC\I\ST\I\K NKHFVF\I\WT\I\DVTSR\I\ASAGL\I\RE AGCCTLA\I\VV\I\VRPG\I\NAGINR\I\R RKT\I\YSLITSFQ\I\WNY\I\LP\I\ST

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met/Asn	SEQ ID NO: in USN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, I=possible nucleotide deletion, V=possible nucleotide insertion)
18673	49041	A	18782	I	528	DNELLDYEDDEVETAAGGSMS/EAPAKKDVKGYSVFSIHSGGFRD FLLKPELLRAIVDCGFEHVPSEV/QHECIPQAQILGMDFLCQAKSGM GKTAVFVLATLQQLEPVVTGQV SVLVMCHTRELAFQTR*KTRPF WNVTVCPSGEDTRVGVKETLL PPPLTAPTPWLPSPASPPPLNPH
18674	49042	A	18783	207	309	
18675	49043	A	18784	85	348	PPHSALLPFPPTPFLPPSQQLEIFVD DETKTLTLHGLQQYYVVKLKDNE KNRKLFDLDDVLEFNQVS*TSS RGMSIGALQL*QKPGY*VHFY
18676	49044	A	18785	I	930	CCCRHTRSPCLVMAENDVDNE LLDYEDDEVETAAGGDGAEAP AKKDVKGYSVSIHSGGFRDFLL KPELLRAIVDCGFEHVPSEVQHE CIQOAILGMDVLCQAKSGSGER QAVFVLATLQHLEPVATGQV CAG*CCHTRELAFQISKEYERFS KYMPNVKAVVFFGGLSIKKDE EVLKNCPAYPSVGTGRLILAL ARNKSNLKHKHFKILDECDKM L\EQLDM\RRDVQE\IFRMTPH EKQVMMFSATLSKEIRPVCRK FMQDVNTLLPSLPLPARCLLPF LALFLRLPCHSSAKKAACAQLG
18677	49045	A	18786	96	1618	LFTPCFHLFCENPSPRSFPSSPAG PVMAENDVDNE\LLDYER*MR WETAAGGDGAE\PAK\KDVKG SYVS\LSHSSGFRDFL\LLKPELLR A\IVDCGFEHVPSEVQHECIPQAQI LGMDVLCQGKSGVMGKTAVF VLATLQQLEPVVTGQVSVLVMC HTRELAFQISKEYERFSKYMPNVKVA VFFGGLSIKKDEEVLK/R RNCPHIVVVG\TPGRLS\LWVRN KSLNLKHKHFKILDECDKM\LEQ LDMRRDVQE\IFRMTPH\EKQV\ MMFQCYLGAKE\IRPVCRK\FM QDPME\IFR\VDDET\KLT\HGLQ Q\YY\VKLKDNE\KNRKLFDLL DVLEFNQVVFVKS\QRCIAL APAY*WEQNPA\IA\NHRGDAP RKERLSR*SSSFKDFPTNEILIG YPTLFGRHGTS\EAGETIAF*FM NMP\GILKTLPCHR\VGPEQGRF GHPRGLA\ITFVSDEE\LP\RS\CD DVQGSALRVKF\SEL\PD\EIGHL PTLEQDTGRRLAHFGNVDR\FL
18678	49046	A	18787	I	363	

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18679	49047	A	18788	78	714	GTTEGKRQEAVGYLCLVPLTLT PLVTRLPPQVADTMLPPMALPS VSWMILSCLILLCQVQG\EETQ KELPSPRISC PKGS KAYGSP CYA LFLSPKSWN\ADALAC\KRPSE KLVS VLSGAEGFSASLLA\RSIS NSY SYI WIGL\HDPKKG\SEPDG DG*EWSSTDVMNYFAWEKNPS TILNPGHCGSLSRSTGFLKWKD YNCDAK\LPYVCKFKD
18680	49048	A	18789	52	186	QSEVH HGI SYY TTQ QG EN LSE PI WKS WQ RQS QDL*QEN HPEI YSL T
18681	49049	A	18790	666	2732	KQLIKMCYFILLL LILSSHIGKD KAIDKNGILVQY\WQE*KLVEPF *KAIWPPCMETLNVDT PFPQPV CLGIYPN E*KLSK/CFKP*APKV YFHGCL*Y*NHWEPTET PPKV GWIK*ILF
18682	49050	A	18791	112	340	
18683	49051	A	18792	3	323	LSSLASMSFTTCSAFT NYWSPG SVQVPSYGTQPV SHA SVYAG LGGSGSRISVSHPS MAGGLAG MGGI QNEKETM QSL RDR LASY LDR VRG LE TEN WKL ESKI QEH
18684	49052	A	18793	1	994	APS YRA/RLV RSV VAS VYAG PGS SGS RISM SRS TSF QGG LGS RSM AA/GMAGGLAGMGGI QNEKET MQSLNDR LAS YLDR VR SLE MG NW KLES KIWEH L EKK GPQ VRD WGH YF KTI EEDLT QI FT STVDN TCI IQL QD NAH LA ADD FRV KYE TEPAT CQS VEN DIH GLH KVID TSV TQL QLE TEI EAL I KEA LLFL KKN HEE EES/WRHTV QALE ID LD WMK NLE ASL ENS LK/EG VEC YTLQMEQLNGILLL HLE SEL AQT WAEGQQQAQ EY QAL PNI KV KL EAEIATYR LLE DGED FNG D A LDSSN STQ TI QK TPT C/RTV DG K VVSET NDT KVL
18685	49053	A	18794	3	377	
18686	49054	B	18795	54	136	
18687	49055	A	18796	149	419	

SEQ ID NO: NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, !=possible nucleotide insertion)
18688	49056	A	18797	83	1402	AEKAGGKKGEAPSYRA/RLVRS VASVYAGPGSSGRSIRMSRSTSF QGGGLSRSRMSAA/GMAGGLAG MGGIQNKEKTMQSLNDRLASY LDRVRSLEMGNWKLTKIWEH LEKKGPQVRDWGHYFKTIEED UTQIFTSTVDNTCILQDINAHL AADDFRVKYETEPATCQSVEN DIHGLHKVIDDTSVQLQLETEI EALKEALLFLUKKNHGEIKGL SRRQIASSGVDPWRVDAPKSSG PSPKIMGRHPGPKYDELARKR TREE\LAKYSSQIQEEST/TQLV TNTSLI/GGLELAEATNLHRS*TY KSRSLEDSTLDSIEKS*KAQAW KKQPLKGWSWKAQRLPLPDWSK LQTGILACTFESRAGNKTARG TSAPGPQEL*GPLLKHQVKVAG GLRSPTLPARLLEDAEAL*SLV DPLDSKQLPCNTIQTTPPPG*V
18689	49057	C	18798	140	283	
18690	49058	A	18799	2	783	VVQFARREKPSSSKVSRHPC EAVREVLHGUNQRKSPQRSWET VELQISLKNYDPQEGQSAFSGT RQALSPPLPRP\KFSCVCPGGTQQ H\CDDEA\KARGISPPhGTfEGA* KNLNKE\KNWSKKAGPRKY*L RFFGPQKSLDQSKIPPNSPGPF K*RAGK\FPFPWFTHN\ENMGG PKLDEGEVPPIQVQFMKERCLC L\AVAV\GH\KMTD\DELVYNI HLGCQLSWVSLLKEKNW\QNV RALYIKSTHGQSPKRFLKAHFE
18691	49059	C	18800	239	555	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met/ codon	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, !=possible nucleotide deletion, !=possible nucleotide insertion)
18692	49060	A	18801	401	3014	TRASSTMSKSFQQSSLRSDSQG HGRDLASAAGILLLAAATQSLSM PASLGRMNQGTARLASLMLNG MSSLLNQQGAHSALSSASTSSH NSQSIFNIGSRLGPLLSQSRHGD ADQASNMLASFGILSARDSDELS RYPSTDITPENLRPILLQLKRRR TEEGPTLSYGRDGRSATREPPY RVPRDDWEERKRHRRDSFDDR GPSLNPDVLDYDHGSRQSSEGYY DRMDYEDDRRLRDLGERCRDDSF FGETSHNYHKFDSEYERMGRG PGPLQERSLFEKKRGAPPSSNIE DFHGLLPKGYPHLCSICDLPVH SNKEWSQHNGASHSRRCQLL E1YPEWNPNDTGHMTMDPDM LQQSTNPAPGILGPAPPSFHLGG PAVGPRGNLGAAGNGLQGPRH MQKGRVETSRVV\HIMGFSTE GKTLRYQLQLVEPFGVYHFKP! *FLNKNLLRAFIEMATTE\DCFK AAVIDYYTTTPA\LVFGKPVVRV HLSQKYKRICKPEGKPDQKFDQ KQELGRVIIHSLNLPHSGYDSA VLKLAEPYKGKIKNYILMRMKS QAFIEMETREDAMAMVD\HCL KKALWFQGRVCVKVDSLSEKYK KLVLRIPNPGIDLLKKDKSRKR SYSVDGKESPSDJKKSKTDSQE AERST\EGKEQEESGEGEJKD TKDQTEQEPNMILLESEDELLV DEEEAAALL\ESGQFSGETSTD
18693	49061	A	18802	3	1013	NCRAAWRAKLEGCLSLRRNAC QCFLIWQTQDPREQSYSLQDLP REVLNQEESKSISIWI\DIYHLLEM GNGLSDQTSILSNLPSFQSFHIVI  GLDCAWKRQLSYTRLQFQLN L*NT\WPYPKGFNTEKI*/RVTLG NSKTVTFHF\WDVGGQEKLRP LWKSYTCTDGV\VVVDSVDV ERMEEAKTELHKITRISANRGV PVLIVAN\KQDLRNSLSSVEIEK LLAMGELSSSTPWHQOPTCAIIG DGLKEGLEKL\HDM\IKRKRML RPTRKRKDEYQFPNIICVGVGF LWSDFDKNRRVSTAGVCLSLAPP WMLLKLCFVEQFRCPTRVALW KMSKCSAS
18694	49062	A	18803	3	1103	
18695	49063	B	18804	34	734	
18696	49064	A	18805	1	1741	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met/Asp	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, ^=possible nucleotide insertion)
18697	49065	A	18806	6460	6635	RTSTERSHLKTRYQRTSCSSNR* LNSSSSKTSFRCSLITSLFWRHT IFNMLLNNRLL
18698	49066	A	18807	5567	5853	IGILEA*LLRNLPNDSIKALVDA *YKSLLSAVERCSFVMLFGEPM NKPPLAILRIQSGVNRRPPVISIM ALIGPLVTPSASTYSGVTNADLS SATK
18699	49067	A	18808	664	992	SCADIHGYZHRGNSSNNDSNLIP KQTNRDCLNNGHQNHSCNG/D *PQPQR**QLTLQNLQMHQ^KQ QYPLPQHQQQE^RTR
18700	49068	A	18809	3	1698	
18701	49069	B	18810	227	883	
18702	49070	A	18811	180	373	PDTLRSILPMLLEQLFCRTFGLL SP**RDTSLHLGHKTEQHT^LV MGSWFYLLASQQPRCCYAC
18703	49071	A	18812	495	701	
18704	49072	A	18813	138	418	AYRLLLCLVYSEGFYMHLEFQ NRLYHQLVF*GRLWHFWIKSIK RFSIY*FWYRW*YICKLNKGR LQDVIGVINT*CHFLS*GLH^TIP GIHRL
18705	49073	C	18814	62	175	
18706	49074	A	18815	644	828	
18707	49075	A	18816	1	1107	
18708	49076	B	18817	84	342	
18709	49077	A	18818	3	1399	
18710	49078	B	18819	1	1377	
18711	49079	A	18820	1	546	
18712	49080	A	18821	855	1099	VTLYSEYQHPSVREYGLYLTSH RIEPLECVHRTL*PVLLSMQPSV LEYYYEQQG YEAEY* LQEECHH QRTSSL* DLLKQLLQ
18713	49081	A	18822	1	1680	
18714	49082	A	18823	1	3951	
18715	49083	A	18824	2	6446	
18716	49084	A	18825	2497	21785	SSPYPPFTKQSSTNNFVFDGNELF NSRDRLSQRSLFYILQSSVHLLNR Q/LEGYYVQHHLNLAEI^HHGLG KDAYIAAMYNNDDGATFQMEI GGIHTNAALAAGDKLQCIWRY LDVNGNAPAAENEFEVVSYEG FGTSNFSVKCKGMLPKFKFIGCD AFYGKYLQTDGPIKQVDSVKW FTNLTVSGSGRKQLQRKYQPQ VVMGMGMTSGFDDGYNLTP RQVKMAYGLGYRDWWTYIG MSHYWKGLTAFQDKETGELI
18717	49085	A	18826	31	479	

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18718	49086	A	18827	255	1002	SQFSLSQVLVDSAEEGSLAAA ELAAQKREQRRLRKFRELHLMR NEARKLHIIQEVVVEEDKRLKLP ANWEAKKARLEWELKEEEEKK KECAARGEDYEVKVLLFISAED AERWERKKKRKNPDLGFSDY AAAQLRQYHPV*PKQIKPVDME TYERLREKHGIEEFPPTSNSLLH GITHVAFHRGKFDRVVLRSGKN QFEKRD/KF*ARRRPYNNDDADI DIYINERNAQFNKKAERFY/GK YTAEIKQNLERGTAV
18719	49087	C	18828	91	225	
18720	49088	A	18829	3	212	
18721	49089	A	18830	88	239	
18722	49090	A	18831	865	1898	QQQQQQHQHRRYPRRRSPRAWC SHPRSPPLLFLPSLAPWPQDQLTEE QIAEFKEAFLSLFDKDGDGDTITT KELGTVMRSLQEPNKKLEL QDMINESGMLMGNGTHLTTPR IF*LMMARKMKDTSSEEGN/LR EAFRVFAKDGNGYISAELRH VMTNLGEKTTRF/KVDEMIRE AIDIDGQGVNYYEEFVQMMTG KMEDLTFLQPLPSPLEESNWNL LLTFLQKKEKKKKVHLFHSCFL YSKTECQKVLLVHTHQLNLHV VGGPCPLKDQATHQFYNNINTCT NLNDNGLLKRSIILLMINTLFLG ASFFHACSFDDWSTSQQLWY KLENGKNQISKPIPNGVLVHFV
18723	49091	A	18832	1	330	WVVLKNVCVGVGLLIAT*MWF SNKYLVQRQSRDYDVEWYGA DVHLNAYPLVILHFQLLFFIN PLPFLKNTVILLYPAPLILLYG SLALGWNFTHTLCSPFYKRVK
18724	49092	A	18833	1	534	VPSNSVNSLVQNGVILNSRDA ARH/TAGAKRYKYLRLFRFRQ MDFEFAAWQMLYLFTSPQRVY RNFHYRKQTKDQWARDDPAFL VLLSIWLCLVSTIGFGFVLDMGF FETIKLLLWVVLIDCVGVGLLIA TLM/WHCHFWKKQVILLYPFAP LILLYGLSLALGWNFTHTLCSP YKRVK
18725	49093	C	18834	295	570	

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18726	49094	A	18835	418	1567	SFTLKNCVLQRVSSILPSNTAEVDFPSWTTQSDWQQTRAQVLLQARARAALRLVLLILRHGDASPPMRTRLSPTATLATGSGASEAPVSGDRKPAATTSGGPRRKMLPSTSVNSLVQNGVNLNSRDAARHTAGAKRYKYLRLFRFRQMDFEFAAWQMLYLLTSP*RVYRNFIHYRKQTKDQWARUDDPALGFPFKYSGFCVSTIGFGIVFLDMG\FFETIKLLLWVGLIDICVGVGLL\IATL\WAFISNKYLVRKRQSRD\YDVEWGYAFDVHLNAYPLL\VLHFQLFFINHVNLTDTFIYG\LVGNLT\WL\VAVGYYILR*LSL\GYSVGLLFSSIAHF\KNTVILL\YPFA/PL*FLPPTGFPLALGWNF\THTLCSFYKVRVK
18727	49095	A	18836	1	888	MPGLLLLRGSQNLKQQAEILCG\LGALAVISAVKPLSKKFMLPLNP\TSMKPESDGIYSINLKRTWEKL\LLAGHAIVVIENSAADVVISSRN\TGQKAMLKFAAATGATGATPIAGH\FTP GTF/TNQIQAAYWEPRLLV\VS D P R A D H Q S L T E A S C V N P P A I\A L C N T D S P L C H / V D I A T C N N K G\A P S V G Q M W * M L A W E V L H M R G\T I S C N / S P W E V M S N L Y F Y R D P E E\T E K E F Q A A A E K A / V T K E F Q G K\W T V S A P E F T V T Q P E V A D W S E G\M Q I C N L G K A Q Q G Q L S S A E D D\F W S L E S L D G Y S I H T V F R
18728	49096	A	18837	74	848	REIFINVRSLLMACFVKEEDVL\KFLAARNP/HVGGTNLDFQME\QYIYIRKSDGIYIIRLKRTWEKL\LLAARAIVAIENPADVSVISSRN\TGQRAVLKFAAATGATGATPIAGRF\TPGTFTNQIQAAFRERPLLVVT\DP R A D H Q P L T E A S Y V N L P T I A L\ C N T D S P L R Y V D I A I P C N N K G A H\ S V G L M W W M L A R E V L R M R G T I\ S R E H P W E V M P D L Y F Y R D P E E I E\ K E E Q A A A E K A V T K E E F Q G E W T\ A P A P E F T A T Q P E V A D W S E G
18729	49097	A	18838	72	528	DEACGVCCYSPGASPMP**GRT\RK E G R T A G K V R P K R P K T P V N\K S G G Q G P K R K N W S K R Q K F R D K\L N N N L V L F D K A I T Y D K L C K E V P\N Y K L I T P S L W S P E R L A K I R G S L A\K G K P F Q E A P * V K G L I / R N L V S K H\ R A P S N F T P G N Y Q G W E D A P S L L

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18730	49098	B	18839	6	125	
18731	49099	B	18840	249	291	
18732	49100	A	18841	128	669	RPGHAQTLGSPSLALGMAGQF RSYVWDPPLLILSQIVLMQTVYY GSLGLWLA/VVDGLRLRIPSQD QMFDAEILGFS/TPFQQLRSLMM SFILNALTCALGFAVISSGEEKQ CLDFTVTVHFFHLLGLGSNSS PFSPSGG*TLVGLGPKPVALII SLAVIGEYLCMRTELKEIPLNSA
18733	49101	A	18842	I	818	MAELTVMRFRHTEPQGSEGLRP RISGSKPKQMHWTVLPLENGI CNGNTGNAQLLIPPGVIFHKYP SHYVTAMLKSLKWPLQTELTS SSGQALWGLVGGGSPHRQAST EKLFSEKVPKTAENFPCSELSCF HGENGFG*GVPCHRLFPRVY AVRGDDFHATAINTG:GGKSHPM GKKFEG*ETSSLKHTG:PGDLVP WQAGPNTNGSPVFLTSCTAQ ELSGLDGKPCGVLAKEV:GM NIVEAMER:FGSRNGKTSKKITI A\DCGTTPNKV
18734	49102	A	18843	4	454	
18735	49103	A	18844	I	978	MRWACDFTKLLSSTWTLIQLYPE NAMIIARWALLADCPETKTKAL RTTEDGIVDAANFEQFLQERIK VNGKVGVLGGGVVTIEKSNSKI TVTSKGVPNSM*IGSASSFVEK KRLLEF*KLLSSTWTLIQLYPE MIIARWALLADCPETKTKALRTT EDGIVDAANFEQFLQERIKVNG KVGNLGGGVVTIEKSNSKI SKGHFQFYVNRLSFLICGKEKA VGILEEIVLNLLIFSSIDILTVKG TCSGCERGFFLEIYDEVEDSSYD NHLKDDDPKREGPGEAQALST PPCCPLEKRPINDQTLIISWSGST NVIEEAGRHSVQEGWGLGV LRTTLPSLPQITGGAGFVGSHLT DKLMMMDGHEVTVDNFFTGR KRNVEHWIGHENFELINHDVVE PLYIEGRAENQLSHTVPGPVDL SDRIVNGYFLSL

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18736	49104	A	18845	167	1440	RDIWLSASAAAMVPVRKLV/AE GGQKTKQVLRTLGC <sup>T</sup> HPIEDG IIDAANFEQFLQERIKVNKGKVG NLGGGVVTIEKSKSKITVTSKG <sup>\</sup> PFNSM*!*GSASSFVEKKRLLEF *KAENLSSKNWNKTRMPTFTTL TQVAPNPITGYTSKGKISTLKR YLAFLRCCHGAREKACGEGG QKTKQVLRTLGC <sup>T</sup> HPIEDGII AANFEQFLQERIKVNKGKVG GGGVVTIEKSKSKITVTSKG <sup>\</sup> QFYVNLRISFLICGKEAVGILE EIVLNLLIIFSSIDILTVKGTCCSC ERGFPLFICDVEVEDSSYDNHLK DEDPKREECRKRDAYAPLKDQ GNAEKRRHNRVRKSWPILLSAKL LKIRTNLTGTEEAELHANHIQQ VPIKCLSYKLTERKNGTQKHLH YALILHVKCDRRETSKFTKYG THPLTLALFVPRAWDGPPSALPE SELAVFLVAYEGNTLHLFLSG AEQRGNSSLKERAGRARFWSH KLNEQTIPPDNLTKSSVQLQSSF SAVHPNSQPTVVWVDMPAHPLS QYLVPARKTVLPIWYGNSCP VIFGSLSDSKLSEGKEFALPLKF
18737	49105	C	18846	713	831	
18738	49106	A	18847	2	303	
18739	49107	A	18848	97	233	RTVT CYHRNSRACHPQQITSCP *HRLAPCLPLWSPKCPSRWPWF G
18740	49108	A	18849	229	359	MKWVYCSVTGMKGQQHRMP SKG*GWVQRYNRDGIPSPRVL LF

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18741	49109	A	18850	1	1185	MSTIDDPRLLQGRRMCLMLRGT PEQKALVIGGEACMWGEYVDN TNLVPRWLCPPTQDLANEGI REMTILHRHIDPRGKGVMRSCS FRTPRPTILACGPEKSLMDPQS QSNSEGASSSLVVKLADTDRER ALRRRMQOMAGHHLGAHFPAPLP LGACCAYTTAILQHQAAALLAA AQGPGLGPVAAVAQMQHVA AFSLVAAPLLPAAAANSPPGSG PGTLPGLPAPIGVNGFGLPTPQT NGQPVAPTRSTTIGSPLI/SGWSQ SRPILRIMKYAEQRIPTLNEYCV VCDEQHVFQNQNSMLKIOPDTII QVWRREDIPVNLYMKELELVTKA GFRALLSAPWYLNRLISYGPDW KDFYIVTEPLSFEGTPEQKALVIG GEACMWGEYVDNTNLVPRWLW AHRIQL
18742	49110	A	18851	231	416	
18743	49111	B	18852	184	594	

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18744	49112	A	18853	247	2296	PVYLSIFMSCVGENGSHIENW HSILRNGLVNASYTKLQLDIKGQ FWNDDDSEGDNESEEFLYGVQ GSACADLYRHPQLDADIEAVK EYSENSVSIREYGTIDDVIAL HINISFL!DEEVSTAWKVLRTE P!VLRRLRFVLSQYLDGPDP\$IE VFQPSNKEGFGLGLQLKKILGM FTSQWQKHL!SNDFLKTQQEKR HSWFK!ASG!T!KKFRAGL!QH\$F SPIPKPSFPYS*Q!DSMAGKGK LGVP!ELRVGR!LMNRS!CTMK NPKVEVFGYPPSPQAGLLCPQH VGLPPPARTSPLVSGHCKN!PTL EYGF!VQ!MKYAEQ!R!PTLN!EY CVV!CDEQHVFQNGSMSLKP!AVC TRELCVFSFYTLGVMSGAAEE VATGAEV!V!D!L!VAMCRAALES PRKSI!FEPYPSVV!DPTD!PKT!AF NP!KKKNY!E!RLQKAL!DSVMS!T REMTQGSY!LE!IKKQM!DKV!W!P !AHP!LLQW!IISSN!NRSH!V!K!PL SRQLKF!MHTSHQ!F!L!SSPPAK EARFR!TAKKLYG!STFAFHGSHI ENW!HSIL!RGNGL!VQWHSYTK LQLHGAAYGKG!YLSPISSISFG YSGMGKGQH!RMP!SKDELVQR YNR!MNT!PQTR!S!QS!RF!L!QRN LNC!A!LC!EV!T!SKD!LQK!HGEH LGCCPV!F!RPM!S!C!TR!L!P!L!*YED G!QVGDAQHY!PHGP!QRV!HERE
18745	49113	C	18854	122	486	
18746	49114	A	18855	1	535	KNAAGNF!SPT!ERLSPNAWKT!T TD!V!LN!G!T!A!F!V!T!L!S!IT!Y!A!ET GSGFV!V!P!S!A!K!A!G!V!E!A!M!S!K!S LAAEWG!K!Y!G!M!R!F!N!V!Q!P!G!P!K! TKGAF!S!R!L!D!P!T!G!T!F!E!K!M!G!R!P C!G!R!L!G!T!V!E!E!L!A!A!F!L!C!S!D!Y A!S!W!I!N!G!A!V!K!F!D!G!G!E!E!V!L!S!G!E!F N!D!L!R!K!V!T!K!E!Q!W!D!T!I!E!E!L!R!K!T!
18747	49115	A	18856	3	356	
18748	49116	A	18857	1	1581	

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18749	49117	A	18858	2	1242	RRLGSPRPIPPIPRRPRQRFPREL CSFCPAPCGPTACGGFRPEFWRI NMKLPAKVFVFTLGSRLPCGLAP RRFFSYGTKILYQNTTEALQSKFF SPLQKAMLPNPFQGKVAFITG GGTGLGKIGMTTLSSLLGAQCV IASRKVMDVLIKATAEQISFSNW EIKVHAIQCDVDRDPDMVQNTV SELIKVAGHPNIVINNAAGNFIS PTERLSP*CWKNQ/ITNIV*NGT AFVTLEMGKHLIKAQKGAAFL SITMMIY/A/ETGSGFCRYPSSAQ SRVWEAHGASLLQLEWG*NM GLRIPIVDSNQGPPIKTKGALYPS GPPTGTFGEKKMIGQKFCGPSP WGLVEELRKSLSLPAFLCSDYA/S W/INGAVIKFDGGEEVLI(SGDF NDLRKVTKEQWDITIELIRKT KRFLRPLWPSSWLQKRE
18750	49118	A	18859	8	432	NSKLPPVVTSQMRMFY/DPQT DQHMKNFPPEQLPLDFEFLQKTDP KDPANYILHAVLVHSGDNHGG HYVYVLPKGDGKWCKFDDD VVSRCTKEEAIEHNYGGHDDD LSVRHCTNAYMLVVIRESKLSE VLQAVTDHDIPQQL
18751	49119	A	18860	1	211	
18752	49120	A	18861	1	242	
18753	49121	A	18862	3	733	LVHSRDNHGRHYVYVLPKGD GKWCKFDDVVS/QLVERL*EE KRINAQKVDR/RQEYVHLYMQA QVASEDQFCGHHQGNDMDEE KVKYTVFKVLKNSSLAEFVQN LSQIMEPQDQIQLWPMQARSN GTRPAMLNDNEADGNKAMIEV SDNENSWTIFLETVDLELAASG VTLPKFDKAHDVMMFLKMYDP KMRSLNYCGHIYTPISECEIRDLL PVMCNРАGFIQDTSLLIYEEVK LNLTERRQD
18754	49122	A	18863	261	659	KHLFYLFIT*EITLYPDKHGCVR DLLEECCKAVALGEKASGKLR LLEIVSYKIIIGVHQEDELLECLS PATSRTRFRIEEIPLDLLEECCKA VELGEKASGKLRLLIEIVSYKII VHQEDELLECLSPATSRTRF
18755	49123	A	18864	107	407	CVFFADTSWRSEATFQFTVERF SRLSESVLSPSPCFVRNLPKIM VMPRFYPRDRPHQK\SVGFFLQR NAESDSTEDSLNDATTNPHIVA FHYWKPNLNSLV



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18761	49129	A	18870	3	885	LVCLVRELLGPRRFFLKVFVFLPTFPGIVPAPVLTATLPPHPEGRLYQVEYAFKAU*PGGPLPSLAVRGKIDWA VIVTQKKST*PNYL DSSVTVSLFPR*LKNIWCVMTGMTS*PADSQV^QRAR^YEA\ANWKLQSMG^YEI^PVD\MLCKKNCP^IFLQVY^HTEM\LMKMA\SLRC\CM\IFNWV\DEEQGPKSY^IRCD\PAIG^YYCGV^*KPTASGS^TKLRS\TGF^LEKKKCKKKFD\WTF^*TRQWET\A\ITLPC\LTVP\IQLDFKTFQ\IEIV^GVVTVENPKF\RI\LT\EA\ID\AQLVAPSKRRD
18762	49130	A	18871	1	471	
18763	49131	A	18872	1	1524	
18764	49132	A	18873	2	719	RPQRAGPVRRAGVMALLDLAL EGM\A\VEFGFVLFVLMW\HM\ AIIYTRLHLNKKATDKQ\PSKL PGVSL\KPLKG\VPDN\LN\LET\ FFELD\Y^PKPLF\FSV^APM\KRIEKT QM**P^CSTY^YEVLLC\QD\HD\ DPAIDVCK\LLGK\Y\PN\VDARLF\ IGGKKVG\INPK\INN\LM\PG\Y\EV\ A\KYDLI\WICD\SG\IR\GT\ME\MP\MSL\ EQSYD\PN\VRD\PI\YR\NN\GD\AD\G\ QH\LV\LD\HF\YQQGSGPK\CS\LN\A
18765	49133	A	18874	200	370	
18766	49134	B	18875	323	448	
18767	49135	A	18876	2	421	FVGP\GP\GD\PPP\SE\TH\KL\VV\GG\ GVGK\G\SA\LT\Q\FI\Q\I\LD\TA\G\Q\E\ EFG\AM\RE\Q\Y\MR\AG\HG\H\FL\VF\A\ IN\DR\Q\SF\NE\VG\KL\FT\Q\I\LR\VK\D\ RDD\FF\VV\LV\GN\KA\LD\ES\QR\Q\V\ PR\SE\AS\AF\G\A\SH\HV\A\Y\FE\AS\AK\ LRL\N\VD\EA\FE
18768	49136	A	18877	2	236	
18769	49137	A	18878	1	763	MTPHS\ALR\A\RGK\GGG\TGG\GSE\ GSSGG\DM\SSGA\AS\GT\GR\GR\PR\ GGG\PG\PG\DP\PP\SE\TH\KL\VV\GG\ GVGK\G\SA\LT\Q\FI\Q\I\LD\TA\G\Q\E\ PT\I\ED\Y\T\K\I\CS\VD\G\I\PA\RL\DI\LD\ PAG\Q\EE\FG\AM\RE\Q\Y\MR\AG\H\T\ GFL\VF\A\N\DR\Q\EF\ST\RW\KL\H\ A\DF\CG\FK\DR\DI\DF\VV\LG\N\ K\A\DI\LS\QR\Q\VP\RE\SE\AS\AF\G\A\ HH\VA\Y\FE\PS\AK\MR\FN\VD\EG\* R\SW\CG\VV\RE\IP\RN\K\EL\PP\SP\PK\ CPP\GR\GG\G\CP\CV\LL\

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met/hod	SEQ ID NO: in USNN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, !=possible nucleotide insertion)
18770	49138	A	18879	2	403	RFLARRTNSTFNQVVLRKRLFMS RTNRPPLSLSRMIRKMKLPGRE NKTAVVVGTTDDVVRQEVPK LKVCALRVTSRARSRLRAGGK ILTF/DEVYRHFKGAPGTPHSHT KPYVRSKGRKFERARGRRASR GYKN
18771	49139	A	18880	1	1006	PKLR*PEPSRNQVLLTRFQIAVHF/LLSRLLQFFFPRPARSRAFLSRK PKPGPGKPKPMALIVEFIGEI.PTG VHARPPSHVETLCNTNFSQIEW HNLRTDRKGNAKSALALIGDTL AAGDNCQLLISGADEQEAHQRL SQWLRDEFPHCDAPLAEVKSD ELEPLPVSLTNLNPQIIARTVY SGRAGGIOTPISSLDLNALGNLP AAKGVDAEQSALENLTLVLIK NIEFRLLDSDGATSAILEAHLRSL AGDTSLREHLLPVGQCANAASS TNHPFTVKKRQQCFVFRQRLLA NGRNDSGWQITHAFWFRFHQH SRIMKYLYGFTARLKEHQPKLR
18772	49140	A	18881	1	716	VCCEFCAERRRHGEWITRHN KIDRKGSGARDPKPEGFLL*RC CVKLYRFSGPEEPNSNIQPRLLW LKRLFMSURTNRPPSVPSRDES GKMKA SLARGKQDPRPVVGG PLT*LMLRVSGRVPKTERYVAL RRGPSGPQAAFLQQGGKIPS LFDQA WPLGLPLKGLLALVPGS SGSLGKGAREGGTRQFSAKAP KETPKPHQNPyVR:SKGRKFE RARGPTGPARGYKLLTGLGSYSL
18773	49141	A	18882	3	168	
18774	49142	A	18883	23	2669	
18775	49143	A	18884	279	396	
18776	49144	C	18885	960	1250	
18777	49145	A	18886	52	925	EVLEPRLGVFSNGCFQGLSSVM ALGLKCFCRMVHPTFRNLYASI RPVSEVTLKTVHERQHGRQY MAYSAVPVRIHATKKAKAG KGQSOTRVNINAALVEDIINLEE VNEEMKSVIEALQG*FQ*GLS1* GPHQDPIDKIAVVTARREALL*T RFSQISMKSPQLNFG*IWASFPE CTAAGAIARESGMNLNPVE/EG TLIRVPHSPK*PESTEKCVKL GQTEHQQGPKTLLREGFTQLN EQAGRNPKD/NSLQEDTIRLTK QISQMADDTVAELYRHLAVKT KELLG

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18778	49146	A	18887	2	389	DSGSHCHAPPTTARRAAPPFGSKSNMATHLKDQIYNNLKEEHTPQNKITAVRVRGADGMACTILM/KDYNVTANSKLVITGGARQQQGESRLNLVQRNVNIFKQFIIQVAKYSPNCKLLIRSNPVDI
18779	49147	B	18888	217	423	
18780	49148	A	18889	27	1217	ARRPTRPPDLIA TRPRRPARCI SRFFGSKSNWQPLKDQIYNNLKEEQTPIQNKITVVGVGAVG MACAISILMKDLADEVALVVDVIEDKLKGEMMDLOHGPFSRNTKVLSGGKRL*^M^LANSKAGSFITGWGHRQEGKKAVALVILVQAVNVNIFKFIIPNVVKYSPNCKLLIVSNPVDILTYVAWKU!SGFPKNRVIG!SGCNL\DSA\RFRIYLM\!ERLGSSPH*ACHGWPWGEHGRFPVLPVMGVCLNVAGVSLEDFWHPDFRTKD\!EQWKEVHK\!QVVE\!AYEVINK\!GTSLG\!IGLSCKP\!DIAES\!MEES\!FRV\!HPS\!SHHG\!LKG\!LYGNKRMNVSLSPCILGQNGIS\!LVKG\!LTS\!EGRGPVGSKSADNNSWG\!STKK
18781	49149	A	18890	1	264	
18782	49150	A	18891	3	736	
18783	49151	A	18892	81	1065	GKGPVAAFIDQSNIFLTDPKIFLGQWREEPKMLLLLGETEPKLLERDCRSPVDPWAAASPD\!ALA CLCHCQDLSGGAFPNRGVVLGGVLFPTVEMVIKVVFATSSG\!IAIRKKQQEVVG\!FLEANKIDFKELD\!AGDEDNR\!WMRENWS\!REKP\!QINGIPLPSQ\!FNEE\!QYCG\!FD\!SFFSAKKENI\!YSFLGW\!WALPD\!S\!KGSEKAEEG\!GETEA\!QKEGSED\!VGNLPEA\!QEKNEEEG\!TATEET\!EEIAME\!GAE\!EEE\!ETAE\!GEE\!E\!EPGEDED\!FLGLF\!MLHFFHFSQ\!KMEAMKQHSNV\!LSTNQ\!TETEY\!FGLPAHPRV\!TEDIMLPDLIR
18784	49152	A	18893	19	445	

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18785	49153	A	18894	1	622	QAAWILKARALTEMVYIDEIDV DQEGLAEMMLDENIAAQVPRP GTSKLKPGTNQTGGPSQA VRP TSHESEKPTITGFLRPSTQSGRPGT MEQAIRTPRTAYTARPITSSSGR FVRLGTASMLTSPDGPFIN*SRL NLTKYSQPKMAKALPEYIFHH ENDVKTALLEAALSTEHSQYK DWWWKVQIEKRYRLGYRE AEKQLSAMKQ
18786	49154	A	18895	1	1651	MKAECICKSRTVKDWHNHQKLG EGNKTDSPPQSEGNTANTLIL DFWPLEMIAACCWETFPQRLLTAE LFMNPTHRWHGYKNQSVGAL RAPLGGQGSPRKGGLPGRVGRQL FTPBPPLSWSAGPSLAAPAAMS SEMEPLLAWSYFRRRKFQLCA DLCTQMLEKSPYDQEEDPPELPV HQAAWILKARALTEMVYIDEIDV DQEGLAEMMLDENIA/PSSTP ITQAGRPTITGFLRPSTQSGRPGT MEQAIRTPRTAYTARPITSSSGR FVRLGRLGMYREAKQFKSAL KQQEMVDTFLYLAKVYVSLDQ PVTALNLFKQGLDKFPGEVTLL CGIARIYEEMNNMNSAAEYYKE VLKQDNTVHEAIAICIGSSNHFYS DQPEIALRFYRPLLQMGYINGQ LFNNLGLGCCFYAQQYDMTLTS FERALSLAENEAAAADVWYNL GHVAVGIGDTNLAHQCLRLAV VNSNNHAEAYNNLAVLGDAEG /RHVEQARALLQTASSISTPV* TAFLILQQSLIRFGDLQRSVYAA QKSEAAFPDHVDTQHLLKQLRQ HFAML
18787	49155	A	18896	2	295	
18788	49156	A	18897	1	4470	MLGLGLLRLRQGSHAVTRCRP LPVRRREGRRDGPWRSSVVCRY CRCRSQGTGASVTTVSLPSSSSP GLDPRGPRQASVKKPAEANPV LRPLVRLHGLPYRDSEEGKREGL SRLRAVCRAGPGRGSFSFSPRD ARASPRLHFLVAAVTTGAASRR QRGARVRQPSPSSRRAKRLRE CERRSLHAPPAMDASYDGTEV TVVMEEIEEAYCYTSPGPPKKK KKYKIHGEKTKPRSAVLLYY YDIYLVKQQELPHLPQS

SEQ ID NO: NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion,  =possible nucleotide insertion)
18789	49157	A	18898	89	810	QRRSGCVRMTEWETAA PAG GQRTPDIKALWGSGAPDDVAR SMNISLQ DYIAS*RRKLCPSYLP  HSCQQGYAAKNI SRKAQ CPI  VERVLNSPMMMHRPQQPARK LMTVRIVQAA HAF ITPCSQAE NPL QVL GEPPS NSG PREDSH HLGAAGTVRQAVDV SPLRVE EPGPFWV ACTRRLVKGLAFPG TFKTI *VAWAD EL NACQGA PSNSYCL*EEGRVAFLHEVAKS NR
18790	49158	A	18899	1	365	DTHFK/DSHHTSTAHHLL SLSQ GPSPPNLPLGVPI S GMLGLPRG EGRANPIPTVLRDQEGLGYRS APQPRVTHFP AWD TRAVAGRE RPPRVATLSWREERRREEKDRA WERDLRTYMNLEF
18791	49159	A	18900	203	427	
18792	49160	A	18901	95	482	ALQSPKLWGYFSGRKVFLNYFF SSQQVSEAVVATGSPRAWLTC LILPLPGIIFSVLPKAMSPRLIITF TPATDPSDLWKGQQQPKEK PESTLDGLAALKFYEALIGDES SAPDSQRSQTEPARERKR
18793	49161	A	18902	348	1660	GVTHLFLFGKRKLRNIGARIK GPGWIFFSYCRSLRLWLLTGP LSLALPCLILPLPGIIFLKFQSQKA  VPGPLLITFTPATDPSDLWKG QQQPQ PEKPESTL DGAARAF YEALINGDESSA PDQSRSQT*T WPEERKRKKRGLL KAPAAEAL AEGVASGRPVQGRSL EADPPMT YRILTSQAQEGD L P*LM RLLEPH EAGGAGGNINARD AFWWTPL MCAARAGQGAAVSYLLGPGIA AWVGVCELSGRDAAQ LAEEA GPEVARVMRRESHGETRSPENR SPTPSLQYCENCDCTHFQD SNHR  TSTVHLLSLSQGPQQPLPLGV PISTPRF*ILLGGVGSPGMGLG PRGEGRANPHPQLILK*GPRKG LGIVKISTPSPEVTHFP SGIPRA VAGRERPPRVA T LNWKE ERR RREEKDRAWERDLRTYMNLEF
18794	49162	C	18903	135	299	

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18795	49163	A	18904	3	2074	ERSRPVALRAAVPRMNPSTPSYPTASLYVGDLHPDVTEAMLYEKFSAPAGPILSIRJCRDLITSGSSNAYAVNFQHTKDAEHALDTMNFDVIKGKPVIRMWQRDPSLRLKSGVGNIFVKNILDKSINNKALYDTSVAFGNTLSCKVCDENGSKYGFVHFETHEA\AERAIEKMGMLVLNDRKVFVGRFKSRKEREALGARA\KEFT\N\Y\K\N\G\EDMD\DGDRKL\DLFGKF\GPALKCE\LM\T\DESGKSKG\FGFVSI\ERHE\DAQ\K\A\DE\NG\K\EL\NG\K\Q\N\VGRAQKKV\ER\Q\TEL\K\RK\F\EQ\MKQ\DR\IT\RY\Q\G\VN\LN\Y\K\N\LD\G\W\DE\RL\RK\EF\SP\G\T\I\Q\LP\Q\K\VM\DG\GL\VA\K\G\LG\F\VC\FS\SS\EV\A\K\A\T\EM\N\F\RI\AT\EP\I\Y\VAL\A\Q\RK\EE\Q\AH\LT\N\Q\Y\RG\MA\SV\TE\A\VP\N\VI\Q\LP\Q\G\APP\FR\FT\M\G\RF\SH\RF\RN\RA\Y\Y\PS\Q\I\A\Q\T\K\T\K\FL\R\W\T\G\O\GA\RT\H\PF\Q\N\MP\G\CP\A\Q\L\A\P\R\PP\I\*G\T\M\R\PA\SS\Q\VP\R\VM\PT\Q\R\I\V\A\N\T\N\D\K\W\VP\RS\CS\Q\AA\AA\Y\Y\LR\PA\PP\Q\Y\K\Y\A\G\VR\NS\Q\Q\H\LN\A\Q\Q\Q\V\T\M\Q\Q\CS\M\PR\Q\G\T\L\W\T\CL\P\M\VG\H\H\LP\PS\RS\SK\Q\ML\G\W\N\G\LP\PS\K\PM\H\PS\Y\SL\V\K\SL\G\ML\LE\ID\N\SE\LL\H\ML\VE\SP\ES\LP\F\RV\DE\AV\AG\TT\PP\Q\A\K\RL\Q\K\A\G\Q\VP\T\G\VP
18796	49164	A	18905	1	988	MAEDGEEA\EF\H\FA\ALY\IS\G\Q\W\PR\LR\AD\T\DL\Q\RL\G\SS\A\MA\PR\SK\FF\VG\G\N\W\K\M\N\G\K\I\K\R\RL\G\EL\I\GT\LN\A\K\VP\AD\T\EV\VC\AP\PT\Y\ID\FA\R\Q\K\I\LD\PK\IA\VA\A\Q\N\CY\K\I\TN\GA\FT\G\E\I\SP\G\MI\K\DC\G\PP\W\VV\LG\H\SE\RR\H\VG\ES\DE\I\A\G\Q\K\VA\HAL\A\EG\I\G\VI\RL\H\LG\RS\*D\ER\G\SL\G\I\TE\K\VV\I\F\I\Q\TK\V\I\RR\I\T\K\DW\K\Q\VV\VL\G\LM\SP\W\GL\W\LL\A\RL\AT\Q\Q\A\Q\EV\H\RS\SS\RG\W\LI\K\SN\VS\DA\VA\SE\PP\T\I\Y\G\G\SS\I\T\G\AT\L\Q\RS\LA\K\P\SP\DV\DG\LP\I\W\GG\A\SL\Q\AR\NS\W\DI\Q\CH\N\NE\PP\SS\H\SL\SL\PL\RC\Q\A\Q\G\L\K\QT\Q\K\PK

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met/Asp	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, ^=possible nucleotide insertion)
18797	49165	A	18906	46	468	TGPTHASAAILVPRPSLHKMPGE ATETVPATEQELPQPQAEKGSG TEDDS/GKSPASDTYIVFGEAKIE DLSQQAQLAAAEEKFKVQGEAV SNIQENTQTPTVQESEEEEVDE TGVEVKDIELVMSQANVSRAK AVRALKNNs
18798	49166	A	18907	1	360	
18799	49167	A	18908	52	513	QLGPHGHRQGPAGPAVPHPRG LVPLPPALLPSGPRRGTQAPR HSGPAL*GHPASDTYIVFGEAKIE EDLSQQAQLAAAEEKFKVQGEAV VSNIQDINTQTPTVQESEEEEV DETGVEVKDIELVMSQANVSRAK AVRALKNNsNDIVNAMEL
18800	49168	A	18909	1	422	RSLCQTGLRQ/VTG/VTKVITGN LENLFV/TKPDVYKSPASDTYI VFGEAKIEDLSQQAQLAAAEEKF KVQGEAVSNIQENTQTPTVQESEEEEV DETGVEVKDIELVMSQANVSRAK AVRALKNNsNDIVNAMEL
18801	49169	B	18910	427	529	
18802	49170	A	18911	122	252	
18803	49171	A	18912	44	189	SKLDYKSSKRHRKPVSFNFTSF QIWD*FLFFF*LKCQLQPRVFSQ PN
18804	49172	A	18913	2	609	PFLPEAHGNQKCQNCNSTSGI CRVSVKVCPGPWVHAKLCAPT LMSRDVTLPDAPVKKPCGEGG AKKKKQVLKFTLUDCTHPVED GUMDAAQF*ASFCKERIKVING KAGNLGGGVVDPSKGARGKFT VTSEVPFSKRVF*KYLTTPKKY LKKNNLRL*PGLPRSLPNQPKEK LPNFRYFQINQGRRKEGGRGF KFPLSGKILL
18805	49173	A	18914	107	524	AGTHLPPFLPVAVRQPMALRY PIAVGLKQGPTKVTPQEP*ASPR HHVRRGRLLTKHTKFRVDRMIRE VCGFSPYEVRRAMELLKVSKD KIRALKFIKKIRVGTHIRAKRKR EEELEQQYWPQIEEKLACQERLE PLPLPSPLK
18806	49174	A	18915	39	465	

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18807	49175	A	18916	439	1586	TWGPPARRLPSGSHVPSA/ASSR LPSHPREEPQLQPAPVITATM SSEAETQOPPAAPP/GAPALSA DTKPGTTGSGAGSGGGPGGLTSA APAGG/DKKVIATKVLGT/VKW FNVRNRYGFINRNDTKEFDVF HQTAIKKNNPQKYLRSVGDGE TVEFDV/VEGEKGAE/AAANVTG PGGVPVQGISKYAADRNHYRR YPRRRGPPRHYPQ\NYQNS\ESG EKNRGIGRVLPEGQAQQRGPY\ RRRRFPPYVMRRPYGRRPQYS NPPVQGEVMEGADNQGAIGEQ GRPVQRQNMYRCYRPRFRRGP\ PRQKTA*ERAAMEEDK\ENQGV WDPRFGSPPP\RRYRNF\NRY\ RRRPQKTPKP\QDGQKRPKAAG SHPA*EFVPLP\PEAE\QGAE
18808	49176	A	18917	1	651	MTAFNSGKVDIVAINDPFIDL YMFYMLYDSTHGKFHGTVK AENGTLVINGNPIT\IFQDQDPS KIKWAP/LAKVIHDNFQGIIEGFM TTVHTITATQTINGPSG\INCHVM AAGLSRTSSLALLA/LAKPVGK VIEPLNGKLGTGMAFHPTANVS VADLTCRLEKPA/KYDDIK\INT HSSTFDAGA\IVLKDHSVKLIS WYDNEFGYSNRV\HLMHNA
18809	49177	A	18918	2	5264	

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18810	49178	A	18919	3	1466	PRSATPRAASWLEDPREVRSVCL SAPPVRQSAAIFFCVVASRATSLR TPMGKVKGVGNGFGRIGILVTL RAAFNSGKVDIVAINDPFIIDLNR YMVYMFQYDSTHGKFHGTVK AENGKLVINGNPITFQEQRDPSK IKWGDAGAEYVVEISTGVFNQ PWRKAGAHLQGGIAKRVNISAP SG*MPMPMFVMGVNHEEV*QTA FKIISNAASCTNQLA*QPLAKG*F HDNFG*SWEGLMTTVWPWPSLG NPRKTVTDGPGSRGNCGPWMGR GGFSRNIFLCLYWALPRAVGKG HP*A*TGKLTGMAFPVSPNTAN VVSGWTLTCRFRKNLPLKYDDI KEGW*KQAFGGAPSKGJIPGLQL SHQVVSSDFNSDTVHSFHPFDA GAIGIAALNDHFVKLWISWYDNE FGYSNRVVVDLIGPHGLQGSKTP WTTEPQARSKKKGKERSPLLGSP CHTQPTTTLNLPSQLPCRPLEE GRGLWEPLHLMVYPSNKKVSLCS TKKKKKKKP
18811	49179	A	18920	3	364	STVINIHSSETSPVDPHV/VLVPVQ HPLLERCCLGFIAYASVSKRSRD RKMVGDVTVGAQ/ALCLHRQVP EHLGPDSGHPHDHWIHPVTGIR LCDSPLYYVTDNTGKTGTLVA AHSLOPLHSTVQCW
18812	49180	A	18921	41	696	PDRRWSSLGHHESHCPNHSSLL STVASSPPNYEDAQGR*SR/EVA VLGAPHNP/APPTSTVIIHRSR PPWPDHVVWSRVQHPLQ*TPA CLGFIAFAYSVSKSRGGQRWL DV\TGAQGLMPPPAKVPTIWG PDFWGIILNDHFVIRHPQWLIFP G\HIGIDQGRHHWRPGALPI/VT IPRILPTTSIPRPAAPSPKSCISPYI LTRFSTMAFNKSARVSGKKKK

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18813	49181	A	18922	127	1016	SNLILRLNLFCPHLALASSAFDKC QEEETVEKTELLAERRGLTEH PGNPITAGHHEPHCANLLSCQQ RPRLPNYYEMLKKEEVAMLGA PQKPCLECPVPIHYPQARPPWP DHVRLGPCFNNPLQ*TTCCPGL SLGISAYFRGSFRGTGKVMVGD VEPGPQGLMPTAQMVA*TSGA PDFLGSLSHEPILAHQSSPPKCW VVPGPADQEVASLRVGA/LPVT C1PRTLSSIPSPPLPEARELLPFD LYSTYSTFHSSPCPHSRVLHQPF ILTRFSTMAFNKVYMFVLVKKK KKKKKKV
18814	49182	A	18923	115	652	VSESTDLVSIGRLVTRA/AFNSG KVDIVAINDPFIDLNLYMVMF QYDSTHGKFHGTVAEENGKL INGNPITIFQ^/RDPSPKIKWGD GAEVYVVES/TLGVFTTMEKA GGSFRCRGGAKRVIHLLPPLA^C PPCFVMGVN^HEKDDN/TLKII N^ASCTTNCLAPLASTGAKG GQGHPEA
18815	49183	A	18924	91	399	
18816	49184	A	18925	26	304	
18817	49185	A	18926	18	203	
18818	49186	A	18927	23	355	
18819	49187	A	18928	1	211	RLLRVRGPPSPRPPGTAPGRQA RHTAPVPARASPSTPPRKLKER APALASPERGSHSAAEG^RAPQ VPPK
18820	49188	A	18929	2	800	
18821	49189	A	18930	1098	1560	VSCPFTVIIFCYNFCRGFFSTTA VMARAKSMFLMLKGKAGPDF GIRFTASSGWFT^FEDRYALHN VNMAESVGADVKAAE^DFGS LIMEEYLPTQFFNMEEPSLFWK QMPERTFVICPKGFPDHCNKE RPWHFCKRKS LTDTRVATPCG
18822	49190	A	18931	33	211	
18823	49191	A	18932	110	624	CILSKMLRSPQELARLPGQRQ LTRW^QRWPLWTIALVLVLR VKSGP^S^RVPSPSP/PVEPVWT LNMAGA/GHGNPAFPPGPPPH VPQPGYPGCQPLGPYPPPYPPPA PGIPPVNPLAPGMVGP/VIVDK KMQKKMKAHKKMHKHQKH HKYHKHDKHSSSSSSSSSDSD

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18824	49192	A	18933	2	664	CEPLRISGRPTRPGERSKP <sup>RRRL</sup> ER*WGWRTHLN <sup>M</sup> WNPNAGQP GPN <sup>P</sup> PPN <sup>I</sup> GCP <sup>G</sup> GSN <sup>P</sup> A <sup>H</sup> PP <sup>I</sup> NPPFP <sup>P</sup> PGCP <sup>PPP</sup> GA <sup>P</sup> HGNPA <sup>F</sup> TGGP <sup>P</sup> HPV <sup>P</sup> QP <sup>P</sup> G <sup>P</sup> G <sup>I</sup> Q <sup>P</sup> LP <sup>G</sup> YPPP <sup>P</sup> PP <sup>P</sup> APG <sup>P</sup> U <sup>P</sup> PN <sup>L</sup> APG <sup>M</sup> VGTKQL <sup>I</sup> S <sup>R</sup> QEDCR <sup>R</sup> KL <sup>L</sup> KK <sup>A</sup> * KRCHKA/HQKHHK/YHKHGKH FLLFPPPSFQAVISGLEYRALDP SLKSHQFCSP <sup>I</sup> KLQMP <sup>C</sup> CTGGM
18825	49193	A	18934	3	409	QTQVVIDAG/ALA <sup>V</sup> PSL <sup>T</sup> NP <sup>K</sup> TNIQKEATWTMSNITASR/QDQI QQV <sup>V</sup> NHGLV <sup>P</sup> FLVSDLS/KDFE TQKEAVWA/GGTVEQIVYL <sup>V</sup> H CGII <sup>E</sup> PLMNLLPAKDT <sup>K</sup> IILV <sup>I</sup> D AISNIFQAAEKLGETEKLSIMIEE CGGV
18826	49194	A	18935	133	400	VLGPHGLGDHLGQF <sup>H</sup> SCSQRA EPIIAGEDIAGL <sup>D</sup> EPDCL <sup>T</sup> KDF LRI* <sup>L</sup> Q <sup>L</sup> S <sup>T</sup> OLH <sup>A</sup> QEE <sup>E</sup> EDQNV VPETTSEGYTFQVQDGAPGTFN
18827	49195	A	18936	218	863	
18828	49196	A	18937	106	1879	TQSALQPLIPPAS <sup>P</sup> SPW <sup>P</sup> KAQARF GAFSLCLITM <sup>S</sup> TNENANTPAC <sup>P</sup> VVH <sup>R</sup> FKNKGKD <sup>S</sup> TEM <sup>R</sup> RR <sup>I</sup> E VNVEL <sup>R</sup> KAKKDDQMLKRERL *AHFLDDAT <sup>S</sup> PLQEN <sup>R</sup> NNQG/T LLNWSVDDIVK <sup>G</sup> INSS <sup>N</sup> VENQ LQATOQAR/KL <sup>L</sup> SREKQ <sup>P</sup> PD <sup>I</sup> NII RAGLIPKFV <sup>S</sup> FLGRT <sup>T</sup> DC <sup>C</sup> SP <sup>I</sup> QF ESAWALTNIASG/TSGQTKAVV DGGAI <sup>P</sup> AFISG <sup>G</sup> WASS <sup>H</sup> AHISEQ AVWALGNIAGDGSVFRDL <sup>V</sup> K YGA <sup>V</sup> D <sup>P</sup> I <sup>L</sup> L <sup>A</sup> ASS**CQSLAC GYLR <sup>N</sup> LT <sup>T</sup> W <sup>T</sup> LSNLCRNKNPA PP <sup>V</sup> DAVEQ <sup>I</sup> LPT <sup>T</sup> L <sup>V</sup> RLLHHDDP GSVRQDT <sup>T</sup> CWGY <sup>F</sup> PT <sup>L</sup> LDGSK <sup>F</sup> WNGI <sup>G</sup> HGWV/VKQGV <sup>V</sup> VPQLVK LLGASE <sup>L</sup> PI <sup>V</sup> TPA <sup>I</sup> L <sup>K</sup> SP <sup>*G</sup> NNW H <sup>I</sup> LGTD <sup>E</sup> Q <sup>T</sup> QV <sup>V</sup> D/IDAG <sup>A</sup> LA <sup>V</sup> F <sup>P</sup> SLLTNP <sup>K</sup> T <sup>N</sup> Q <sup>K</sup> EATWTMSN <sup>I</sup> TAGRQDQ <sup>I</sup> QQV <sup>V</sup> *NHGLVP <sup>F</sup> PLSVFLSKAD <sup>F</sup> KT <sup>K</sup> QEA <sup>V</sup> WAV TNYTS <sup>G</sup> GTS*TEL <sup>V</sup> VL <sup>V</sup> H <sup>C</sup> GII EPLMNL <sup>F</sup> YCKRL <sup>P</sup> R <sup>I</sup> LL <sup>I</sup> L <sup>D</sup> AN FKISFOPAENLV <sup>V</sup> DE <sup>L</sup> KEPSINLE <sup>\</sup> ECGGLRP <sup>K</sup> L <sup>K</sup> ALPKP <sup>M</sup> KM <sup>M</sup> ESV YKASVKA*FEKYFP <sup>C</sup> RGK <sup>E</sup> GR <sup>I</sup> KTVV <sup>P</sup> ETT <sup>T</sup> SEGYTFPSSRMGPP

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18829	49197	A	18938	2	251	KVTNVKDGTTH/QTSLELFMYL NEVAGKKGHGKVGRIDIVENRFIGM KSR/GMNQVQGDYEPPTATGFIN INSLRLKEYHRFQSKEVTVK
18830	49198	A	18939	I	888	
18831	49199	A	18940	1	1155	MSSKGSMVLAGSGGLNTSICLV WLKEQGYDVTLANTGKE DFEEARKKALKLGAKKVFIEDV SREFVEEFIWAAIQSSALYEDH YLLGTSLTRPCIAHKKVETVQR VGAKYEGPWRAPWRMPEFYN WFKGRSDLMEYAKQHGPILVT PKNLWSIDKNLMHISYKAGILE NPKNQVPPGLYTKIQQDPAKPN TPDILKIQFKKGVPVRVTSVKD GTTQTSLELFMYLNEVAGKH GVG/YIAIENIFTRQRPISPECF VRPCIAKSQEPAEKGKVQVPVLK QQVYILGWESPLSLYNEELMSV NVQGDYEPIDDTGFININSRLK EYHCLQLSLLEFAGCRLQTLFAW VSPAGAAEQQRLLPVPPSSGNFIP EGHLPDASWSSPV
18832	49200	A	18941	I	993	MSSKGSVVLAGSGGLDTSCILV WLKEQGYDVIAYLQAVKG QLLPVSLVKRKTTTGPQAQYANR LSPRVGRFINAAGTTGFTGKR AGNDQVRFELSCYSLAPQIKEM GSLKVRNE/LQEVTVPMPAST QLPADTQCKLAE/LSAPVKK*T LGLSKT*QTQVMSSQSADSMR AWYRN*LFTNPTVRRGLGNSPVT GSSLPRLPG/RGIYETPAGTILYH AHL DIEAFTMDREVRIKIKQGLG LKFAELVYTGAECKLIVASVPE PWRRGGVVEGGRDIKEVQEHH GSDSAESSTHPPASRPGEGLCA CIFCGKWRHLNTPLSCERYPRH SRDHRPH
18833	49201	B	18942	324	1035	

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18834	49202	A	18943	29	1516	KQIPDAGNSRLQSQTLLSSKGS VVLAY\SGGLDTSCILVWLKEQ GYDVIAYLANIGQKEDFEARK KALKLGAKKVFIEDVSRFVEE FIWPAIQVQAHLY\EDRYLPGH LSLPGC\IARKQVGNSPSGRGA KYVVPPTGATGKG\NEQV\RFEL SICYSL\APQI\KVIAP\W\RMPEFY NRIFKGRNDL\MEY\GKATLGFPI PVTPKNPWSMDENL\MH\I\SYE AGILENPKNQAPPGLY\TKV\TQGP SQKPTPLDILGDS\SKKGVPVE GGPTFKDG\TT\HQTFL\ELF\MY LNEVAGIKHGRR\AVF\DIV\ENRF IGN*SPRGILRR\I\PL\AGHHSFYH AHLDI\RG\LS\SPWDRGSCGKIKQG PGAWKFAEL\VTGFP\AQAPE\I CEFCPTGIAK\VP\RKPSGKGKV QVVR\SF\KGP\QVY\I\LS\REI\PHC LLLTMREL\VKHGTC\KG\DY\WRP ID\H\RGSSK\H\Q\IP\K\AEG\N\YH L\PR\AK\VT\Q\ID\P\V\Y\NE\EL\G\PPQ FSGSPQ\VTG\ANCC\DNL
18835	49203	A	18944	1	560	GRARTPAN\MALRV\VR\SV\RA LL CSLRA\I\W\APAVP\CLP\PR\WP\QLG AGAIW\T\LL\T\GP\V\LL\W\VC\K\FT\TE K\H\W\IT\T\EN\G\I\G\T\V\G\I\N\F\A\N\E ALGDVVY\CSL\SE\VG\TKI*TKPS WSL\VL\LE\VS\K\A\A\SE\LF\SP\LS\G EV\PD\N\EA\LA\I\N\G\O\I\V\T\K\SR\Y ED\G\W\I\K\MT\LS\N\P\RT*M\H\L M\SE\EA\YE\K\Y\K\I\K\SE\EE
18836	49204	A	18945	3	108	
18837	49205	A	18946	1	845	MAIPGIPY\ERR\LLIMAD\PR\DKA LQD\Y\RK\KL\LE\H\K\I\D\G\RL\K\EL\R E\QL\K\EL\T\K\Q\Y\K\SE\N\DL\K\AL\Q\S VGQIV\G\EV\LK\Q\LT\EE\K\I\VK\AT NG\I\PR\Y\VV\G\CR\Q\VI\EL\PL\TN\PE LF\Q\RV\G\I\PP\K\G\LL\Y\G\PP\G\T\G\K T\LL\A\RA\VA\SQL\DC\N\FL\K\VV\SS\SS IV\DK\Y\I\G\ES\A\RL\I\RE\MF\N\Y\A\RD HQ\PC\I\I\F\M\DE\I\DA\I\I\I\DL\PN\E\Q\A R\LD\I\K\I\H\G\P\I\T\K\H\G\I\D\Y\EA\I V\K\L\SD\G\F\N\G\A\DL\RN\VC\T\EA\GM F\A\I\RA\H\DF\VV\Q\ED\G\K\MA\VR\K V\AD\SK\K\LE\SK\LD\Y\K\PV

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met/Asp	SEQ ID NO: in USNN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, !=possible nucleotide insertion)
18838	49206	A	18947	3	1181	LLIMADPRDKALQDYRKLLHEKEDGRIKELREQLKELTKQYEKSEN DLKALQSV/GQ!VGEVLKQLTVEEKFIVKATNQPRYVVG CRRQL!QKVSLPGVTRVAL\DMTTLT\MEDILPRI\EV DPLVYNMSHEDPG\DVSYSEIGGLS\EQIRGI*GEVIGLPLYKPKQSYFQRVG IIPIPK\GLLYGPPTGKNT\LLARAVASQLD CNFLKVVSSIVDKYIGESARLIREMFNYARDHQPCIFM\DEIDAI GG\RRFSEGTSADR EIQRTEIMELLNQMDGFDTLHRVKMIMATNRPDTLGPVALLRPG RLDRIKIHIDL PNEQARL DIL\KIHAGPITK\HGEIDFESNC*FMRMG FNGADL\RNVCT*SQACSPIRAD P*FC*YREDFUMKA\VRKVA
18839	49207	A	18948	1	220	VNMRDRFGQIM\ENLRRQCELAGVETCKSLES\RIESLEFLDEM *LLEQLM/RHYCLCWATKGGN ELGLKEITY
18840	49208	A	18949	1	645	
18841	49209	A	18950	10	1226	AAPAEPGRALPSSVAFLSLWLAP SPAARRPRFHVPGGAAQLP GTVH ARWPARQR\ESS\TSCCSTSSCD ADDEGV RGT CEDASLCKRFAV SIG\Y\W\HD PYI\QDL\VR LSKQR\ KAPEINRGYFARVHVGCSVQLK\ AFLRKTECH\CSNCNSL\LGQGM GSPPFWRLKDEDLSSQVNIFEV DFPMIVTRKLHSIKWLAFPLSS PILELHSEDTLQMASDCICDGH ILDSKRYA VIGADRLDLEEE KLKKCNMNTQL\PTP*IAECVL VYMTPE\QSANLLKWA\INSFE RAMFIYYQQVNMGDLFGQIMI ENLRGRPV\CDLAGVETCKSLE SQKERLLS\NGWENK HRPVRT* LEFVPPGLPSKLK*SRIESLE\LD ENWELLEQ\QI\H YCLCWATQRK\*SLGLKEITY
18842	49210	A	18951	3	502	TEANTLN*RGLQNME/ARLAE/ RKF M/NPFNMPNLYQKLESD/P RTRTLLSDPTYRELIEQLR NKP DLG TKLQDPRIMTTLSVLLGV D LGSMDEEE\IA T P P P L P S S S M S L S P A P S C C L G C S P I V G F F F I W G S GHVMGRGGGSSSLRSQSLSHVV YSASP SPIKQASW A WL
18843	49211	B	18952	1	1071	

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18844	49212	B	18953	67	1026	
18845	49213	A	18954	2	1910	PVASSMFQKAARAVGNAERTD SIQRCGSPRCAAMEQVNELKEKG IKALSVGNIDDLQ/CYSEA/*R LDPIHNVLYSNRSAAYAKKG DYQKAYEDGCKTVDLK\PDW GKGYSRKAAALEFLYRFREEAK RTYEEGLKHEANNP\QKLEGLQ NMEARLA\K\RKFMNFNMPNL YQKLESDPKTRTLLSDPTYRELI EQLRNKPSDLGTLQDPRIMTT LSDLLGVLDGSMDEEEEIAATPA PPPPAKKETKPEPMEEDL彭K KQALKEKEGLNDAYKKKDFT ALKHYDKAKELDPTNMTYITN QAAVWFEKGDYNKCRELCEK AIEVGRES\REDYRQIAKAY\ARI GNSYFKEEKYKDS\WIFYNKS AEHRTPDVLLKKCQAEKILKEQ ERLAYINPDLALEEKKNKGNECF QKGDYQP\AMKHYTEA\KRNP KDAKL\YSIRAACYTLLFQL ALKDWEEWYQLEPTFIKGYTR KAAALEA\MKDTKAMDVYQ KALLDLDFSCKEAADGYQRCIM AQYNRHDSPEDVKRR\AMADP EVQQFMS\DP\AMRFILKQMQK DPQALSE\HL\RNPLLPREIQKL MDVGSCKFGDDLFIPAFLCPS CGKRSWDRGEQAARSGRESST ERKGEQGERRPSSPY\T
18846	49214	A	18955	2	293	
18847	49215	B	18956	53	182	
18848	49216	A	18957	2	403	
18849	49217	A	18958	3	1646	
18850	49218	A	18959	3	408	
18851	49219	A	18960	1	2458	

SEQ ID NO: NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, =/possible nucleotide insertion)
18852	49220	A	18961	88	1511	LWPLGMASNSSSCPTPGGGHL NGYPVPPYAFFPPMLGGLSPP GALTTLQHOLPVSGYSTPSPATI ETQSSSSEEIVSPPPSPLPPIYK PCFVQDKSSGYHYGVACEG CKGFFRRS1QKNMVTYTCRDK NC1INKVTRNRCQYCR1QKCFE VGMSKESVRNDRNKKKEVPK PECSESYTLPVEGLEIEKVRKA HQNETPPALCQLGKYTTNNNSSE QRVSLID1DLWDKFSELSTKCI KNGEGRQGRPLPGFTTLTIAQDQI TLLKVAACLDILILRICTRYTPE AGTP*PSWDGTLTNRVTQMHNA G\FGPL\TDLVFAF\ANQLLPL\& MDD\ARETGLLSAICLICGDRQ DLEQPDRVDMILQEPLEALKV YVRKRRPSRPHMFPKMLMKIT DLRSISAKGAERVITLKMIEPGS MPPLIQEMLENSEGGLDTLSQGP GGGGRDGGGLAPPG\SCSPSLS PSSNRSSPATHSP

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met/Asp	SEQ ID NO: in USN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, ^=possible nucleotide insertion)
18853	49221	A	18962	143	2159	LTHSSTWLGRSCNHDERRQMGSKVMSYVVAGRGTCAQETPIYTIRYLEDKEQYQGSSLGVDSVLARLFSGASVLFISGPPFSSYLSGVPPGHPMEDSMIDM/DMSPLRPQNYLFGECLK\ADKDYHFKVD\N DENEHQQLSLR\TVNLGGLVAKG*VAHLLKAEAEIEFTEAASPNLKVTTWAT\KMSISVPAQRV\PFPLGGLLKTTPTRWVWKGLKVVWVQGPVHISGTAL**LWEGRQCSPEDEE\EDVNRVLFMFKPKGRGLKHMFGLVCSWKLAIAETQSSSE\IVPSPPSPPPLPRIYKPCFCVQDKSSGYHYGVSA\CEGCKGFRRS\QKNM\Y\TCHRDKNC\IINKVTRNRCQYCR\QKCFEVGMSKESVRNDRNK\KKEV\PKPECS\ESY\TLP\EVGELIEKVRKAHQET\TPALCQLGKYTTNNSS\QRVSL\IDILWDKFSELSTK\CIK\TVEFAKQLP\GFTTLIADQ\ITLKAACLDIL\LRCTRY\TPEQDTMTFSDGLTLNRTQMHNAGFGPL\TDLVFAFANQLPLEMDDAETGLLSAICLICGDRQDLEQPDRV\DM\QEP\LL\EA\LKVVYVRKRRPSRPHMF\PKMLMKITDLRSISAKG\AERV\ITLKM\EPGSM\PLI\QEM\LENSE\G\LDTLSGQPGGGGRDGGGLAPPGSCSPSLS\SPSSRN\SSPATHS\
18854	49222	A	18963	748	1075	ILPTSLFFLFCFV\FFFVCF*DRVLL\SPG\WSA\AVRSWLYCQCNLSLRGFKGFSCLSLSNW\DYR\CTPLRSANFVFL\CRDRVSPC\WPT\TSVNS*PQ\VIHPPWPPK\VLG\ITRV
18855	49223	A	18964	3	674	GRRRLLRDAEGPEETVRLWPA\RAAMDAAEVEFLAEKELV\TII\PNFSLDKIY\LLIG\GDLGP\FNPG\LP\VEVPLW\I\ARLN\KQ\RK\ICRL\LP\PEWMDV\KLEKMRD\H\RK\EE\FT\T\MP\K\PF\TT\W\EL\T\K\LL\LN\H\A\IS\DN\I\PK\GR\TE\FRD\PG\SR\VF\WG\HSY*\AK\FR\VF\G\DS\VF\VR\QQ\EA\H\AK\LD*\LG\PW\MG\D\QQ\PA\VT\FL\Q\AL\N\PH\VT\NS\RT\N\PP\SP\LE\ST\SV\LR\TS

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met/Asp	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
18856	49224	A	18965	261	876	VAQKIDMPEYQGEPEDEISIQKC QEAVRQVQGPVLVEDTCLSFN ALGGLPGPYIKV/WFLEKLKP/E GLHQLLA/GF/EDKSAYALCTF CTQAPGDP\$IQPVVRLVSGGRDL RGRIRWHEPGCQIDFGWDI\$PC/F QPDGYEOTYAE\$MP*GRRNA V\$H\$RFRAPCWE\$AREYFWQV WPSLTSASWKEGP\$RPGDLGK GLAPKPSPHRGRA\$P
18857	49225	A	18966	2	181	TAEKMAVLAPIJALVY\$VPRLS RWLAQPY\$YLLSALLSAFL\$LR KF\$PLCHGLPTQREDGNPCDFD WREVEILMFLSAILMMKNRRSS TK*AHPTRRR
18858	49226	A	18967	5331	5454	ETEA*RINDLL*LLEFFCNI*QN* P*IRPTVIRSSLKYNT
18859	49227	A	18968	5186	5308	ETEA*RINDLL*LLEFFCNI*QN* P*IRPTVIRSS\$KYNT
18860	49228	A	18969	4570	4691	ETEA*RINDLL*LLEFFCNI*QN* P*IRPTVIRSSLKYNT
18861	49229	A	18970	5666	5788	ETEA*RINDLL*LLEFFCNI*QN* P*IRPTVIRSSLKYNT
18862	49230	A	18971	5630	5752	ETEA*RINDLL*LLEFFCNI*QN* P*IRPTVIRSSLKYNT
18863	49231	A	18972	224	456	
18864	49232	A	18973	5543	5665	ETEA*RINDLL*LLEFFCNI*QN* P*IRPTVIRSSLKYNT
18865	49233	A	18974	4602	4725	ETEA*RINDLL*LLEFFCNI*QN* P*IRPTVIRSSLKYNT
18866	49234	A	18975	3	313	
18867	49235	A	18976	5480	5602	ETEA*RINDLL*LLEFFCNI*QN* P*IRPTVIRSSLKYNT
18868	49236	A	18977	269	394	
18869	49237	A	18978	5322	5445	ETEA*RINDLL*LLEFFCNI*QN* P*IRPTVIRSSLKYNT
18870	49238	A	18979	164	434	
18871	49239	A	18980	5364	5487	ETEA*RINDLL*LLEFFCNI*QN* P*IRPTVIRSSLKYNT
18872	49240	B	18981	18	1904	
18873	49241	A	18982	1296	1973	RILPGQQNNSWNFSEDTVISIL NTINEVIAENLEAAKKLRETQGI EKLVLINKSGNRSEKEVRAAAL VLQTIWGYKELRKPLEKEGWK KSDFQVNLLNNASRSQSSHSD STLPLI\$PGPKNO\$RNLI\$GKFR* AIWDQTQNH*IT/DYSTPNERGD HNRTLDRSGDLGMEPLKGTT PLMQDEGQESLEEELDVLVLD DEGGQVSYPSMVCPSVTPKIVL EEGGS

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion,  =possible nucleotide insertion)
18874	49242	A	18983	5844	5967	ETEA RINDLL*LLEFFCNI*QN* P*IRPTVIRSSLKYNT
18875	49243	A	18984	5781	5904	ETEA RINDLL*LLEFFCNI*QN* P*IRPTVIRSSLKYNT
18876	49244	B	18985	1	1477	
18877	49245	A	18986	152	1539	
18878	49246	A	18987	5571	5694	ETEA RINDLL*LLEFFCNI*QN* P*IRPTVIRSSLKYNT
18879	49247	A	18988	4551	4674	ETEA RINDLL*LLEFFCNI*QN* P*IRPTVIRSSLKYNT
18880	49248	A	18989	2	1043	GVRLLRSPIAVVMVGAEGRDL RRRRAVAVTAEKMAVLAPI/S LSVYSPVRLSRWLAQPYLLS A  LSAAFILLVRKLLPLCHGLP TQ\REDGNP\CDFDWRE\VEILM FLSAIVVMKNN\RSIT\TEQHIGN  FMFK/SKVANTILFF\RLDIRMG LLYITLICIVFLMTCKPP\SPYPM GPEYIKYFNNDKFDEEELERDNR VN\W\ILLEFFGNWSNDWQSFAPIYADLSLKYNCTGLNFKVVDV GRYTDVSTRYKVSTSP\TKVQLP TL\ILFQGGGGQQCGRPQI*QKG GR\ALFSWDLI*GT\KEQENVIREFN\LNELYQRAK\KL\SKAG\DNIP\EEQPVASTPTVSDG\ENKKD
18881	49249	A	18990	I	1105	MESTGEDAVNIVEMVTEDLVY RLVVLKSLQVWLSPGDFGMGSE GTECMLIGPWVAMGRPSESTLS SHSGPRSPHGTGSPAPRLQAVH VLCKCPKSRGVQGGWGLASOCL PEHRHTQLSCDSTQAWPQLCSA QSLRHNRSGQGAGAVTSEPAG AGGLPRPPRTQGCLGAES\PAG QLHSQQRGGPEEGRLLSVDVHP DLSSQQQRGP\QVAGGWCV SAAWSSTTHLAGPQQRWDQEEA RQWEQIPLSLLMMGDPPGYSR APGDPGPQPPQRLQLCLGSSH PTNS\GAE\LP\PPVPGSAECAALT VLPSLHLPQWWQVGRGP\T\*V DPRVGLPGQQAPEQRVYSLTHPEQLPVLPQVPLLIYRYSSTNGV
18882	49250	C	18991	105	393	
18883	49251	A	18992	38	230	LYWQKRKGKLLNNL\TQGIVAD P\VR\KKFHKCPNSNCPKI\HNTES A\YAVSFMKYS\AHVLGSLYEM
18884	49252	A	18993	487	747	
18885	49253	C	18994	179	649	
18886	49254	A	18995	3	3187	
18887	49255	A	18996	274	423	

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18888	49256	A	18997	1333	2243	RCWRPRTLGFASPPTRPCSPTH APGCEMTPRDWHRVLSFASPLR IEEIFQGYDKTFGLKNKKGAKQ QKFIKAVTHQVKFGQ/SKSTS TE*SWKRKLKKDDKKELQEL NELFKPVVAAQK!/RVKGADPK SVVCAFFKKQQQCTKGDKCKFS HDLTLGEKM!EKRSVYIDARDE ELEKETKSSL!QADTMNDNWDE KKLEEVVNKKHGAEAKKKPKT QIVCKHFLEAIENNKKYGFWV CPGGGDICMYRHALPPFVLIK KDKKKEEKEDEISLEDLIERERS ALGPNVTKITLESFЛАWKKRKR
18889	49257	A	18998	1	322	
18890	49258	A	18999	1	822	MGKAKEEVFLADELVHAKTNR NKECDYSVTANSKIVVVTAGV RQQEGERSLNLVORNVNFKFI IPQIVKYSYSPDCIIIVVSNPVDLT YVTWKLGLPKHRVIGSGCNL DSARFRYLMAEKLG!HPPSSCHG WILGEHGDSDDHPGRPRPHPVPI KPPETLPGRTSSWTSRGAHWR RNTQAAGRREHIDRHQQAIDR WNNGV!GRGGQRRARLLSDLT PTGKSSYSVSLLAPPSAESYFH SIKPCIHSPS*CMQRPIEIKN/RD YSVTANSKIVVVTAGVRQQEG ESRLNLVQRNVNVFKIIUPQIVK YSPDCIIIVVSNPVDLT YVTWK LSGLPKHRVIGSGCNLDSARFR YLMAEKLGHPPSSCHGWILGEH GDSSDHPGPRPRPHPVPIKPPETL PGRTSSWTSRGAHWRNNTQA AGRREHIDRHQQAIDRWNNG FGRGGQRRARLLSDLTPTGKPS SYSVSLAPPSAESYFISIKPCIH SPSPREIQQFGYTKARNPRVQK

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18891	49259	A	19000	1	1337	MEKPKRLRWLWGPAPSSLLAE PAPEETHAADFVFSARLLQRSP EPSLSWGGRALAEEQKAEAGSSC GSAERLVAFAAKTRPQLSCK MATKEKLIAPVAEEEAATVPPNN KITVVGVGVQVMACAIISILGKS RAMEHTTAGAPYTPRQQTQC NMMSLADELALVDVLEDKLKG EMMDLQHGSFLQTPKIVADK DYSVTANSKIVVVVAGVRQQE GESRLNLVQRNVNVFKIIIPQIV KYSPDCIIIVVSNPRDILTYGTW KLSGLPKHRVIGSGCNLDsarF RYLMAEKLGIHPPSSCHGWILGE HGDSSVAVVSGVNVAQVSLQE LNPEMGTNDNSENKEVHKM VVESAYEVIKLKGYTNWAIGLS VADLIESMLKNLNSRIHPPVSTM KGMYGIGENEVFLSLPCILNARG LTSVINQKLKDEVAQQLKKS DTLWDIQKDLKDL
18892	49260	C	19001	462	728	
18893	49261	A	19002	1	1033	MSGISFLMFLPKADMPAPMLVQ PAERFDWSWWAGPEQQLHSNQL PGDADALLLGRNLTKGTRRLC TEEQVKIPQPEPGPPQKLCVLSA AGGQACLVLTFRRTVWEPP PPGLVGVKACARWWGKGEPD RKAPAPPPPPPGTEKVDQTESE RGTLIQRPPAPALPGWVRKTGR P/PPPA/TGRLQQVPLLGASTQPE /PPGRGV/PPGVSPGLGEDVE/N DGMSLSSYLAE*POATSQRAP*G ENTVALSGRLGRNSSSYTCRPA GERNFHPRGGSSTAALHLRK MPGTPQCEGRRAVPRALPET*M LQGPGTTR*T/PPGPLAFSSPSSP TGPQKVKS LGNNSARTILPPKW
18894	49262	A	19003	2	212	
18895	49263	A	19004	1	425	PTRPAAVAEDEGGLKKCKISSYC RSQPPARLISGEEHFSSKKCLA WFYEYAGPDEVVGPEGMEKFC EDIGVEPENCDCTEKLQNKFDF LRSQNLNDISSLFKNIYRYAFDFAR DKDQRSLDIDTAKSMIALLGR TWPLFSVFY

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18896	49264	A	19005	229	1028	GASKRTGTPFPGFPAHPAREGR KMPVKKKRKSPGVAAVAED GGLKCKKISSYCRSPPARLISG EEHFSSKKCLAWFYEYAGPDE VVGPEGMEKFCEDIGVEPENII MLVLAWKLEAESMGFFTKEEW VKGIMTSQCNLHRKGYKPNF DFFAAHS*IDISSFKNIYRYAFDF ARDKDQRLSDNDTAKS1MLAL LLGEGHzGPLFSWFYQVPGGQS KYRVMNKKD1QWYNVSEFSRTV HADLSNYDEDGAWPVLLDEF VEWQKVRQTS
18897	49265	A	19006	3	373	
18898	49266	A	19007	3	418	GRAGSRKWLLTGSLASTSPSL LSGGGPWAPLQRAMKPPGGS SNLFGFPEEATPSSRPNRMSSNI FGPTEEPQNLKRTNPPGV*GSG IFDESTPVQTRQHLNPPG1GKTS DIFGSPVTATSRLAHPNPKDH VFLM
18899	49267	A	19008	1	684	
18900	49268	A	19009	3	81	
18901	49269	A	19010	1	465	
18902	49270	A	19011	120	344	
18903	49271	A	19012	3	1334	SPQLISSASRPAVRNSRHDATRP VVFQIMSGGSADYNSREHGGPE GMDPDGVIESNWNEIVDNF/D VTMNLKESSSLRQH1YAGFKEP SPIQQKA1IIPCKGY*CGLLKLQ SGTGTATF/SLISLQPVGRLSF KETQSTSYWAPTRELAAQQI1Q VIALGDYMGATCHACIGIGTN VRNEMQKLQAEAPHIVVVGTPG RVFDMLNRRYLSKPW1IKMFVL DEADEMLSRGFKD1Q1YE1FOKL NTSIQVVVASATMPTDVLEVTK KFMRDPIRILVKKEELTLEGIKQ FYINVEREEWKLDLCLDYETL TITQAVIFLNTRRKVDWLTEKM HARDFTVSALHGDMDQKERDV IMREFRGSSRVLTIDLLARGI DVQQVSLVINYDLPTNRENHYH RIGRGGGRFRGRKGVA1NFVTEED KRFLRDIETFY1NTTVEEMPMN
18904	49272	A	19013	75	540	

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18905	49273	A	19014	774	1529	RWGERILLTWRKRQLQVPPSAL EAGGGSSGLEVLPLLLQQADELH RGDEQGKREGFQLLL/TQQAW CMEAGRTFLWRLARAYSDMCE LTEEVSEKSKYALDGKEEAEAA LEKGDEE/SLTCHLWYAGALW SAG*AMRASRRRIQELALTFKE HCGQKPFALQP/KTPMAHFLLG RWCYQVSHLSWLEKTTATALL ESPLSATVEDALQSFQKCYREL GKNSEARWWMKLALELDPVT KEDLAIQKDLEELEVILRD
18906	49274	A	19015	97	452	GTERRTGKLPALLTPNLVQLRR LLFPGIQT*VPAQQGRGHLLQRP AAA/RPRTRRSAPPAAAAPPQV EARPP*LQPTRQEEAAELQATAR AGLWELWAGPQSPRDLNSLESI RITCSPTP
18907	49275	A	19016	1299	1800	FWGGRSGTVGYGADMGKFKN NTTNQNS*K*YRNTSRNPDHKD *FLKGMDPKFPKNMHA*KHN EKGLEKMQDNNMRAEAIKA/L PKPMEVQPRVPKSASRKLD/LA YTAHPKAGKHARAHIATGLRL CWPKAКАKДQTKAQSASAA APASVLAQASKGQАPMKA LE
18908	49276	A	19017	410	1323	RQEGTLIGVFIPAAAAAAVA AAAAAAA AV/GTSFSKPHKLMEHKKEKPS KDSREHKSASFKEPSRDHNKSSK ESSKKPKENKPLKEEKIVPKMA FKEPKPMKSEPKPDNSNLLTITSG QDKKAPSKRPPISDSEELSAKK RKKSSSEALFKSFSSAPPPLITCS ADKKQIKDKSHVKMGKVKIES ETSEKKKSTLPPFDIVDPNDS VEENISSKSDSVPQGSPTVNIFF TSSSTPTILKSYQLDNSDQQGA QEASDKQIEGYFSGEVPAYRQG ELILVASRQ

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18909	49277	A	19018	91	890	GAERLPEGPGKRMVFRRFVEV GRVAYIVSFGPHARK/MWVAIV DVF*SEQGLVE*PCTQVRIQQA MPFRCMQLN*FHPSPRFPNSAQP ESMFRAWQKVADINTKWGSP HDGAKKIEAQRKGKPKDDQIF D RFKVMEGQKKMREQE*SKE* S*RSFKRAALLELSPKKHHLG T*GYCCLLAAAAAAACCLLLACCLKVPSKRRSPAAS KKAPAAQKVPAQKVATG QKAAP APKAQKGQKAPAAQKAPAKPAS GQESISGNHKK
18910	49278	A	19019	280	1249	SLNEGIMYAQPVTNTKEV W QKVLYERQPFSLDKLWWDRRF LGRSSGKNIHAPENTQY WGCG *FESSVIVIQQLCSCVCFVVIR W YMDEGLLAPHWLVTGLASSL IGVLFDLIDGGGERKKG QTR WADL*ELP*SFITFTV G SPVVLK TLTEFCSALTPIYAMSVMLLR HLIFFDYG ANAAIVS STLLVN MAIFASVCVWASRLP RSILHAFI MVA FAIQIFCPGGPML QKKLK  ACTP RS YVGVTL LFAFSAVG GLLSISAVGA VLLA LLMSISC LC PFYLFH FACSLFKENI HMPG WDEA E KEDLSPGSLS
18911	49279	A	19020	1	310	
18912	49280	A	19021	2	411	
18913	49281	A	19022	374	1275	VLTRLIRKRERRKAQSQRERCR CVLAKDFLAGGVTAASIJKMAV APTE RVKLLLQVQSASKQ TAD KQYTGVVDCMVRIPK EQVQLS LWHIGIQFWHKFAGSLASGGP GATSLCFVYPL DFARTLAA VGKAGAEREFRGLG*PAGLRIY KSDGK LRGLYQGFNVNSVQGII YRAAYFGIY DTAKG MLPDP Q NTHIVISWMAQTVTAVARVDF PIPFDITVRRRNE*MQSRAPKEL TIHVHQARFDCWAEGLLRDEG G KAFFKGAW PMFLRGHGVG AFCALSLY GWKSKEGTHKLIS
18914	49282	A	19023	461	705	TERKKKGILPGNGNGFMSLRRT IRVWRNTPNYLGTNAVSPURQD *IGKKGVQCQRKQAGPCCPSNIQ GILEWRKHRISETKP
18915	49283	A	19024	2	408	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USNN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion,  =possible nucleotide insertion)
18916	49284	A	19025	1	885	MTQHAGKRDSELPVIVQDTETVPSVMDGKEYQAGRFARGLRLQCFRRRRRRRTRRRRKKEEEE EEEEEEEEEVEEEEGMKKEEGRRKKKKKAEEEEEKKKKEEEEKKRRREPPRPRNDDARRRKKEEEEGRRRS/MLGKRDSELPVIVQDTETVPSVMDGKEYQAGRFARGLRLQCFRRRRRRRTTRRRRKKEEEEEE EVVEEGMKKEEEEGRRRKKKKKKAEEEEEKKKKEEEKKRRRREPPRPRNDDARRRKKEEEEGRRSMKKKEEEEEE EEEEEEEEEKKRKIGPASKMMGGFEELRRLNVGPTMAIFFLQSAALAPAILYFCPSLKSNIKCNFQFLMFCQLLGRVTIPFLVSQRSRIEVGRHSLSTLNETAHELYLGRTEPDEC GKTAGLGTGLDK
18917	49285	A	19026	1	378	
18918	49286	A	19027	36	3415	ESAAANAQVLAAPSPCSPFAFTLSKVNMSLKNEPRVNTSALQKIAADMSNIENLDTRELHFEGEEV DYDVSPSDPKIQEVVYIPFSAIYN TQGFKEPNIQTYLSGCPKAQVLEVERFTTTRVPSINLYTIELTHGEFKWQVKRKFHKFQEFHREL LKYKAFIRIPITRRTHTFRRQNV REEPREMPSLPRSSENMIREEQFLGRRKQLEDYLTALKMPMYR NYHATTEFLDISQLSFHDLGPK GIEGMIMKR
18919	49287	B	19028	37	147	
18920	49288	B	19029	10	264	

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18921	49289	A	19030	3	1255	HASGRAANMAADRGAVQQQ SQDMMEVDRRVESEESGDEEG KKHSSGIVADLSEQSLKDGEEP G/EEDPEEEHELPVDMETINLAD RDAEDFDLNHYRIGKIEGFEVL EES*RLSCLRQNLIKCL\ENLGR ELPESFRELDLYDNQIKKIEENLE ALTELEILDISFNLLRNIEGVDK LTRLKKLFLVNNKISKIENL\SN LHQL\RLMLGAGDLNRRQGFSK YPTTLTNL\ESWFLGKKTITN FQNPGCASPNTLTVLSMOSNRLT KIEGLQNL\VLNRLELYFSHNGIE VIEGLENN\NKL\TMLDIASNRK KI*KISAHLTEL\QEFWDGTTIPL KWSSDLDELEGEPALEDSVP WGGNPLARRTPKYRRK\WMLA\ LPSVRQDRCPRSVRFKSLFLGSL MWSLSSEELPSHG\VFNPCCS
18922	49290	A	19031	138	564	YREVMVSE*ETPAGAGRPPVY FSAPGTAP\PAINVHPPPPSLSAT PHPPQPOQPPPHQHNAKARVAT IRT\KRTSNCRIRSRKVRKSPPEK WVGFNRRPKASC\SPPPGAARV DVGGETERREREQAA\PGEMGK WARPGEEYFHS
18923	49291	A	19032	1404	1586	ENESRFSDRNQASAGLGLYLSDS L*QWIVGNGHATDLWQNCSTS SSGNVHCFSSSPNGSG
18924	49292	A	19033	187	701	AELAARMLLL\LLSII\VLHVAAL VLLFVSTIVSQWIVGNGHATDL WQNCSTS\SGN\VH\HCFSSSPNE W\W\QSCSRGTM\DPV\QSSFSILSL FLFFCQL\FTLT\KG\G\RFYITGIFQ ILAGL\CV\MSAAAIYTVR\HPEW\ NLNSGY\*RFA*ILAWVAFPL\ ALLSGV\YVILRKRE
18925	49293	A	19034	1	493	
18926	49294	A	19035	105	307	
18927	49295	A	19036	32	302	
18928	49296	B	19037	119	641	
18929	49297	A	19038	496	653	
18930	49298	C	19039	568	747	
18931	49299	A	19040	522	656	ESSQSHGKNFYMGKRIKLSLY WNVWRMLNSKSETTNCPLIRH RLSKR\VGAPFLPAVLVLT\KITIY QT*KFQIRNHKLPSNKTSAI

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18932	49300	A	19041	111	277	RHVVAVVLDGVGRSPRMQYH ALSLAMHGFSVTLLGFCNSKPH DELLQNNRJQIVGVLTEQLSЛАV GPRVFPQYGVKVVLQAMYLLW KLMWREPAGAYIFLQNPQPGLPSI AVCWFGCCLCGSKLVIDWHNY GYSIMGLVHGPNPLVLLAKW YEKFFGRLSHLNLCVTVNAME DLADNWHIRAVTVYDKPASFF KETPLD\IRTHRLFTKLTMHSPP RARSEPEDPVTERSAFTERDAG SGLVTRLRRPALLVSST\SWTE DEDFSILLAALSERV*TTDS/SIG HNLP\SLVCVITGKGPPREYYSR LIHQKHFQH\IQVCTPWLEADEY PR/ILGSVDLGVCLHTSCSGLDL PMKVVDMFGCCLPVCNAVFK WQEQNPNLSDSFTDPLRRKQ CRASCPQ*GPAPGLHELVKHEE NGLVFEDEDSEELAAQLQVLFNSF PDPAGKLNQFRKLNRESQQLR WD*SWGSATPNPMMSSCRTE
18933	49301	B	19042	110	2294	
18934	49302	B	19043	81	1538	
18935	49303	A	19044	21	1158	AVVAALPTSSSRHSL\TQKPGS RRLRIESLLPPSCE\FLFSYI\FR LCEKPYHQT\RSAS\NVT\KT\DP\PR SMNS\RV\FIG\N\LNT\VV\VK\SDV EAIFSK\Y\GK\I\VGCSV\H\GCL\CS VQVMLMRRN\NAPGLI*QGE\DG RMI\ALGQVLD\INLA\AEPK\VN\RE REKSSV\KRS\AA\EMY\G\GQ\QNT LLRPLYFSSSF\LDYDF\ORDY\Y DRMYSY\PARV\PPP\PIARAV\VP SKRQRV\SGNTS\RS\GPRGFNS\KE WNSGVSSKFW\KR*KGDDLQ\AI KEELTQ\INQK\VDS\LL\ENLEKIE KATGANKQLEMK\NDK\SEE\QQ SSS\REGK\MR\TNV\KD\G\*GGV PDDSAEGG\GPT\WMN\DD\NV\KS GGMT\SW\ELI\K\D\DEKE\AEE\GE DD\RD\IS\ANG\GG
18936	49304	B	19045	93	303	
18937	49305	A	19046	1	246	
18938	49306	B	19047	123	487	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met/Asn	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
18939	49307	A	19048	584	1664	SGLFLFLFYSEIFLIFSYIFRLCE KPYHQTRASASNVNTKTDPRSM NSRIVFIGNLNTLVVKSDVEA IFSKIYGKIVG/CSCFIKGAFAPFK *C**EEMPRACCSGRVGRVGRIDL GQVLDI*PGLAEPKIVNPREKPG VETILPAGDVRGQ*QNTLLRPL YFSSSFDLDYDFQRDYDHRMY SYPARVPPPPP\IARAVVPSKRQR VSGNTSRRGKISGFNSKEWNSG VSSKFWKR*KGDDLQ\AIKEEL TQINQK\WDSLLENLEKIEKAT GANKQLEMK\NDK\VSEEQSSSS REGKMRRTNVKDGV*GGPVDDS AEEGPTWMMNDDNVKS\GGMT SWELIKDD\VEKEAEE\GEDDKR QGPMARNDs
18940	49308	A	19049	158	1001	KRLGSSAISMSKYKLIMLR\IIGE GAWNKENR\FC\SVWDQ\KLNSE GMEEARNCGK\QKL\KALN\NFEFDL VFTSVLNRAIPTARL\I\AEELGQ EWVPV\ESSWRLN\ERH\Y\GALI GLNREQ\MA\LNHG\I\EQVRL\W RRSYNT\TP\PP\IEE\SH\PP\Y\QEIY NRPGIKVCDVPL\DQLPRSES\I LKDV\I\ERFLPY\WNERIAPEV\I RGK\TILISAHGK*AVGALLKH\I GRYPSGLKTS\N\IY\SFLLGVPILL E\LDIENLRAVGP\H\QLDQEA\I QAAIKK\VEDQGKV\KQAKK
18941	49309	A	19050	1	521	SASWVG\VA\MSR\VL\SA\Y\VSRL PARFA\*PRVRMLA\VARH\I\ST ALCSEG\T\TRL\G\T\Q\AL\PL\VL\A\I QVPW\I\ELHMLC\Q\Y\SD\MP\I\PLR TLEGIQ\DRVRLA\*L\K\T\L\SD\K\VD PREAFQ\I\H\I\FM\K\DL\G\LD\SL\DP KWK\I\MA\LED\I\EG\FE\I\P\I\DA E\K\LM\T\PP\RL\K\VL\H\QC\Q\DK\KKD
18942	49310	A	19051	1	516	IRALTM\I\W\RR\ALL\AG\T\RL\W\VS RSGSAG\W\LD\RA\AG\LR\I\DCG\I\TA ASGMESNT\SS\LEN\LA\T\AP\VN\Q I\Q\ET\I\SD\NC\VV\I\FS\KT\SC\Y\CT\I AKK\I\FL\I\DM\I\VN\N\Y\K\VV\EL\DL LEY\G\N\Q\Q\DA\SL\Q\K\*L\V\RT\I\TV PR\I\F\VN\G\T\FIG\G\AT\T\H\RL\H\KE GK\LL\PL\V\H\Q\CY\LL\K\SK\R\KE\FO
18943	49311	A	19052	825	1080	KRK\I\Q\NF\H\K\LS\K\KA\I\KD\Y ESG\SS\SV\N\Q\Y\K\RI\RP\T\DN\VV\K\Q Y\W\PG\A\VA\HT\CS\ST\SV\G\QR W\I\T\*G\Q\EF\ET\SL\AN\VV\K\PH\Y
18944	49312	A	19053	80	429	

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18945	49313	A	19054	3	752	FKNAVGNLAMEGGGGIPLETL KEESQSRHVLPPASFEVNSLQKS NWGFLLTGLVGGTLVAVYAVA TPFVTPALRKVCLPFVATTK\Q QIENVVKMLRCCRRLDPLWDIGS GGRDGIVHRRRLRKGFTAVGF MEFKPMG*FWVFPYRRAWRE GVHGSAKFYISDLWKVTSQYS NVVIFGPQMMLQLEKKERE LEDDARVIACRFPFPHWTPDHV TGKGIDTVWAYDASTFRGREK RPCTSMHFQLPIQA
18946	49314	A	19055	157	829	TWGKGDPPKKPRGMSSYAFFV QTCRGGHKKKKHPDASVNFSEF SKKCSERWKTMSA*REKGKFE DMAKAIDKARYEREMKTYIPP QRGRQKRKFKDSDLHPPRPPSG LLSSSCSEYRPKIK*GEHPIGLSI GDVAKLGRDVGINTAAD\DK QPVYEKK\AAKLKEKYEKDIA\A YRAKGKPDAAKKG\VVKAEKS KKKKEEEEDEEDEEDEEEEEEDE EDEDEEEEDDG
18947	49315	A	19056	85	267	GHLSHAWCGTYKPWPSPKEQS RAWKKDGGLFPPPP/PLPPTGLK VRGRESF*SVELIRPQG
18948	49316	A	19057	1	1158	
18949	49317	A	19058	452	517	
18950	49318	A	19059	93	1069	YEGVTTSLPELPRGCLVLQEQ ELVQMSGMEATVTIPIWQNKP HGC/SLRSVRRIGTNLPLKPCA RASFETLPNISDLCLKRCAPSSL PWLVAWLGLFAE*KGSQKARV\RS DTRPLRHTWKPSPLIVMQRN ASVPNLRGSEERLLALKPA/L ASPKAALLSCRTS*ATLRTKICK DSGKLMQLRLH*RQISYLOEVQ MSLLPLPCFGSSFHSTTSFCH*/ PSPRRQRWRSLSFHQSPCFVLP ALNVANQNTKLPAVRLKRMTA SLCPRAAALQDMMMGILKGLFTG MKQSQDLNRSLLKEEDPAVLIS EVLRKFALKEEDISRKGN

SEQ ID NO: NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion,  =possible nucleotide insertion)
18951	49319	A	19060	162	1410	GQASCPPPALGQQTPASSYTVQ IQTYAPSSPHPRQPGPGQGSSDPR GLRGAIPRGRQGQGV*QQGPRC RPPSPSPVLPHIPQLSCCGHDGRD PEEGLGLILETLTLLHHAHPWSPN SW*KDSPSPHGEFPAPHSR DQTSPTATTKHEVQPLPQASLS QPSLGIGCLVDWLRLQLRTTQGS /PQDAAQDSTWERP*DAS/GKP WLL*PGVPTPGPPCPQAERKPP FMGNCP*SRVPWPSRLPEEL/P AMPLAPPVAGEAAGPASQHQL SPSQDPTPLPGADRREKERGGE EGSSWPQTPLITHTTSPPEKQ QQIESPPPIRLSSFKTGFLASSGH SYAIKPNSTKTAEKVQGQVRVPR SHTIREQRQGKRPGEHRRTER DAKPOQEEDHQATVVSQKLGT DRRIKKQRTSVLSATAES
18952	49320	A	19061	1	340	GSVGS GTTLNQ LGFWSSPGTSP LEPPCPWLD SHI FWPFWKDV A FGEGVCLP PPGAPQPRC PRRG QQPEFQQEEPE TIPERTP ADPGV LPPAFPGICL PRR L RAPPDPGP A A*AVPPVADA*GSVGS GTTLNQ LGFWSSPGTSP LEPPCPWLD SHI FPVFWKDV AF GEGVCLPPGA P QPRRICP RRGQQPEFQQEEPE T PERTP ADPGV L PPA FPGICL PRR L RAPPDPGP A
18953	49321	A	19062	3	396	IPLASLHLALPGHQRG PPPGRL P SCSSQGTVP PPPRAGPYQAGCPG TAPAPAAPASAPW SAQASATG GTAHAAGPGSGGARSLP PRA HPPARCWQGRPLRSLLL*PSSVP ETGGPEKARLVKALSPNTAP
18954	49322	A	19063	563	1269	LEESTGRITHFKATLHCTMSNN LAWG GTKWLQESRVFFHIRRLP SDASAGPGCVYRVVPDGGSQG RPQGAPP*AAQA/GTPRGRPPV P GAPS ALL PPPSGT SVGP GGLQ QRRPTGQEDS PTERGFWK PRL WRSHL ATSLATRCTM QGEPAR AHPPGGRGPAA SEERHQ RG PPP GGCFA ALRYCATPRPDLSGRCP GTAPAPAAPASAPW TRLRH QPL AAQLMQPGQVWWGPAA SW

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met/Asp	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, +=possible nucleotide insertion)
18955	49323	A	19064	1	1158	MELKAKARELREECRSLRSRCD QLEERVSVMENEMNEMKREG KFRERKIKRNEQSLQEIWYDVK RPNLHHLIGVPESDGNGTKLEN TLQDIQENFPNLARQANIQIQEI QRTPQRYSSRRATPRHIIVRITK VEMKEKMI.RAAREKGRVPHK GKPIRLTADLSSETLQARREWG PIFNILKRIIFSPQRGGTGGRRM VKLTAEELIEQAAQYTSAVDR LDLRYGYKIPVIENLGAATLDQFD AIDFSDNEIRKLDGFPLRLRKLT LLVN/NNRIC/RVLDFQKV/LK ERQEAEMFKGKRGQAQLAKDI ARRSKTFNPGAGLPTDKKKGG PSPGDVEAIKNAIANASTLAEV ERLKGLLQSGQIPGRERRLGPT DDGEEE MEEDTVTNNGS
18956	49324	A	19065	2	431	RKLDGFPLRLRKTLVNNNRI CRIGEGLDQALPCLCTELILNTNS LVELGDLTPLASLKSITVLSILR NPVTNKKHYRLYVIYKVPQVR VLDFQKVKLKFNPAGGLPTDK KKGGPSPGDVEAIKNAIANAST LAEVERLKGLL
18957	49325	A	19066	92	303	NCFLVFSPARSTVGEFASMSE ECI*MHVVFVFLPLTLCVVSILYER QEAEMFKGKRGQAQLAKDIAR RSKT
18958	49326	A	19067	208	293	LLLLWWFPLGPTDDGEEEMEE DTVTNGS
18959	49327	A	19068	22	904	ARNPWSTHASGWREATGFPQR GGTACCTGMGKLTAEELIEQAAQ YTNAVRDRELDLRYGYKIPVIEN LGATLQFDAIDFSDNEIRKLD GFPLLRLRKTLVDTTRIAGIGE GLDQAIPCLTELILNTNSLVEL GDLTPLASLKSIVAYLTYLRNP VTHKKHYRLYAIYKAPHVRL DFQNVKLKERQKAEMSKGK RGAQLAKDIARRSKTF*FPGA GLPN*PKRKGGP/SLPGDVEAIQ ECP*QNAFNSGLKVERLKGVC KSGVQIPGRERRSG/PTDDGEEM MIEEDTSHQTGS
18960	49328	A	19069	1	395	AINYNEKIELRVMETKPKDKA VSIIECDMNVDFDAP/LGYKEPE RQVQHEESTEGEADHSGYAGE/ LGFRAFSGSGNRLDGKKKGVE PSPSPKPGDIKRGIPNYESKLG/ EAGGRFVAFSGEGQSLRKKGR

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18961	49329	A	19070	1	1108	
18962	49330	A	19071	353	693	GSLFLVKRREPER/QVQHEELTE GEADHSGYAEGELGFRAFSGSG NRLDGKKEPSPPIKPGDIKRGP NIEFKLGKTPFIRNACPLVKKF EEDEAGGRFVAFSGEGQSLSKK
18963	49331	A	19072	2	1112	RLGAAAAAAAGRAVGGVSSL HCPERSGVCVVSIMFSFNMF HPIPRVQFNRFSTQYRCFLSLS LAGPNDR/SSIGEKELIIMPLPL PGTKLSLSL*HYRIPMLFKLTK NSGPHGRHCGVAGSLWA**GA SAYLPHWDGRTYSLGRKAA WVQGGRSVNLSSGPLISNFQPOQ SPDFLADITNP\KAVFEN\ALRNF ALS*PPGDV\IAINYNEKILRNCV VMETQTPTPRVSHH*SVNH*TV EL*LLPPGATKEPRKDQVQP*G VRTEGESRPHSGYAWKSLGFP RFSRGS\NR\LDGKKKGVEPSP SPIKPGDIKRGP\NYEFLKGKTT F/VSRSNSRPLVKKVEEDEAGGUR FVAFSGEGQSLRKKGKRP
18964	49332	A	19073	1	415	SGGGRNRSATGSWVGTMAGIT TIEAVKRKIQVVLQQQADDAEER AERLQREVEGERRARE\RGMK VIENRALKDEEKMELQEIQOLKE AKHIAEEADRKYEEVARKLVII EGDLERTEEPSSLWQESKCSLE EEEELKNVT
18965	49333	A	19074	1	421	
18966	49334	A	19075	3	388	
18967	49335	A	19076	1	1332	
18968	49336	A	19077	49	483	
18969	49337	A	19078	227	1030	AVSVWGTMAGITTIEAVKRKIQ VLQQQADDAEERA\ERSQREFR EERRARE\QA\EAEVASLN\RRIQ \LVEEEELDRAQERLGHCPCKKL *RS*KKLADESERRY*RLFEN\R ALKRLKEKIGTSREIPTSKKKPH HCRKEAD\RKYEEVARKLGDH LKEDLERTEERA\ELAESRC*EI DEQIRLIDQNLQCLSAEADKYS QKEDKWAEEEMKIL\TDNLKAEAE THAELAERSVAKLEKTIDLED KLKCTKEEHLCTQRMIDQTL DLNEM
18970	49338	A	19079	50	864	
18971	49339	A	19080	1	1014	

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18972	49340	A	19081	1	1650	MGFHHVGQAALELLTSGFSQT QELQKFLFLFLVYVTTIVGN LLIMVTVTFDCLRLHTPMYFLR NLALIDLCSVTSPKMLVDFL HETKTISYQGCMQIFFFFHLLG GGTVFPLSVMAYDRYIAISQPL RYVTIMNTQLCVGLVVAAWV GGFVHSIVQLALILPLPFCGPNIL DNFYCDVPQVLRЛАCTDTSLE FLMISNSGLLVIIWFLLLISYT ILVMLRSHSGKARRKAACSTCT HIVVSMIFPCIVYTWPFPTFL MDKAVSISYTVTMTPLNPMIY TLRNQDMKAAMRRLGKCLKG PAVAVGPGPGPDAEAAAER RVKVSSLVPSVDALVSDKKPPK EASPVPAAKSASSGATLRLLLL GHGAREAHSPGPKLKFETASV KWENSQDGAAWMQEPC*YSP PPRHKAHKTNPKPRTAFTTSQL ALEGKLLQKQYLSIAEGADFSS SPNLTETQVKILFQNRRAKTKR LQESELEKLKMAAKPMLPSSFS LPFPISPLQAASIYAAASPFH VLPPIPPVGLYATPVGYGMYHLS
18973	49341	B	19082	62	440	
18974	49342	A	19083	1	902	METEALMPGLGVAVAGAQVTL GFLAETQLPFTGHKRILRLFFS SPRDPPHVPSPKGKLRKGWARR GRTFALREAEPQRPLSLSRAFG TLARPYARLVRPGNPVVPPLA GSAEAARAATCERQARTCPM PGVTVKDVNQQEFVRALAAFL KKS*VGKLKVPEWVDTVKLA KHKE LAPYDENW FYVRAAST AQAPCTIRGGAGIVGSMTKIYG GRQRNNGVMPISHFSI RGSKSIV RRVPPKPWRG*KMVEKGTKNC GPQNLTPSRDKRDFGTETAGQV AAANKEALEQIHCFCGLIHLAHS
18975	49343	A	19084	1	673	AGPDAEASERVPEGPEAPGAGP SRPLEPRPRASGRPGHGRCLGV TVKIDV\NQQEVRLWAAFLS KSLR/LRVS*TVPEWLDTVQAG QAQKSLLPYDE\NW FYVHAELAS TAIRHLYHPGSALGVGSMTKIY GGTSDETASMPKPLSARGFQEI WARRVILQSPGPRGLKMGKRD QELRAAKLDTFKGQKRFWDRI RRNRLAVAYKEALEQTMAGV NKLPOFVKKKK

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met/hod	SEQ ID NO: in USNN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, ^=possible nucleotide insertion)
18976	49344	A	19085	1	427	HPVRFVHRGPH/VDFSLEVVSVWYELVVFTASMEIYGSAVADKLDNSRSILKRRYYRQHCTLELGSYIKDLSVHSDLSVFDPSD TALLNLLPMLDALRFTADVRSVLSRNHLHQHRL
18977	49345	A	19086	2	832	WNSAELGRGGPGAGGAGVIGM MRTQCLLGLRTVFAAKLWS FFIYLLRRQJRTVIQYQTVRYDI LPLSPVSRNRLAQVKRKILVLD LDETLJHSHHDGVLRPTVRPGT PPDFILKVVIDKHPVRFVHKRP HVDFFLIEVVSQWYELVVFITA SM <sup>AEI</sup> YGSAVGRLNWDSRSIL *GGRYYRQHCTELGS <sup>YIKD</sup> P LLWFHSDL <sup>S</sup> GIVIL <sup>DN</sup> SPGAYR SHPGYGGRUDNAPIKSWVSVT <sup>P</sup> ANTAILNLLPMLDALRFTADVR SVLSRNHLHQHRLW
18978	49346	C	19087	69	206	
18979	49347	A	19088	312	438	
18980	49348	A	19089	635	826	QWISLWKCYKPEESGGQYLIFL KKSIFNDEFHVKP <sup>N</sup> *AS*GKEK* TPLQTSNC*GILSPPGLP
18981	49349	C	19090	1	390	
18982	49350	A	19091	336	551	ARPLGSLASAPFPAPM*NVYPT GP*YNADCPNVTAPV <sup>CAS</sup> NGH TFQNECCFCV <sup>E</sup> QREFHYRIKFE KYGKCD
18983	49351	A	19092	76	309	KGRFVIALFTFT*HSNLEKSCSK ICKIKUNKSLVCKHQLAKSIQS <sup>P</sup> S **WNGMNN*FTTLFICCHNTEK TFIHCGKRP
18984	49352	A	19093	181	447	NKYQTNDNIKLSNDNL <sup>T</sup> I <sup>G</sup> HQTG NTTAHIC/RYIMLFRSFQ <sup>Q</sup> MAIT <sup>T</sup> ILS*YRKNIYPLW <sup>K</sup> E <sup>T</sup> L <sup>K</sup> R <sup>M</sup> W <sup>Q</sup> RHREKVGSEKVN <sup>D</sup> IKL <sup>F</sup> HHW
18985	49353	B	19094	1	639	
18986	49354	A	19095	1	160	NLHSQMLWNQ <sup>R</sup> IR* <sup>L</sup> TSV* <sup>LE</sup> L LCKNP <sup>N</sup> RVATRDQLL <sup>C</sup> LSGHL GMGR <sup>I</sup> ELGG
18987	49355	A	19096	2	456	YKNITITDYYE <sup>H</sup> LYAH <sup>K</sup> L <sup>E</sup> EN MNKRASTIC <sup>T</sup> ETIPKKL <sup>RR</sup> RD SSLTHSMRARRLSV <sup>D</sup> V <sup>K</sup> PQ <sup>D</sup> RS RGP <sup>S</sup> ECT <sup>I</sup> FRAGV <sup>P</sup> EG <sup>T</sup> RGALW LPHFQ <sup>T</sup> ESDPGSKPA <sup>I</sup> LLV <sup>I</sup> H <sup>P</sup> DE <sup>L</sup> QIYV <sup>R</sup> TKTC <sup>T</sup> /URMFIA <sup>L</sup> FI JAKT*KQPRYPSCL <sup>I</sup> ST

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18988	49356	A	19097	138	1193	LCFFGQHAPIYCSLRHSLLS TRY PASLICCLPGSHRYLEFVLLLK HHRLHEDLNHCPIGSRSGRDVR SQTTEQHVIAMPFPLRKLEPL HSGLYSHSCCSRYLAGWLALA TGGAARSPPAISILQPQEPSPVTPS DTQRACGRSTEAFESKEQKASV RVEVVVFSCS1KVVDGGLLEPKR ADTGWHGHCRPASITAGWV PARYLLYVFFSRQCVLMSVCGP QYTRGEIPGAVLKEECLPSLLT GRFDLSGRARRLSVDVKPQDRTS RGPECTIFRAGVPEGTRGVVLW LPHFQTESDPGSKPAITLVIHP DELQIYVRTKTC/T/RMFIAALFI IAKT*KQPRYPSANTLLL
18989	49357	A	19098	3	247	
18990	49358	A	19099	1	1048	MQLKPMEINPEVSARCTATRRA RGRGRGSRVADRGFFAFAFA FQMLNKVLSRLGVQAQWRFV DVLGLEEESLGSVPAPACALP ACLFPLTAQIHENFRKKQIEEL KGQEVS PKVYFMKQTIGNSCG TIGLIHAVAQ*SKTNLGFEDGS VLIKQFLSETKKNVPLKDRAKC FIEKNEAIQAA\HECRGTRKGQ CRVDDK\VNHFYSG\PTVDGP PSMNLDDGRMPPRGPMPMAPS\Q GDTLLEGRPRSCRURSPRERQR RSPASSARGFSCKGSLNALWGG TWLISPLSPQHENILP HASLKC FSTCETQA VLLFCQTRPSPQPH RHLSTSRVHSCPLGHCGVSRW
18991	49359	A	19100	57	450	VGDCLTSGMSWVQATLLR/ ALCRAWGTT/CRGALTGTTSIQ VPRLA P\PRGLHCSA/ASVSEQS LVPSPEPRQR/PPGGERDKASF LQTVOKFADTSVVDGSHIDFIY LALRKMR EYGV ERDLAVYNQL LNIFP
18992	49360	B	19101	307	390	

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18993	49361	A	19102	431	1267	SGTRITSTAARTSRTWRS*TPLL ACTPRPCGSALKATATSRCTIRP *SPSATQTLTGTKVPLPKDSTG AADPPQPHIV/GAQGMYVSTPG IQSPDQQAAALARHNPAPRVFVE GPFSLWLRNKCVYYHILRADLL PPEEREVEETPEEWNLYYPMQL DLEYVRSGWDNYEFDINEGKE QHVTI/LCSSGEC*ILRRRQNV* LLDW/LAGKALTSPCTCAPKIC VPLALPTPYCSGQNLNSSCSMT SVSDHLSPTVPTLLSTISKAHGP PPNTKVVTKVTVRQ
18994	49362	B	19103	49	691	
18995	49363	A	19104	89	95	VGDCLTSRGMSWVQATLLARG LCRAWGGTCGAAL/SQEPPSLR SLASLPRGLHCSAAAHSSSEQSL VPSPPPEPRQRRAHQGWSVCPRL/VP VLGQQAGLGERGQQGRAFL/LD GCRNLRTTTSVRKRGPH/VDLFY LALRKMR/EYGVERG/DLAVYN QLLNIFPKEVFRPRNIIQKRIVPHY PRQQECGIAVLEQMENHGVMV NKETEFLLIQIFGRKSYPMLKLV RLKLWVPRFMNVNPFPV/PRDLP QDPVELAMFGLRHMEPDLSAR VTIYQVPLPKDSTGASKIPPKH IVGI/QRSPDQARPLARHNPS/IR PVFVEGPFSLWLRNKCVC/YY HILRADLLPPEERVRA*SKACV GAGEWAGTTLRVHGRGWRRE TERALASDPACTPHLG/EEVEET PEEWNLYYPMQLDLEYVRSGW DNYEFDINEVEEGPVFAMCMA GAHDQVATMAKWIQQLQETNP TLAQIPRGLSAFAGSTRKLQTS SAGLEPP/HCPRTTKEEDDNLQ RQSRAQS*SPCAGIRAQQQDRA GLESAGRCSR

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18996	49364	A	19105	1	1199	EFGALRRTRLGSSFPRRDSSA MESYDVIANQPVVIDNGSGVIIK AGFAGDQIPKYCFPNVYGRPKH VRVMAGALEGDFIFGPKAEEHR GLLSIRYPMEHGIVKWDWNMDE RIWQYVYSKSQLQTFSEEHPVL LTEAFLPNPRKRNERRA\EVFFET FNVPALFISMQA\VL\YATGR TGVVLDSDG\DGVT\HAPV\IYEGFA MPHSIMRIDIAGRDVSRFLRLYL RKEGYDFHSSSEFEI\VKAIKERA CYLSINPQKDET\ETEKAQYYL PDG\STIETG\PSRFRAPELLFRPD LIGEESEGIHEV\LV\FA\QKSDMD LRR\TLFSNIVLSSG\STLFGFGD RLLC\VVKKLAPKDG\IRISAPQ ERLYSTWIGG\SI\ASLDTFKKM WVSK\KEYEEDG\ARS\H\RKTF
18997	49365	A	19106	1	3288	MPSGDQSPPPPPPPAAAASD EEEED\GAEADAA\PPA\ESPTPQI QQR\DELCSRLNMDEA\RAEA WDSYRSMSESYTL\EGSGLWLP RGLFQHPG\HCTGL\LL\LLRSGCV RSQPSDRACR*EK\CHSSH\IEFF N\KMKK\WEDMANL\PHFRERTE R\LERNFTVS\AVIFK\YEP\IFQDI FKYPOEE\Q\PRQ\GRK\Q\RRQP CTVSE\IFHFCWV\LF\IYAKGNFP MIS\DLV\NSYH\LL\CALDLVY GNALQ\CSN\RKELV
18998	49366	A	19107	56	3552	GPAAQGCAMPSSGGDQSPPPPP PPAAAASDEEEED\GAEADAA\P PAESPTPQI\QQR\DELCSRLNM DEA\RAEA\WDSYRSMSESYTL EGNDLHWLACALYVACRK\VP TVSKGT\VEGNYVSLTRILK\CE QSLIEFFN\KMKK\WEDMANL\PP HFRERTER\LERNFTVS\AVIFKK YEP\IFQDIFK\YPOEE\Q\PRQ\GRK KQ\RRQ\CTVS\*NFSIFC\WVLFIC AKGNFPH\*LS\DDLV\NSYH\LLG ALDLVYGNALQCS

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18999	49367	A	19108	1	1193	GRRRRFWWRKRIGGGGGGMA MPAEAPWMASSFNGFLSLPPG WLLLPPPSDRNPPLQPSRRPLC VRMWWMNAFTPLISLFFWASLV SSGARRLHPIQOPQPQCREQAPMP APGAARSAVAASMSDCTVAGP CTGSHTPCHSTSDQSOP/CGGVG SSLVV*AE <sup>R</sup> SCAQCRMSPRKGH  CCCCCCCCCCCC/SCCCYCHYC CCYCCCCCCCCCCCCCCCCCCCC CCCCCCCCCCCCYCCRCYCC CCCYCCCCCCCCRCCCCCCRC CC*HYCCCCCCCF/GCCCCRYC CCCYRRCYCFCCCCCCYCY CCC*RTAHAWP <sup>S</sup> MNKSQCVLP/ CICKVPLGRLAVTTGCPFGF*G GCWEDCMFPAKGPSIRLEQWFS TTAILLPSGP <sup>G</sup> DFWQYLGTLLV VTTREVLLESGG
19000	49368	A	19109	1	762	GTRDATAEENRVLLAMVNPTV FFDIAVDGEPLGRVSFEVRGLD TKK*LLI*SIKLC*QIGGSSIFITS D*KN <sup>S</sup> CLPLIVQQCLLFRILP/L FADRVPKASQKIFVALS/TGEKG FWL*GVP <sup>C</sup> FHRLFP/GFV <sup>C</sup> SRGG DFHTAINGTG <sup>C</sup> GKSI <sup>C</sup> LWGENL <sup>C</sup> K DENFILKHTGPGI\LSMANAGP NTNGSPVFLTSCTA\KT\EWLDG K\HVVF <sup>C</sup> GKVK <sup>C</sup> EGMNIV <sup>C</sup> AMER SLGPRMGKTSNKFTIADCGQL RIKF <sup>C</sup> DLVFY <sup>C</sup> L
19001	49369	A	19110	95	240	LHSEITVCL*GSEHHFFENGTYI PHRSCHDPLEARAEDFL
19002	49370	A	19111	1	1644	
19003	49371	A	19112	237	632	AIGFPSYSSMQLVNIFGLLNLFSI ISSSF <sup>C</sup> RHQG*HS*ELPYPLEPGA EDFLR*GPLAGHGH <sup>C</sup> TGSQPFFC RVSEA/CGSHLVNSSRAALKRW AGV*RK <sup>C</sup> WPRGS <sup>C</sup> PETPRNLKD <sup>C</sup> SVLEYENTPDTS <sup>C</sup> GKKALED

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19004	49372	A	19113	274	2704	GISVLHGCGYRFQPRGMAAPGP FSEKPVPGCDAGDLQTPALSSW TQTFIISHEQQGIKFLNQRWSCWS KERNIGHCVRGRHVTAACQCDL FGNGLKHNLDLHHDNRDASK NVKKSTNYGKMSFYTYCECTP TGEKLWDHNQHRKIIYGVKPASS QDQKLYSGEKSYECAEFGKSF WKSQFKVHLKVPTGEKLYVCI ECGRAFVQKPEFITHQKTHMRE KPYKCNECGKSFQVSSLFRHH RIHTGEKLYECSECGKGFPYNS DLSIHEKIHTGERHHECTDCGK AFTQKSTLKHQKIHHTGERSYIC IECGQAFIQKTQTLIAHRRIHSGE KPYECNNCGKSFISQLQVHQ RVHTRVKPYICTEYGVFVSNNS NLITHEKIQSREKSSICTECGKA FTYRSELIIHQRIHTGEKPYECS DCGRAFTQKSALTIVHQRIHTGE KSYICMKCGLAFIRKAHLTHQI IHTGEKPYKCGHCGKLFTSKSQL LHVHKRHTGEKPYMCNKGK AFTNRSLNITHQKHTHTGEKIFI CSKCGKAFTQRSDLITHQRIHT GEKPYECNTCGKAFTQKSNLNI HQKIHHTGERQYECHECGKAFN QKSILIVHQKIHTGEKPYVCTEC GRAFIKRSNFIITHQRIHTGEKPY ECSDCGKSFITSKSQLT+EH*AV HSG^KPYVCAECGKAFSGRSN LSKHQKHTGEKPYICSECGKT
19005	49373	A	19114	3	180	
19006	49374	A	19115	95	433	PVLRTHPGPQSLPRLPGVPCGG LLEPLSRAEVSPRLGLRRDILG GMAPSGSSTVFLALLTHIASTW ALTPTHYLTKHDVERLKASLDR PFTNLESAFYSIVGLSSLAQVP
19007	49375	A	19116	196	706	ISISNETKDLLAAVSEDSVTQI YHAVAALSGFGPLASQEALSA LTARLSKEETVLATVQALQTA HLSQQADLRSIVEEJEDLVARL DELGGVYLFQEEGLAEETALFV AAATYKLMDHVGTPEPSIKAEDQV IQLMNAIFSKKNFEVSLSEAFSV ASAAAVLSHNRYH

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19008	49376	A	19117	275	2192	MVVSPQGSSTVFLALLTIIASTW ALTPTHYLTKHDVERLKSALDR PFTKRLCFSWFTTCVTT*H*LFP TV*KACTYIRSKSLPCLPQIAKT CSKTLCLPILS*ISISNETKDLLL AAVSEDSSVTQIYHAVALASGF GQVREGVSG*NKTCCHSLGFYSL PSRTVDGSCISFLLLDIQHISV LLWQDLVARLDELGGVYLQFE EGLETSTAVALPPSQQRKRNSCI SHFFQDQVQLQLMNAIFSKKNFE SLSSEAFTVASAAAVLSHINRHPR INKILCSCSLCCNK*FFIYFQLQV TNVLSQPLTQATVVKLFLVISM F/RT*VLAKEPIVILNRDVFELNF MNVKFYICM*IEHPHPIDLATVF SIFL*LRVKISTDIFSACSQRYTD PL*RLTLYASFRVTYPAKAGT FIADRDSMLGPGRJLKLSDERL YYSSI*TFVRLHNQKTCQEVVF VAEPDNKNVYKFELDTSERKIE FDSANIIY*VSPTSLPLCFYRLSL FF*ADVVVINPGIHCPCVWEGHIL KSSWCVFRQHLFREPEKSWHG LCCFPFKF*CLFLFLPIIQLWILT FLNRRASLCFI*LDVMTPLLAA MLGLMVYVWTQLNMFQTLKS LAILGSVTFLA(GN\RLMA QQA
19009	49377	A	19118	3	413	PRKEAPSTFLSQ(NLFTPKQEIQ)\ HLF REPEKR PPTVVI SNTTALI LSPALLLFLALWIRIGANVSNFT FGLPSTH PHWG HAAMLG LSM YVY*TQAQPCSQTLEVPWPILG QCDRFLAGQSGMLAQRTA VQE NQHN
19010	49378	A	19119	2	535	GRVDPKAKKEAPAPP*SLPKA *AFKGPRKAVLK GV HSPQKA GRSRSTPPFRAGRKTADSR PAPKIIILRKSRVPGGNKLD HYA  I KFPADH*SASA VKKIED NNT L VFIVD V LKANKH QIKQGCE RSLYD D VGQGQH P W RP D GE KKAYCSTW L D YD G FG MFAN QNWGSI

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19011	49379	A	19120	159	801	GAAGRRRLPEGEGEDEASAWR RLARCLMPKKNRRIAYEYLLFKE GIVMVAKKDVHMPVHKPHEILAE VKNVPQPFMVMKGHAGLSSPR GYVKGTSFAWRHFLTGTLTQ* GVSQSPWITLH LAPGRFVPCP PLRPVARP RRMGRPVRPKVVLG GVEATWRGFHKRGEV DRGYL TRRSACCQLGAIDKKS RRGWGL GSSNPNFQF RGI GF/GCGRGQ/PP
19012	49380	A	19121	334	989	EPPAETLPVAARDPTGLSPTYLS SHKHEKFQVQRHFPVLLGYPIA SSGASPEVRQRRTTFFRFRPGES LCGDMKLLTHNLLSSEHV PAGG SLPFSGGMVGRGPVLA*TP/LAL QATEGRMICPVEINPQLGRVMI P*KWKWS\AFLEAGPDKLAV*I PGARKGPG*GDMRENEEFS*GP WHHLACWEVGSD*EGTLQVP GNLGRYFSPFKPRGSPNMLAE
19013	49381	C	19122	61	177	
19014	49382	A	19123	4	191	
19015	49383	A	19124	1902	2187	
19016	49384	A	19125	55	340	GELV LKALSAFIRA FRC PEA GS DPVGRAADP SPPAPRGIQS QGS ACGSPFLPGP ITESLPLP PGLG S SELPSL YLVSGI YGGV RRG PPA RLEA
19017	49385	A	19126	1228	2447	TSQGSSPPA HIGR WSSN HKKG L GSSFSQSCCKAEALV KNAW WPPT QA*VSICCFEQDLRGQQKGKS GGK WQKTAES REAVTEC PACY RAAR CRAAGD RGLRA EGA A HTASPSA YRV RGERGH RDMHS ASARL SHP GET NMLG LAE PSV TSH*SHP F RQS*LP*QAGP**EM/ PLPPSARDSSDLCSGSPSH DLLP LPNTVIFWGPSPQDWQPLPLSP FCV SQAAGSPC SP LLLQ GLE PGG I STSCCPG PAPYIDFGA VSGA QOS AAQRAHFP AAMAERPSAGTS GSSG ISG AIAATV VSW VAE GEQ AVKCLAE GSTR QTG QPS R RAPS RGCPAPG APPG RAA PQQ PAP Q PAAGGG RGP PAA PRAP A PRP QP QGA PRP VSP C RGTGA APP PTLV WGLS SE AEG

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19018	49386	A	19127	164	563	CEAALKGDSGGSPWPDEPKPE GVKTEENNNDHINLKVDGAEVMT VVIQFKIKRHTPL**TLKAYL* TDRGLSMRQIRFRI*PGNPIN*K QTHLHLQLNGNRIEDYNQLMCFQ QARPQGVYLKKGTCFFYSKNS VSF
19019	49387	B	19128	166	426	
19020	49388	C	19129	76	285	
19021	49389	A	19130	3	179	
19022	49390	A	19131	93	172	
19023	49391	A	19132	1	2742	
19024	49392	A	19133	1287	2571	ILRQWLLASPEEKTRGPALASG SAETLSWLRAQGRPRGPA*SA VGAEHRTTRTAPGSDPRCGILPS GRSPSP/PARLFLASVPA*AM TPSPTRLPAWPPP CRG/PDASPE VVRKCGGKAGQPRGSPQPWRSG AEEIEVGLLPLTRAILFPQVP TALPAVYIIFLAACEGICPHSCA APSMIELWDFLIQQHQPEKAVA CTTHIPGLRISALNKHRAWGG TDDDVAASEMPLGAAGAEPW D/VE*LLPAALKIPTGHTATTSW GAGP*SPQGSCKGISGVGSGAT ADLLAPTAGVGTTSRTACGGGT QFMSEGAPGVMNNGSPDWSSN QFMSEGAPGVMNNGSPDWSSN LSQPQPMHLLYLTTLWFLERPM CCPDITALTQTLPVPSFSYPVCT SHIRQNPHLHFRLRAPSPHYTTA CSFEPQRFLEQQQQDLL
19025	49393	A	19134	31	202	ILITYIIKLNLNQADFSTP*FMSHLI VSSRLCLTEKWNFHFPPHF*D*Q QTFCTLQFL
19026	49394	A	19135	410	867	LLTLSRTTPLMSLGFPGIPKMIN RPRQSSPIKLQNSSLNLNLLFFQ EDSSTLDSGLERSQLGLDSTGGG EDICRVTAS*SFICLSDPQKVQ IQSAPNRKAWCLVILVVVSHSS TPFSWQKVMKWIKKISFRVFAA GQGLLGGYSNPRYSFSF

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19027	49395	A	19136	111	743	VITILTPMLADRTTERRIERPPKKK GTTSLGQRKWLLTQDWPSVYP VAIHPFKPSA/P/PLPV\RMGYPV KKGRAHGDRRGNLELLKISQFF WILTSCSNLKSTCFALKD/PCTG VGQPHWDSGRKKMLKKHFSN WKFGQHLDLCFHQGPSSGSPN RARVVVLKSKAFLV*1*HDHAK KTLITLVGERYCKTPDVLTIKQ NRWPLRSQ/TIMPVYL
19028	49396	A	19137	305	2291	YLDAEKMGQKASQQQLALKDSK EVPVCEVSEAIHVAAQKLKE YLGFEVPPSKLCPAANTLNEIFL IHIFITCQEKGVD/EWLTTKMT KHQAFLFGADWIVWTWFGSNKQ IKLQLAQVQTLQMSSPPVESP CDLSNPESRVEESSWKKSRFDK LEEFCNLIGEDCLGLFIFGMPG KPKDIRGVVLDSVKSQ/MVRSH LPGGKAVAQFVLETEDCVFIKE LLRNCLSKKDGLREGGASPGSL RLAAGPPLTLNAACPLRLAHL AAMAAAALPAWLSLQRARTL RAFSTAVYSATPVPTPSLRVDD LHLTEIVGMLDSVLTEDSSGK YRFISGEVLCRITGCFTGVRVEA KDLFGGCCSNPNEVMVTWIKVI VEKEVWLYRLYILKALPPRTEK MAVDQDWPSVYVPAAPFKPSA VPLPVRMGMYPVK*GVPMAKEG NLELLKIPNFLHLLTPVAIKKHCE ALKDFCTEWPAALDSDEKCEK HFPIEDSTDYVSSGSPVRNPR RVVVLRLVKLSSLNLDDHAKKK LIKLVGERYCKTDLTIKTD CPLRRQNYDYAVYLLTVLYHE SWE/TEEWGKK*D*SRHGKSIY GENSSSERKYPGERFSSR*KL KNMGN*LKKSS/CGTEIEEYK KSVVSLKNEEENENSIQSQYKES
19029	49397	A	19138	3	233	
19030	49398	A	19139	1	256	
19031	49399	C	19140	5	114	
19032	49400	A	19141	8	444	TTDKEQ*EL*LLDTE*GSYTKE CHTDLSRY*TSSTS AEDRDDS L LRRSGSYRDL*E*IPYSCR LDKD DSTD CIKLYE QILAE\NDKLKAQ LHD TMEL\TDKLQLEKATQR QERFADRS LLEMEK RERTALQR RISEMEERLQM
19033	49401	A	19142	1	287	

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19034	49402	A	19143	211	346	
19035	49403	A	19144	175	3381	EDPAAGEGMKMDAKHKRNE QLKRWIGSETDLEPPVVKRQKT KVKFDDGAVFLAACSSGDTDE VLKLHRLRGADINYANLH/LSH ALHQACIDDNVDMAKLLVDNG ANINQPVNNDGWLPLHAAPSCGY LDIAEFLNGQGAHVGVAVNSE DTPLDIAEEEAMEELLQNEVNR QGVVIEAARKEEERIMLRDARQ WLNSGHINDVRHAKSGGTALH VAAAKGYTEVLKLLIAG\YDV NIKDYDGWTPLHA\AAHW
19036	49404	A	19145	1	2406	
19037	49405	A	19146	1154	1365	
19038	49406	A	19147	1	293	MGVSVLDFSHSDKCEVASRFA GMPEPTNIVLPKLEVADTLGGC TTIPESDLEERSVEQDSTELFT HRHLTAETPR/PW*RLDGLHKQ VSPLOGVSE
19039	49407	A	19148	3	1290	VSQATDVEVGTDLVPSTVVK TLQNRVILQKAKLSQLVYVQPPLE LTCDOFTFEFMNRNPDGIPRVIQ CKFRLPLKLCIPGQPSKTASHK ITIDTNKSPVSSLSSLPFGFASQSD DDQVNVMGFHFLGGARITVLA SKTSQRYRIQSEQFEDLWLITNE LILRLQEYFEKQGVKDFACSF GSIPLOQEYFELIDHHFELRINGE KLELLSERAVQFRAIQRRLLA RFKDCKTPAQLQHLDLTLGTYK QVIALADAVERENQGNLQFSFR LKSATHL.VILLIALWQKLSADQ VAILEAAFLPLQEDTQELGWEE TVDAISHLLKTCLSKSSKEQA LNLNSQLNIPKDTSQLKKHITLL CDRLSKGGRLCLSTDAAAPQT MVMPPGCTTIP/ESDL*ERSVEQ DSTELFTNHRHLLTVEPRPEVSP
19040	49408	A	19149	48	642	WNSALREPRLNAGDMA/KSKN HTTNNQSRKWP\RNCGIKP\PRSP KIRLLKGVAAPPFL\RNMRFAQ ESPNKKGP*RRLQANKLPRAMS ATLPRAIKALVKPQGGLSPKIP\  KGVSSRKLDSTCLTFQAQPQALG SVARCP\LPRGPRL\CPKAKAK AKAKPRPKPRPRAKDQNQGPG LQPQASVPAQ\APKRTQAP\TKA SE

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19041	49409	A	19150	1953	2447	WTPQYMDTEYKNGP威MMEK KVWLDP/NETNEIPNANFRQQIR KLKDGLILRHRKPVTVHSRAQ CWKSTLARRKGRHLGIESKKID RHMYHSLYLLKGNVFKHKRIL LTEHSHKLKADKARKKPLADQ AEARSGSKTKEARKLREEHLQT KKEEIKTLSQEEKAKK
19042	49410	A	19151	1	693	MAVMEKLYWVNREESYASLR VHLPICNATTMSMMSLQLQR LAS SVLRCGKKVWLDPKETSEIAN ANSHQWIRKLKDGLIHKPVTV HS/*ARYR/KNTLACQKGRHMG /*KATANARMPEKIMWM/RM RILCQLLRRYCDSSKKIDHHMYH RRYHESKKVDRHMYHSLYLLK V KGNVFKNKRILMEHHIHLKAD KACKKLADQAETRSRSKIEAR KHREEHHLQAKKEEIKTLV
19043	49411	A	19152	34	280	EVIIHAIGEKGSY/NA**PWVE EQLTRQPLIHHQPSLHSVY/RC RYHSLYLLKVKGNVFKNKRILM EHIHKLKADKARKKLLA
19044	49412	A	19153	2	625	HEAMSMRLQKRLASSVLRCG KKKVWLDPNETNEIANANSRQ QIRKLKDGLIIRKP/VTVHSRLR CRKNTLAR/*KGRHMGIGKRK VPANA RMP EKT/WTWRENEG FCRRLASEDTRESKKIDRPHVV TALYL EVKGNGFKNKRIL ME HIIHLKAIDKARKKLADQA ARRSKTKEATKRREERLP/APR KREII*TLSKEEETKK
19045	49413	C	19154	154	291	
19046	49414	A	19155	3	253	
19047	49415	A	19156	2	474	FKDKQNKPTGFA LGSIEGRVAI HYINPPNP*V*LCQLADFTGLFL TKEDLHEPLSFSAKDNFTFKCH RSNGTNTSAPQDIYAVNGIAFH PVHGT/ATVGSDFRSFWDKD ARTKLKTSEQLDQPISACCFNH NGNIF/AYASSYDWSKGHEFYN PQKKK

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19048	49416	A	19157	97	1728	IRGFFRGSQGSFYRRLKEASGS WDFCPRSWPSSLRARSQSTPE TLLLPGAVFRRSETPMFKMSLF GTTSRFGTSGTIMGSATTDNH NPIEGY*K*HSFSLMDSIGCSCL FSPPTLPGNFIAGSWANDVRC WAEVQDSGQTIPKAQQMHTGP VLVDVCWE/SDGGSKVFTVASC  KTAKMWDLHQ*PRRLQIAQH  DAPVUKTIHW KAPNYSVCVMTG SWDKTLKFWDTRSSNPMMVL QL VERCYCADVIYPMMAVWATA  ERGLIVLQL/ERIQPSEFRRIESP L KHQH RCVAIF DKQNKPTG FVALESIQGRVAIHYINPPNPA K DTFTFKCHRSNGINTSAQ DI YAVNGRAF HPVHGHPCNCGD LDGRFSFWDID ARTKLKNFRE QLDQP LSSAC CFNHVNGKHILP YAS SYDWVKGDH EFYNP QK KKFTFFPA*MQAEELKAPGNKE VVAGRTLGSQAQSFLHHSGLIS VRIWAPNLVGVVSPWTMEFQP PGENDIVVQQLESPPRRAAGDLP VFSIPTGLVAEVFSGKPKGGLK
19049	49417	A	19158	1	1254	
19050	49418	A	19159	1	921	
19051	49419	A	19160	1	1386	
19052	49420	A	19161	49	731	

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19053	49421	A	19162	61	1533	PLKAKMGKEKTHINIVVIGHV DSGKSTTGHLYKCGGIDKRTI EKFKEEAEMGKDSFKFAWW LDKLKAERERGTTIDISLWKFET SKYVVTHIDAPGHRDFIKNMITG \TSQADCAVL\VAAGVGEFEAG IS\KNGQTREHALLAYTLG\WE QLIVGVNKMDSTEPPYSQKRY EEMWLREVSTFVKKIWLQPPTQ *HFVPISWFGIGDNM\LEPSA\N MPWFKGW\KVTRKDNGASGTT LLEALDCILPPTRPTDKPLR\PL QGVHKLGGIGTVSSAPMETIGF SNPGMVVTFAP\SSTVTTESKIL SKMHP*SFEVVKLLPGDQCGPSM SKNVFCQGMFRRGKRLLLGDQQ KMTPPNGKAAGLHWRSVII\N HPRPK*GAGPMLYLDC\HGTG HLHAKFAELKEK\DRRISGKKL EDGLKFLKSGDA\IVDIVPGRP MCVESFSFDY\PLGRFAVRDMDR QTVAVGV/ISKAVIDKKGCWEL GKVTKVWPRKAPEG
19054	49422	A	19163	1	514	EFGTRAKKEAPAPP*SLKPKRK AFKGPRKA\VLKGV\HSHQKEE DPARSPTFPGGPKTLR\LRQPK YPRKSRVPGETRLDHLC\LS\INF PLTH*VLPMKKIEDNNNTLVFIV DVKANKH\QIKQAVKKL\YD\ID VAKVNT\LW\RPDGEK\KAYVR LAPDLP\IAFGMFANKIWGF
19055	49423	A	19164	433	1015	GLISNLDMASRGAS*PTGPDTG N\KICQFKLSTSGESPAVCKSSLV LRFVKGQF\HEFQESTIGAAFLT QTVICLDDTTEKFEI\WDTAGQE RYHSLAPMYRGAQAAIVVY DITNEESFARAKNWVKE\QRL ASPNIVIALSGNKADLANKRAV DFQ\EAQS\YADDNSLLF\METSA NTSMNVNE\IFMAIGKINISF
19056	49424	B	19165	1	2511	
19057	49425	A	19166	2	360	

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19058	49426	A	19167	125	211	FRPGSPRQPRAQPISAPDCTRA MVGRRAL\IVL\AHERTSFNYA MKEAAAAA\KKKGWEVVE\S DLYAMNF\NPIIS\RKDIT\GKLE GPLRTFQ\PGRSFLAY\KEGHL EP\EIICGLNKKLEAADLV\IFQ FPLAVGLEVPAIL\KGWFEPSVH KESFA*HFTAGHVMDKGPPG VKKAVAFFFTGGS\SMYSC QGIHGUDMNVL\WP\I\QSG\ILPF LGLPKSLDPQLT\Y\WPP\PLPAR RPEFSI\LE\GWKK\I\RE\N\IWDET PLYFAP\SSLFDLN\NFQAG\FLMK KEVQDEEENKKF\GLSVG\I\HHL GKSIPTD\NQIQS*KRECTV\HYT RDSHKVAAGAAQLTES\LPAR VAPATTSPANQRPGHLHQSHGR
19059	49427	A	19168	2	331	WVDSQQK\ARY\VPVKGDHVIGIV TAKSGDIFKVDVGGSEPA\SLSY LSFEGATKRNRPNVQVGD\IY\G QFVVANKDMEPE\EMVCID\SCGR ANGMGVIGQDGLLFKV\TLGLIR
19060	49428	A	19169	145	350	QEFHLSSEPSIRLGRSLY\H\HHL FASKK\VL\*QWLDSL\*VCSW EHMRRSQ\GIFSRLANRGFQNG DC

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19061	49429	A	19170	1	1863	MAVAIRLSADTQWEDSPGKSL ELHMSCTKIPERCEADKKESTS SWCTRKRIFRMDLEKECKVLLS GGGGSRMGSQKGDGVGRWSSP RVLGLPSSQTLLRPPPTDFHIAPL SKARQHLLVSVSVLFCFSAPLD VQPLKVLDECQNQRACHLLVN SRVFGPDLCPGSSKYLVLVSFKC QPKQMFITQQQGPGPVLSIGETQV STSSVTRSSSPVGPDIHCEFHTN MCKIPDELKNKNTVCEDQELKL HCESKFLNISATYGRRRTQER DICSSKAERLPPFVFTRYYCFLY APVSSIANPVKGCFHLGKQDC LSYSALQVLSRRCYGKQRCKII VNNHHFGSPCLPGVKKYLTVT YACATLSSMGPILAEVPPEAKK VTLSTSLDSSSGRMEDGRDTG HTEVPVTSGLFIRVNLKKQNFS LQIRCFSFGRGGPKLRHCWAGA. AIALGTEYILVKGDQVTGIVTA KSGDIFRVDVGGSEPVSL\SYLS FEGATKRNPVNQVGDLIYQGF VVANKDMEPEMVCIDSCGRAN GMGVIGQDGGLFKVTLGLN*E SLLASQICE/ISIQEVGKL\LPLEI VFGMNGRIWG*GQKTHPSQTLI LA\NIL\EACEHMTSDQRKTDL
19062	49430	B	19171	29	82	
19063	49431	A	19172	1	427	

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19064	49432	A	19173	1	1548	MTMAAAVVARGAGARAATA AALRGCGCTAARGRPCAGPAR PLCTAPGTAPDMKRYLWERYR EAKRSTEGETKKYTTSLNARHY YTHFTEENEDEINSSSSYASQKK TFEINPRHPLIRDMRLRRRIKEDED DKTVLDI/AVVLFETATLRSGYL LPDTKAYGDRIERMRLRLSNNID PDAKVEEEPEEEPEETAEDITE DTEPDEDEEMDVGTDDEEEETG KESDDPMAYI^HTAEGEVTFKS ILFVPTSATPRGLFDEYGSKKSDY IKLYVRRVFTITDDFHDMMPKYL NFVKGVIRKKLVRKTLDMIK KIAADDKYNDTWFKEFGTNQKLG VIEDHSNRTRLAKLSRFQSSH PTDITSLDQYVERMKEQDKIY FMAGSSSRKEAESSPFVERLLKK GYEVIVYLTEPVDEYC1QALPEFD GKRFONVAKEGVKFDESEKTK ESREAVEKEFEPPLN\WMKDKA LKDKit^K/ALWVSSAALTESPVL LLVAQPVRDWS/GQHWERIMK AQAYQTGKDISTNYYA
19065	49433	A	19174	37	266	WADRAAGGVRILTTQGCVGGG GSCDRRGLETSPARTPVRALWV LGICCVLLTFGSV/READDEV VDGTVEEDLG*KYEKDQVTDD EVVQREEEA\QLDGLNQASQIRE UREKSENFPF\QAEVNRMIELTF IQFHCKNKEIFLERLINSSSCAL DRLSLISLT\DENALSGNEELTV K\KCDKEKNLLHVQHTGVGM TREELVKN\LGTA\KSGTKRKF *TKRPEA\QEDGPSQPS*IDWPS LGVRF
19066	49434	A	19175	233	664	RAPEQSSGVSAAEQERVPNAG WPCSVAPTCPSPRSAE\PARCT* GKEEGG/CEDSDRADSGSPFQE PRYPSGSPFPPIPQASFPCCPCLLVL GIRGHSTILQYRGQEHVHLFTG RCLLVDPPLLVLVVKKSPNAA RDQPARYPRGPL

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19067	49435	A	19176	1	672	MAEAGPKPQRTLWAWESVL SQRKPRAEAGRLSEGCVVKATGTP GFGWQARPDKQEHLRLDGRVID PKDRHGLVKDTEPRLNEFQSLCG GLNPATEEKIREYLAASLGRRR PVKKVLEKKFHTVSGS/KCGPQ VPPSWSETYRTRA*SGDQLGTP AAPNPRWPME*EQEIEAQRRSA HSGARAPWPPWPPRDPGPNP GPKFMVSLSCWNISLRLAGLLY AGCCSP
19068	49436	A	19177	3	684	RHASARKKYNPPSWFHRLGPPP EDQEDEMSVSEELEPITLTPSSA LKPSDRMTMSSSLGERACCRDY QRLGLGTLSSSLRAKSEPFRIS PVNRMYAICRSYVPGLLIVPQSV QDNALQRVSRSCYRQNRFPVVC WRSGRSKAVLLRSGGHLHGKGV VGLFKAQNAPSPGQSQADSSL EQEKYLQAVVSSMPRYADASG RNTLSGFSSAHMGSHGKGV RTSGRSSGLG
19069	49437	A	19178	1	341	
19070	49438	A	19179	1	3710	MVSGARAAAAAAAER TRGVPGHPDSTGRLPAHQQLQ RGLLFRQLGITNVLSVCATLM EHEVFLSRSYQQLTDACRSLL ALLFPLRYSFTYVPILPQAQLEA LSTPTPFIJIGVNAAFQAEQTEQELL DVIVADLGETVTPICEVHIPPL LEPLQSQTHSVLRMVLDEPEL VDLAFPPPM/HDKELRLFHQLL QGYLWCLHVVCIHPEVIRFH KAAFLGQCGLVEDNFLMNVLE GMAFALFVLECGV
19071	49439	A	19180	1	303	
19072	49440	A	19181	14	942	TKLTGSRG*LA*NPCM/HNCE SCVDLLFVRGAGNCPEGTPLR KSNFRVQLFEDPTVDKVEVIRK KVLKIYNKREEDFPLSREYNDL LEEVEIIVFNLTNNVLDLNTKK KMEIYQKENKDVIQKKNKLKT REQEELEEALEVERQENEQRRL FIQKEEQLQQILKRKNKQAFQLD ELESSDLPVALLLAQHKDRSTQ LEMOLEKPKPVKPTSTGIKM SVGITLCPAEEHTFNDERSFNLS SSWSKFNKPPSTLPKVLDDEER LVELKVPNTLITKLVPFAISPCS EAIQDHPAILLAYKKTPFWRLQ
19073	49441	B	19182	49	456	

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19074	49442	B	19183	53	333	
19075	49443	A	19184	2	208	VYPELQITNVVEANQPVTLQNW CKRGRKQCKTIPHL*FPYRCLG EPAGRGAGVWDWGPGLERKRKG CSC
19076	49444	B	19185	51	300	
19077	49445	B	19186	148	3568	
19078	49446	A	19187	1	3411	
19079	49447	A	19188	2	2416	NSRGA CAGPRETAAVAAARE QGRGGSHSHSSALGAPRVRAM LPGLALLLLAATWARALEVPT DGNAGLLAEPQIAMFCGRLNM HMNVQNGKWDSDPSGTKTCID TKEGIL QYCQEYVPELQITNVV EANQPVTLQNWCKRGRKQCKT HPHFVIPYRCLVGEFVSDALLV PDKCKFLHQERMDVCTETHLHW HTVAKETCEKSTNLHDYGML LPCGIDKFRGVFVCCPLAEES DNVDSADAEE\DDSDVWWAG ADTDYADGSEDKVVEVAEEEE VAEVEEEEAED*LTRTDEDGDE VEEEA\EPYQEATERTT\SIATT TTTTESVEEVVREVCSEQAET GA VPSNDPLVIL*CD*REVCPIL LRRMWRQPEQL*HRRVLHGRV WQR\PTTAASTPDA\VDKYLET PGDENEHAHFQKAKERLEAKH RERMSQVMREWEAAERQAK NLPKADKKAVIQHFQEKVESL *QEAANVRQQQLVETHMARVE AMLNDRRLALENYITALQAV PPPRRHVFNMLKKYVRAEQKD RQHTLKHFEHVRMVDPKAAQ IRSQVMTHLRVIYERMNQSLSL LYNVPAVAEEIODEVDELLQKE QNYSDDVLANMISEPRISYGN ALMPSLTETKTTVELLPVNGEF SLDDLQPWHSGFADSPANTE NEVEVPDARPAADRQLTRPG

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19080	49448	A	19189	1	2355	MKSIFTSEISSVLFVNPEPGRRV SFLGSGRREHAEERARGPRETA AVAAARAEGQRGGSHSSALG APRRVAMLPGLALLLAATWTV WALEVPTDGNAGLAEQPIAM FCGRI.NMHMNVQNVKWDSDP SIGTKTCIDTKEGILQYCQEYYP ELQITNVVEANQPVTIQNWCKR GRKIQCKTHPHFVPIYRCLVGEF VSDALLLVPDKCKFLHQERMGC FAETHLHWHTAAKETLQ*RRS TNLHDYGMLLPCGIDKLRGVVF VCCPLAEESDNVDSADAEEDDS DVWWGGADTDYADGSEDKVV EVAEEEEEVAEVEEEEADDED DEDGDEVEEEAKEPYEEATERT TSIATTTTTESVEEVVRVPTT AASTPDAVKYLETPGDENEH AHFQKAKERLEAKHREMSQV MREWEAERQAKNLPKADKK AVFQHFMPEKVESLEQEAANER QQLVETHMARVEAMLDNPRRL ALEVNYITALQAVPPRPRHVF NMLKKYVRARTEGLVSTSL*HF EHVRIMVDPKKAAQIRSQVM*T HLRVIVYERMNQSLSLLYNVPA VAEEIQCDEVDELLQKDANYS** RLWPTMISEPRISYGNDALMP SLTETKTRGSSVPVNEEFLSD DLEPVHFFWWLTSVPANTENE VEPVNDARPAADRGLTTRPGSG LTNIKTEEISEVKMDAERHDS
19081	49449	A	19190	103	463	PLLYAMSTGKRWLGSFGSMIPPV AICASNKIRWPFSMSLSFMAW NKEMMFPVSGSLYPTVARSAD RSFSLNSMPTRPLL*ASSTGNLK LLTGSTIKPVAAWASSNSRAVP GRTKPIFMAS
19082	49450	A	19191	1	182	
19083	49451	A	19192	3	437	MVHAEIISDEGFFLSAPIALTOA WLNIPKTRRTFCKKCGKHQPH KVTQYKKGKDSLLYAQQKRY DRKQSGYGGQN*KPIFRKKAKT TKKIVLKLALSAPTCRSKSKC WLFKRICKHF*TGEEIKRKGQ VDPVLKCHLLFMEGH
19084	49452	C	19193	341	421	

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19085	49453	A	19194	15	1066	VLACTVEASVIGGQKREMNMG SIVREGFMEEAGPRIGNQLSFFI QSTVTGSSVGSTQLQPLSLPPA TAGQEPRGTGPLGSNHNSCPAPE PVSYGRLNDPPATTHPGSFTRF HSKPLTSSCWDSEMEGCVSNL MVCNLASFLNVSTNPACAFFPW YFYYLLLL*AGWSPLHIAASAG RDEIVKALLGKGGVNVYNTNT DRFLHCFLLSSPSFQIAVMLLEG GANPDAKDHYEATAMHRAAA KGNNLARNPNHYIELVVINWSL VVPDFRHLACDEERVEEAKLL VSQGASIYIENKEEKTPLQVIAK GGLGF*YSREWVGRFKQLGFIL YFVLLCLLSPVSYKMLYCLTRH
19086	49454	A	19195	1597	1923	
19087	49455	A	19196	551	747	
19088	49456	A	19197	1059	1296	
19089	49457	B	19198	1	1281	
19090	49458	A	19199	3	565	LPGRLLLLNFRQRQIDRPSMN DTRNLSSRTRKFHAPTRPTSEEN KWVIDVLSpagRPTVP*DQKFR EK\LAKMYQAPHPDV\ILVFGF RTVHFGGGKTTGFG\MIYDSPWI MQRKNEPIKHRLARIHGLYEKK KDLKKATEKERQPELKVQG GLAKGPLLGAQQKEEMKCLAV ELEIGSQPKELKVQ
19091	49459	A	19200	2	476	

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19092	49460	A	19201	1	2448	MRGSLIKECGSKERASQVDLEY SRGNTASFAMCFHDRARIMKG SQRSRKLTGGEGREEGERVENK DFLDLHGQIQVRL VVKTASLLS RVTYIAEVEGRETDAGWRNEL QVGRLDGPDILVVSISTDHTLV DTHLEAVGGHSHEPYFKNHL ACHVESELQRDRNGHRDAGWR NMRHGITDKEMQDSQGSSDNH VLGSILRWSARAAPALPGLPEE AFVEMSTEGGFGGTSRSDAQS LKSFWLRPRFFITELTLRAWIHT EDNNCRTYVAMAITKFDQLDF LIDIVLRLDELKPPKCQEVEVLQSV TPAEPVQYYFTLAQQPTA\QVQ VQGQQQGOTTAASSMTTMQPGOII IAQLQQGQTTPVTTQVGEQQ VQIVQAQPOGQAO*^AQSGTGW TVQQJQTLATSAQPI\TQTEVQ QRQQ*^FSQFTDQQLYQIQQVS IPAGQDLAQPMFIQSANQPSD GQAPRSHEVIAAAPAARRERER ELAGRGPFCPPPAGNVRALKSR RCLPGERRERARKKPEGGAA ASERGETDSHPGASGQGPRDSG RVPLGMWSRRGLGVSRAPLHL LLGVSTSFPLPLTPIPTTAVVN PLKPLKNRIKAPHRRMPLVPGG SQNLGTVRARISTRQSHAEPST DNERVLSMTQDIHSIFLNKNIT WICTLQSCGFLLSNLCKDIVHK AGSGEARTRWSPRAQAGTHED
19093	49461	C	19202	124	369	
19094	49462	B	19203	739	870	
19095	49463	C	19204	787	969	
19096	49464	A	19205	101	331	
19097	49465	A	19206	137	415	
19098	49466	A	19207	86	221	
19099	49467	A	19208	1	1347	
19100	49468	A	19209	120	899	FGARGNLKKAYSTRSKMAELN THVN\KEKIYAVRSV\VPNKS N\NEIVLVLQQFDNFVNDKAVQAF VDGSAIQVLKEWNMTGKKKN NKRKRSKSKQHQN\KND\AKDK VERPD\ACPLQPQQPQI\QNGP\M NGCEKDSSSTD\SANEKPALI\PRE KKISILEEPSKALRGVTGPNIEK SAKDLQRCTVSLTRYRVMIEE\ VDSSVKKITA\FAELHNCIDKE ASLMAEMDKGIEEAMEI\LTAR Q\RKAEALKRLTDI\AS\QMAE

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19101	49469	A	19210	211	2150	ADTKPERGVSSAVFASGSERRLGCVLLSSSETRLLSGTLWIPRAYSTRSKMAELNLTHVNVKEKIYAARSVVPNKSNNIEJVLVLQQDFVNVDKAVQAFVDGSAIQVVLKEWNMTGNKKNYKRIRSKSKHQQGNKDAKDKVERPEAGPLQPQPPQIQNGPMNGCEKDSSSTDSANIEKPALIPREKKISILEEPSKALRGVTEGNRLQQKLSLGGINPKPIHGTTERSDGLQWSAEQPCNPSPKAKTSPVKSNTPAAHLEIKPDELAKKRGPNIEKSS/VKDLQRL/CTVFF*LEYRVMN*REKWDSSGERRRSKLPFAE\HNCIIIEQKEVSLMGRKWD*SLKEGRPWEILDWLVRKKSKKKLKLRTDLGQSRAEMAEMQLGPKLRAEIKHFVSEAVNYDEELGKSCPGFSCDIEQLKVAQIIALPGKITHPKVNNYFLKELPCSSL\PLLNAAARSKPLGKTEVTFSRKSSTHNKPSEGKAAAPKMVSSLPTADPSHQ\TM PANKQNGSSNQRRRFNPQ\YHN\NRLNNGPAKSQGSGNEAEPPLGK\GNSRHTQEGQPH\NRFGRFPK\NKGRCQKIQEASLGIEGPPRAPAHFLKRPRAKGSHAADTFGRA\RAFGVGS/GSVRGSQCNLFPT\RIEVSTDAAVLSPGCDRWVA
19102	49470	A	19211	93	180	
19103	49471	A	19212	3	39	
19104	49472	B	19213	1	888	
19105	49473	A	19214	863	1509	GCAGPCLVNQMFNSTSILCKSHCHSLVSINQGHNAPWKAAG\PLPLKAGY\QSFSPCDDSLKG\QSWDEKDLTVQPQDTRKASVLRWISQRGKPLAVDMEEG\HCL\CLPPG\N*NVLGCKTPIVHLFNSELGRK\AALWEARHVG\SNAAALLFTP\LRCLGGEKHKGGLHAIHPGIVPS\LELNYDIDSFAHVVFVVAVELPLIITLLPYCIPLCNNEK
19106	49474	C	19215	289	510	
19107	49475	B	19216	534	1686	
19108	49476	B	19217	1	1062	
19109	49477	B	19218	1	1878	
19110	49478	B	19219	1	747	
19111	49479	B	19220	230	786	
19112	49480	B	19221	67	6011	
19113	49481	B	19222	1	3455	

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19114	49482	B	19223	1	4763	
19115	49483	B	19224	65	4534	
19116	49484	B	19225	512	4782	
19117	49485	B	19226	345	2194	
19118	49486	B	19227	267	7391	
19119	49487	A	19228	578	739	
19120	49488	A	19229	419	1410	KQRQARERHLPRIPQLSAVVTIE TL*RK*RNFAELKIS/RLRKKFA HKMLQKARRKLIYEVKVKHCK EYRQMYRTE/QMAMT MARKAG NFFVHPKPKLAFVIRISAISGVSP KWKNKQLCPLNHVFGLGMGD LRAFLADGTGPSGGIEITGMRD LRGPLSVRAPSAGVVAEPRHLIV FEDVVNGKFLQTSRCEISGSKN KVVQTLKKNKRERQLPLTGFG RLADQRAYGEAKNNCGQVGL VETLWERHLLRIGVYIATSLA VPTLSSNYNGLAHDQSCSDTVQ RSTGAPEAWDRGYCVRGQAQG  PIFFLDRPLTLSFDEARGSSSS
19121	49489	A	19230	3	307	AGTMEGVEEKKKKEVPAVPETL KKKRNRNFAELKIKRRLRKFAQ KMLRKARRKLIYEAKAHYHKE YRQMYRTEIRMARMARKAGN FYVPAEPKLAFTVIRIRGI
19122	49490	A	19231	3	160	GRVLL*DKTTSRGITRQQQLLFT NICCSAASA/G*YPGKQGLEWT SSRLQQTCs
19123	49491	A	19232	303	570	GLCIRHVLVPSAAGLLEFAGGP LQTLFAWVSAEAAEQQIWVN SKCC/CPDRSSGSFVSEEYLAV* GVGLTLSSASLMLGAVDWSCS HSA
19124	49492	A	19233	1	176	MQYVQQKPKLKFQVHICAYRK TVLQQPLLIQRT/WVWSGPPA NSNRPAGGADC*KEN

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19125	49493	A	19234	1	1977	MFAVILQAPLVIPRQT/WVWSGP PANSRPAAEGPDC*KEN*RQT GSGVQLQQPTPTDLQLRVLIVRR KTNEQKQGHPHQNPICTPSSKT KVDTTTNMGEKQSRKTEKN QSASPPNLKKKREKNQIDA NDKGDIITDPTE!QTTIREYKKH LYSNKLENLEEMKFLDTYNL GLNQEEVESLNRPTGEIEVIIN SLPTKSPGPDGFTAEEFYQRTK DKNHMISIDEEKAFDQIQQPFM LKTLNKLGIQDGTYLKIRAIYDK PTANIILNQKLEAFPLKAGTR QGCLPLSPLLFNIVLEVLAIREIRQ EKEIKGIQVGKEEVKLYLFADD MIVYLENPPIUSAQNLLKLISNFSK VSGYKINVQKSQAFLYTSNRQT ESQIMSELPVTIASKRIKYLGQL TRGVKNLFKENYKPLNKIKED TNKWKNIPCS WIGRINIMKMAI VPKVITYRFNAIPIKLPMFTTEL EKTLKCIWNQKRAHIVKSILS QKNKAGGIMLPDFKLYYYKATV TKTAWVYVQNRHIDQWNRT PSEIMPHIYSYLFDPDKPDKTRNG ERIPYLIRWCWCWQNWLAICR KLKLDPFLTSYTKINSRWKDL NVRPKTIKTLLEENLGIITQDIGH GKDFMSKTPKAMATKAKIDK WDLIKLKSFCATAKETTIRVNRQ PTEWENISAIYSSDKGLISRIY
19126	49494	A	19235	206	456	
19127	49495	A	19236	2	385	NLCCSAASAGDTQANRVSWSGT PTNSSRPEVSSGAMDGEWGWL PVDPPLTGHQDALPWQRCYHP CSSSVPPRQACASPA CSSSSA W/TSASTGPWHSGCGSSCGSC CWGPSASVGVAGAIRSRTV
19128	49496	B	19237	1	642	
19129	49497	A	19238	128	584	
19130	49498	A	19239	4054	4578	QSGPSAAGLLEFAGGPLQLTFA WVSAEAAEAEQRLVNSRCCL VPIRKFLRGVASHVRQC SAPY DVFCHGITLAKCWCSALGLPSL QSCEPNALFFINYPVCGI/TAPCC KVEGTMGIVGPKSPQLSYNVL GSDNNNGVLLGMSMAIFTIL LICH EHGMFFHLFVSSFISLSSGL

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19131	49499	A	19240	1	948	MVLEKAREEVDPMSLIPPVTVQ CGQLPRSQCPQPTLSRMLTLEV GISLGIVLMLISWPDTVKKEYQS REALSFKKYKNKNPGLLK FAGDP LQTLFAWVSPAEAEQQISALC FLWKLRLPRGAPTRCQPLLSYTR CLSAPAGSFVYTMRGKPPQAS VMADASPPTRKIEHPRTTSDCCV ASKNFKPVLDLSSLCMVGSAE LDHWATWLQSPPQGSERFCLA GVPGTTGV*KETPAASSVSAQM AAQFC*NAHRTLVV*APKGIL WVCGLRRPWEKRSICAGVHHS SWHSPSWLPLARGSSSTCTS WVRRCP TLHL
19132	49500	A	19241	171	1345	YCPKEGTLDNFNAFNMTAVNV ALIRDTKWLTLLEVCREFQRGTC SRADACKFCAHPPRVCVHENG RVVACFDLSKSVTAVPFLFMAL GLSREPETVPASMVQFTSLGVG GGAGSV*PDENCKYLHPPPHLK TQLEINGRNNNLIQQKTAAMAF AQQMQLMLQNAQMSSLGSFPMT PSIPANPPM/SFESLRYHILGMG LVPAAELVPNTPVLIPGKPTSQL PGSCLGPKLMAFQINWEVLPRN FQRGVNCISRGENDICRYAHPTD ASMIEASDNTVTICMGIYIKGRR TVGVWGIKAKSSKQRLDITKGS HQGNSFVROTDYLIPICTNMSK AKGTAFLKWMQKLVYNGSS QCSPAFFCCAWKEHSEKAGRA SGAKCNRHRHTNPVFLMREGA IS
19133	49501	A	19242	61	544	KFNPVFVTSRPRARIRKRAF/NAP SHIPKGRLLSFPPLSPKSLRPEG TNRADSHAPIPKRMIESSRLYR GHL*GSAKLAKVVPFRTRKKY VIYIERVQREKA\NGTTVH\VGI HPSKQV\ITKAKTGTKTRKKIP PNRKAQSRQVGKEKG\KYKER TIEKMQE
19134	49502	A	19243	652	1042	TPLSSCFLSREKA\TQLLFPVVVA VPMLVLSAMGFTAAIGIASSIAA KMMMSAAAIANGGGVAGSLVA TLQSLG*VSWRGLPTVLPTELP RQACPTLSTLCFFPGATGLSLT KFILSIGSAIAAVIARFY
19135	49503	A	19244	48	397	

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19136	49504	A	19245	42	296	GCVGVRPSLHPATSTASGSASP TLARAMASVSELACIYASALILH DDEVTVTEDKINA/APAEEKKV EAKKEESEESDDDMGFGFLFD
19137	49505	A	19246	172	519	LGPSFLHDDEVTVTEDKIQMPL KAAGVNVEPFWP/G/LCFAKAL GKRSTLGLSLILAMLGPPGVPGS QPAACLQPAAGGSCPPSTCCWF QLEGEEKWEAKERKIPREF*LID MGFGLFD
19138	49506	A	19247	3	175	
19139	49507	A	19248	2	390	GWDWNCVWEPHHWLQLCQL/N SVTQAGVQLCNLSSLQPLPLGF KQFSCSLPSSWDYRNPNSLKQQ LFSYAILGFALSEAMGLFCLMV AFLISLPCEGAVSTSHSSPASG WPRVFLFLYLPQRQPGERGWLR
19140	49508	B	19249	139	13320	
19141	49509	A	19250	28	450	TNDFNLLQNPQSCFPSACPAGVG SERLPVLGWFVGNRSEPPPQST LSVLGKRLGRNGAIAAGVFGA LFIGYCIYFDRKRLK*PQLKDAE AVQKFFLEI*LGEEILAKGV HLTNPSA FFG/QPNHFPLQMDSF GPFLRFQA
19142	49510	A	19251	164	420	
19143	49511	A	19252	1	329	STHTTYWEGCRTTSAGLLRKH EPGEEAF/FYHST\SKKPGIAGLI KVNQFVRMMKRSIPWAELNP YHQAHKATGGPLKNMVLFTQ RLSIQPLTQEEDFVLSLEEKEP
19144	49512	B	19253	39	368	
19145	49513	A	19254	1014	1290	
19146	49514	A	19255	122	680	LARITRIVRTKVPCSVTSMSRPRK RLAGTSGSDKGGLSGKRTKTENS GEALAKVEDSNPQKTSATKNC LKNLSSHWLMKSEPESRLEKG VDVKFSIEDLTAQAKQTTCD GVRNYQAS/RNFLRAMKLGEE\ AFFYP*OLAKKPGIAGLMKIVK EAYPDHTQF*EK\NPHYDPSSKE DNPKWSMKSLILF

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19147	49515	A	19256	2	1005	RISTSTLCPKPKKKLIAPPGRAGL ASMGLNEEQKEFKVAFDFAA REMAPNMAEWWDQKDRKADGK GGAVTQEVAQQLI.VKHGQKL VSRFQLSSFSYVDSVRTTQSKQ EHLQTDKGKLSGKRTKTENSGE ALAKVEDSNPQKTSATKNCLK NLSSHWLMKSEPESRLEKGVD VKFSIEDLKVQPOQTTCWAEQ VRNYQARNFLRAMKLGE\AF FYHNSNCIEPGIAGLMKIVKIEA V\PDHTQFEKKQPPPL*PPS*QR GTTPKWPHGWMV/QWWFGMM KRFHSPSLAEVLKS\HHIQAHKA\IS GGPL\KNMVLFTRIQRLS\QPLT VQEEFDVLSLEEKEPS
19148	49516	A	19257	3	727	VRLQFLPTLRAARTMAAPPQL RALLVVVNALLRKRRYHAALA VLKGRFRNGAVYGAIRGSPSR WVMTFLFREWAAASREKLWAIL Q\ATYIHSWNL\ARFVFHLLTRV FRCPAVPYITRARTYPA\AHAPFG AGLSFGGIL\VFGRKQ\TFSNQI\I NMYLLSTRPCLP*SR\LAVERRK GLHP*NPRLWDPP\VC\LTAVVVW GLVLWLFEYHRSTLQPSLQSSM TYLYEDSNVWHDISDFLVYNK SRPSN
19149	49517	A	19258	1	849	MSGALDVLQMKKEEDVLKFHA AGTHLGGTNLDFQMEQYIYKR KSDGIYJINLKR\TWEKFLLAAR AVVAIENPADVSVISSLNTGQR AVLKFAAATGATPIAGHFTPGT FTNQIQAAFREPRLLVVTDPRA DHQPLTESSYVNLP\TIALCNTDS PLRYVD\ICNNKGAHSIDPEEIE KEEQAAAEEKAVTKEEFQGEWT APAPEFTATQPEVADLSEGQVQ PSVPIQQFPTDDWSTQPATENW SAAPTAQATEWKMQQQSTILE AESSHQTPNLPAPWSRTSQPPE

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19150	49518	A	19259	1	1309	GNLAAGKTIQAAQDRDAVGILSSRTGESMENLQKNLLPKQRRRTRETFTMSGALDVQLQMKEDVLFKFLAAAGTHLGGTQFLLSRGHGYFYKGKS/DGLSFNPKRAEE/LLLPARQIVPHKTPS/DVSVISSGNTGQVCGTVRA/VCLKFAAATGAATPVAAGRFTPGTFF*PRSKAAFVPRPLLVVT*PPGADPPALSRSASYVNLPYHLLRCGNTDS\QLRYVDIAIPCNKNGVAHSGVLMWWM\LRGSCAMRGTISREHPW\EVMPDLYFYRDPPEIEKEEQA\AA*E/RQVTKEEFQGEWTAPAPEFVTATQPEVADWSEGVQGAPLVPYSAIPTEDWSSQPAMEDWSAAPTAQATEWCSRSLRQNPSDTELKKEGLYSARSISIKTHVSKTELPNQGTTKCSRTSHRQNPSVTELKKEGLYLARSIGKTHISKTEL
19151	49519	A	19260	965	2495	AFTTRSTFSTNY\RSLSGSVQAPSYGARPRQAARPASAYAGAGGSGSRSIVSRSTSFRGGMGMGSSGLLATGTSPGVMAAGMGIGIQNEKETMQSIVNDRL\ASYLQGE*RSLEDRRTRKLGRAKFREHFGRKKGPQVARDWSHYFKI\EDLEGFRFRKILVGGQCPASVSRFDNAPSLLD*F*EFKY*GQSWPMCPVLLENDIPLSAKV\DDTNYHTDQLQ\ETEIRGSSRRELLFQ*RRNHEE\EVKGGLQAQIASSGLTVEV\DIAPKSQDLAKVIMADIR\AQYDIELARKEPEKEA*TKYWSADLRESTTVGHPHKSA*GWLKLAEDDASQKLRRTVQSLEDRPWTSMRKSERPALENSP*GEVEAPLRLPLQDWSQLQTGIPACHLWSQELGTRHRAQRGQRPGPQGV*GPPLNHNQGSSLEAEICHLTRPPSWKIGEDFNLIGDSVLDERNSMQTQKTTTPPG*VGLGVVS*DQLTPKVLKALSQQEAVVFPFWGSRRPIKSFRVQKKKEKEF

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19152	49520	A	19261	387	1125	CCRPCATPYALRSPLR*PACPPPRWRPSSMPTSRPPVSPAASPTC GTCMLSP/CPPAEHLLHLPHQDQDPALLQPCHPAPPLRPRALHA AHHVGVPAAPHQPLLPPPVLCPGGAGRGGG*RCPWWRGPSSSSPG PTIAGQDQPGAQQP*TWQP/PTL TSVSATASPKAPLPLAAA VPGAPAEGCCPPLLQRQALPAGOLPPGG RRATSAVPPAVPGD/PAQPTM PGSMSCWALAPARPCPPGRCW AWRS
19153	49521	A	19262	3	1097	RGNNSRLRYSHEDELQLPRLPEL FGNCRQLLEEVETADPAGFR\IVQEKFVKG\LDLLE\RAAEML\SQSTLFGRECRFWKDLSPTHLIT FWGPQAFQGALTMKQVNPSKR LRSFCGSCAREHT\INLYTQCHIC YHVGQSFEL\PKT\MNNSAENH TANSSMAYPSLVA\MA\ASQRQA KIQRYKQKKELEHRLSAMKSA VESGQADDERVVRGYLLHLQR W\WV\DIS\LEE\JESIDQEIKILRERDS SREASTSN\SSRQERPPV\KPFHS HFGTWLHSQSTFGAGY\SKGWP TYGR*VSWYE\QHRKLW\STYP DQGNM\PRAAPEGISEKA\AQQQ EDQEEKEEDDEPNNFH\RA\RE W\DDW\K\WTHP\RG\Y\GQRQNM
19154	49522	A	19263	2	262	
19155	49523	A	19264	3	1062	GRTAENPARAVSSPNFYAHRKTEVLFPCLTQPLARGPKKHLK\RVAAPKH\WMLDKL\TRVFA\PR\STG\PHK\LR\ECLSR\UFLRNRLK\YAL\TGD\EVKK\N\CMQR\FIK\ID\GQGSELD\IN\LP\LLGF\MGCP\SAFDKTGEENF\RLD\LD\TQ\GVRFC\WY\IR\PPW\RKAKL\QV\W\QC\K\*GK\IL\CGPTK\RESP\SSGL\TH\*CPA\PH\PA\Y\PP\PH\PR\*NG\Y\IPD\*I\*E\DL\AK\N\L\I\Q\SS\EE\HW\*TLC\MD\LE\GA\*P\*GR\N\W\VL\T\PT\TER\GHP\G\I\FL\TV\G\SR\*D\A\N\Q\Q\A\F\G\H\G\L\FO\H\FL\VI\G\K\G\N\K\T\H\G\I\SL\PR\G\K\G\I\RL\H\H\I\LE\ER\DK\RL\A\AK\Q\SQ\W\G\EM\G\SL\G\VD\I\Q\I\FW\RN
19156	49524	A	19265	62	298	

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19157	49525	A	19266	1	555	MAWQMMQLLLALVTAAGSA QPRSARARTDLLNVCNAKHH KTQPSPEDELYCQ/SP/WMCKG SCRKTKSWNI/HRKSCKCEVGLA/ WEACSVSAGTGRGPCCGRWV GAPQGP/CPRKCSSG*PTW/VQR SQNMEEMA VNVNQSWRKE RLN VPLCKEDCERW/WEDCRTSYTC KSNW HKG WNW TSAPS AVCDP LL
19158	49526	A	19267	216	974	MDMAWQMMQLLLALVTA GSAQPRISARA RTD LNVCMN AKHHKTQPSPEDELYGQCSP WKK NACCTASAT SQELHKDTS RLYN FNW/DHCG*KWN PCTCKR PLYPQD SCLY ECL TPTLGPW WIR QFN QNS WRKE FLNV\\PL CKEDC ERW WE DCRTSY TCKSNW HKG WN W NTS GINK KGR PGAF* STFES YFPT PA AL CEGL LWS HSFK VSNY SRGS GRCI QM WF DSA QGN PNE EVA KFY AA AMN AGA PS RGI UDS
19159	49527	A	19268	345	2138	QRLTATSSWTTMAKNRRDRNS WG GFSEKTYEWS SEE EPVK AGPV QVLIV KDD HFS E DET AL NR ILL SE AVR D KEV V AVS VAG AFRK GK KS FL MD F ML R Y M YN Q S VD W G D Y N E P L T G F S W R G G S ER ET T G Q I W S E I F L N K P D G K K G K H F Q K L Y K L P W A Y F R S R G A * D I * R S N G G L K I T C R G L V E Y F K A Y I K Y Q G E E L P H P K S M L Q A T A E A N N L A A V A T A K D T Y N K M E E I C G G D K P F L A P N D L Q T K H L A T * G R N L W K L F R G V K K M G G E E F S R R Y L Q Q L E S I D E L Y T N I S S H I N D S K I N T F C P S S Y P Q P T L F C S H P L I T Y V I A G V T G F I G L D I A S L C N M I M G L T L I T C T W A Y I R Y S G E Y R E L G A V I G P R W L Q L C G T R E V Q M R P W N K L Y Q C Q Q A T P T D I L Y P S K P F P L H P K V G N L T E Q I Q K R K K M V M P K F

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19160	49528	A	19269	351	509	VVPLPPLPPLDSWTCESWLRSHI LTGESENPDHKRI*PYTSDLPEG PGPWATD
19161	49529	A	19270	781	4324	ESVREKVLCGLIQQTVTSVC/W SGTYIFAVLLVCFVVFHSGAQEK NYTIREEIPENVLIGNNLKDLNL SJPNKSLLTTTMQFKLVLVYKTCGD VPLIRIEEDTGEIPTTGARIDREK LCAGIPRDEHCFYEVAVILPDE IFRLVKIRFLIEDINDNAPLFAT VINISIPNSAINSKEYTLPAAVDP DVGINGVQNYELIKSQNIFGLD VIETPGGDKMPQLIVQKELDRE EKDTYVMKVVEDGGFPQRSS
19162	49530	A	19271	3	644	FRSLP RRCRCLPRWQPSSFLGHG PPFRRP CEA P KIVK KENPRK FIR APSQTGY\AKLSVN W RKTPEAI DN RVRV RRF\KGQILM P NIGY G SNKKVTKHM\LP SFRK F L VHN VKEPEIA DVA TNLTV P RSLTM FPPRN RKAIRGKG\ACPI GPF RSS PNPIARVAQQLKEN*VRQLMCN KSYCAEIAHN VSSK NRKA IVER AAQLAIRVTNP NARA Q
19163	49531	B	19272	27	161	
19164	49532	A	19273	80	430	RWLATHYLTVKLSSL PNLAVT CQPKREQNITSNESTD C*VIVTS TKSDSL YTVGML ALSVRAIRCP LYLLTGLIFVSKNDLWYCE LQS HYTVVLLL FMRKRSRFQSNVQ RKLMTNF
19165	49533	A	19274	482	832	RWLATHYLTVKLSSL PNLAVT CQPKREQNITSNESTD C*VIVTS TKSDSL YTVGML ALSVRAIRCP LYLLTGLIFVSKNDLWYCE LQS HYTVVLLL FMRKRSRFQSNVQ RKLMTNF
19166	49534	A	19275	121	20I	SMYMDEN* RLELITL* FSSMYM DHSLL
19167	49535	B	19276	I	II47	
19168	49536	A	19277	305	442	AGLF KSRKVSSICIRFE* ILT SCL GVRIST GKL VARI JHG SFADAE
19169	49537	A	19278	133	527	GFLER PRILIKVTL SIKQKSTS IF VGGQFSKFRFLTVL WAKCL SQP CF* A* TPASQHVS* SIRAISSMIS KRS ELL VRLWRRPSP* AGLFKS RKVSSICIRFE* ILT SCL GVRIST GKL VARTH HG SFADAE
19170	49538	A	19279	531	669	AGLF KSRKVSSICIRFE* ILT SCL GVRIST GKL VARTH HG SFADAE

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19171	49539	A	19280	80	428	RWLATPYLTVKLSSLPNLAVTC QPKREQNITSNESTDC*VIVTST KSDSLYTVGMLALSVRAIRCP LYLLTGLISVSKNGLWYCELQSH YTUVLLLFRMRKRSRFQSNVQR KLMTNF
19172	49540	A	19281	10	426	
19173	49541	A	19282	1	900	
19174	49542	A	19283	314	451	AGLFKSRKVSSICIRFE*ILTSCL GVRISTGKLVARTHGFSFADAE
19175	49543	A	19284	1	1139	MWGIGSRTPIYKILVYSSPEVS CEPKPYVKSQSTHTGFESHKR YIFYLRLVGKNLHVSAMGLGK SQERRKKALKSQPQQPADSFPS LPTVEGLTTSGEVAAGFWLSGE ALSSC*LLSASVHLLACLGMG KCSCSGFWLYF
19176	49544	A	19285	1	864	
19177	49545	A	19286	306	444	AGLFKSRKVSSICIRFE*ILTSCL GVRISTGKLVARTHGFSFADAE
19178	49546	A	19287	189	1089	HHTAHCQ*CWL*S/DHGINPLRS WVGTG*V/GVRGKVQYADLGA ENWKPISNLHDMSSSHSKTLGY KRLTKSNPISCQILLYKRSRSKGR KNQRSTRTRTHCHHPSK1YASA KEPWVLTATNLPVIEIRTPKQLVN IYSKRMQIEETFRDLKSPAYGL GLRHRSRTSSSERFDIMILLIALML QLTCWLAGVHAQKQGWDKHF QANTVRNRNGSLLTNPWPSVPP TIKEEENSEEELAATTSSKEQEP IGTDLDAVRTPEPLEEPKREDQ EGSPETSLPYKWWVVEANLLI PAVGSSLSEALDLIES
19179	49547	A	19288	1	549	
19180	49548	A	19289	80	430	RWLATPYLTVKLSSLPNLAVTC QPKREQNITSNESTDC*VIVTST KSDSLYTVGMLALSVRAIRCP LYLLTGLISVSKNGLWYCELQSH YTUVLLLFRMRKRSRFQSNVQR KLMTNF
19181	49549	A	19290	80	430	RWLATHYLTVKLSSLPNLAVT CQPKREQNITSNESTDC*VIVTS TKSDSLYTVGMLALSVRAIRCP LYLLTGLIFVSKNDLWYCELQSH HYTVVLLLFMRKRSRFQSNVQ RKLMTNF
19182	49550	A	19291	773	1015	AGLFKSRKVSSICIRFE*ILTSCL GVRISTGKLVARTHGFSFADASF STDLYHGTLPKASLTMSGVVLL GRMLARSARNWS

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19183	49551	B	19292	1	1488	
19184	49552	A	19293	2	133	YAQTDDNRRNLILNGTPLRRVK VLVFDIEYP**KVVGYNSTLA
19185	49553	B	19294	1	879	
19186	49554	A	19295	80	428	RWLATHYLTVKLSLLPNLAVT CQPKREQNITSNESTDC*VIVTS TKSDSLYTVGMLALSVRAIRCP LYLLTGLIFVSKNDLWYCELQS HYTVVLLLFMRKRSRFQSNVQ RKLMTNF
19187	49555	B	19296	1	1575	
19188	49556	C	19297	1	2187	
19189	49557	A	19298	473	613	AGLFKSRKVSSICIRFE*ILTSCL GVRISTGKLVARIHGSFADADT
19190	49558	A	19299	410	547	AGLFKSRKVSSICIRFE*ILTSCL GVRISTGKLVARIHGSFADAE
19191	49559	A	19300	876	1005	
19192	49560	A	19301	167	263	KLIEAIWSS*FITGSSLRHNERLG ASTSGEY
19193	49561	A	19302	258	396	AGLFKSRKVSSICIRFE*ILTSCL GVRISTGKL.VARTHGSFADAE
19194	49562	C	19303	1	1641	
19195	49563	A	19304	1221	1327	ALHPRNRHLHKERLGCIPVAC* LYLFGQYDAHCTC
19196	49564	C	19305	1	1353	
19197	49565	B	19306	1	2047	
19198	49566	A	19307	80	429	RWLATHYLTVKLSLLPNLAVT CQPKREQNITSNESTDC*VIVTS TKSDSLYTVGMLALSVRAIRCP LYLLTGLIFVSKNDLWYCELQS HYTVVLLLFMRKRSRFQSNVQ RKLMTNF

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19199	49567	A	19308	1	2597	MAMFMLLAALLSTFLTNDA LYTVVPLTILKRLCEIPYNRLL FEGAGSQRWFATDANWQPAK YSYLGTFWSFVCRIVCPNGTAG WRNDADAPAPVLMQVHTGV QTPEWKPRLLWSCLGLYIVFLT ALEFKQELWGVVIAAGFALL ARRVVLVSDWTLLLVFAMFI DVHLLTQLPALQGVLGIVISNV PSTILLNNYVPPSLLLVWAVNV GGFGFLTCRHARIAAPADLKD LAVHEKRETRSLTEKTKMMLLP KLGVGSRCCGNVKEVGIRAI EFGPYKINGDKEIMRRMDDLLQ GFDAQHMRMKLPAQPTSLATKS ARRVRYPLFCPSIFNGFFEEFIFH RFLAEQALEFFNLLHGGSKFRG RNNLFSGGDSSRKNQRSTRTHC HHPSPKIYASASAKEPVLATNL PVEIRTPKQLVNIYSKRMQIEET FRDLKSPAYGLGLRHRSRTSSSE RFDIMLLIAMLQLTCWILAGV HAQKQGWDKHFQANTVVRNRR CKMATLKEKLIAPVAAAAATVP NNKITVVGVGVQVGACAI SILG KSRA MEHTTAGAPYTPRQQT QC NMSL ADELALDVLEDKL KGEMMDLQHGSLFLQTPKIVA DKDYSVTANSKIVVVAGVRQ QEGESRLNLVQRNVNVFKFIIP QIVKYS PDCIIIVVSNP RDILTY GTWKLSGLPKHRVIGSGCNLDS
19200	49568	A	19309	435	777	RWLATHYLTVKLSLLPNLAVT CQPKREQNITSNESTDC*VIVTS TKSDSLYTGVGMLALSVAIRCP CRLVDWADIPEQKQLMVLRAS VALHGRSVTLYEKAFFA FRAM FKRSS

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19201	49569	A	19310	69	1270	LCLLRHD CYRGLQSLLL LCKM ATLKEKLIAPVAEDEAATVPNN KITVVGVGQVGM A/CAISIPGK VSWPDEL\ALVGCFWEDKLG GNDGSFQH GELIFFQT*NCGQ DKGLFL*PANS*RFVSW*LAGS PVQPRGRIRLQLSQWPEKWL VFQIPLFLKIVQVQSLICHIIGGFN PQLDILTYVTWETKVGGLPKHR VIGSGCNLDS\ARFRYR LMAEK TWHFIPSSCHGWNFGGNMGDS SVAVWNG\VN VAGVSL\QELIN PENGNL\TNDKLKIWKEGA*IW WLKSA\YEV\T\KLKGY\POLGAI WI*VLAESYWNPMKLKSYPR\I HPGCPTNG*RQGMYGHWRME SPSLEPSLCIPQCPRGLNPAVIQP RSLKDDEVASASRKSKARAPILWD NPEWTLKRPLT
19202	49570	A	19311	52	406	HVEAAGSR*CAA PAG ALLRFLG TPSFEDVS\PEPKPKLRFIERAPLV PKV RREP KTLSDIRGPSTEATEF TEG\N\I\A\L\G\G\G\Y\L\H\W\G\H\ F\ E MMR\LT\N\R\SM\DP\K\N\M\FA\I\W\ R VPAPFQAH
19203	49571	A	19312	1	783	
19204	49572	A	19313	15	397	LLAEWTM GHTPVGGRGAISL DAAP*EQGTM LVS WLCDLFLV LRLVVGKT VSSKKNIFERVN GDG KHENIPMSSPPRSWPFSEKRF TN RRKTTSHQLNVLGA VSLRQH WRGGVPRNL TRAPAGAAH
19205	49573	B	19314	127	181	
19206	49574	A	19315	242	1067	CAAPCGCPCQIPG\ALLPASAGV KTLLPVPS\ FEDVS\PEPKPKA*DL LERAPTC\AQK*RREP*KFKV\TIR GPISH*KPTEFYRKAI\FAILGIGV VGY\LHWG\HF*K*WRLTIQPAL WTPRTWFAI\W\RV\PA\PK\PI\TRK SVGASHGGEAKGAI*HYLTP\ V KAGRLV\ VEMGGRCF\ F\ A\ S\ A\ K V\ S\ L\ T\ Q\ V\ A\ L\ R\ S\ C\ P\ F\ A\ S\ K\ R\ L\ *ACG TPREGCEQDQEERERQQPRT\ PW T\ I*AE*PTA QHG\W\ A\ Y\ G\ K\ V\ P\ E\ P\ H MTLTPQGEIL\GARFYMPK\TCV V S\ V\ G\ D\ I\ L\ Y\ I\ G\ Y
19207	49575	A	19316	1	520	

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19208	49576	A	19317	104	763	SAAADGPDRRLRRRPPANLARP VLAPASATASARRACSPHPQT MSESKS SCPEYASFFAVMGASA A AMVFSALGAAYGTAK SGTGI AAMSVMRP PEQIMKSII PVVMA GIIAMLRPGWVAVLIANSNDD ISLYKS FLQLGAGLSVGLSLA QPAFA IGFVG DAGV RGTA AADIFRGA* FLI FAEVRLIY GLIV A LILFI KVDLFRAHQPT
19209	49577	A	19321	36	164	
19210	49578	A	19322	190	743	NDRGKEGS LSTVPSI RTDSGH LAPRRKPQLLKP SLNTSPKAR KIHKG HEHEVASAGGN PPA PILP KVPP* FNIHRRGPPWPDHVRFG SLF NTLFL NW CCLGVSLA FRL LP* KSRDTGKMLG DVEPG AQ ALCLPPPKCLN I WALIL GIL MT IGFIL LL VFGSVDSL TILWFQI Q GKTGGY
19211	49579	A	19323	2	257	
19212	49580	A	19324	1	1227	MGRARKSGL GQRSPRTASRSEA AVQPGVRKARGAGN WRVGLQ TGEAAPSPHRDLR DTPDPRPW L ARTHRM TTL VSAT FDLSEVL CKGNKMLNYSAPSAGG CLLDR KAVGTPAGGGFPRRRHSV LPSS KFHQNQLLSS KGEPAPALSSR DSRFRDRS FSEGGER LLPTQKQ PGGGQVNSSRYKT ELCRP FEE NGACKYGD CQFAHG IHEL RR LTLHTKD* TELCRTFHTIGFC PY GPRCHF IHNAE ERRALAGARDL SADRPRLQHSFSFAG F PSAAT AAATGLLDSPT S TPP V LSADD LLGSPT LPDG TN NP FAFSSQELA SLFAPS MGLP GGGSP T FLFRP MSESPHMFD SPPSP QD SLSD QE GYLSSSSSSHSGSD S L D NSR LPI FSR L S IS DD
19213	49581	A	19325	204	456	
19214	49582	A	19326	1	323	IVEYH GP V D S S CTGMATCN MGA E GAT TSV FPY N H RM KKY LSK T G RED IAN LA DEF K D H L VP DPG CHY D Q L IE IN L SEM V P DM LP AP R LA H G V T V V V G FLK
19215	49583	A	19327	2	131	
19216	49584	C	19328	2	283	
19217	49585	A	19329	1	206	
19218	49586	B	19330	217	435	

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19219	49587	A	19331	1	565	PWE*SPKGIGVSCGPLSGWS/SP KD\VIKVQ/GILRKGKGTQIV ESTGLG*TPFSCTGMRQFCNMG AEIGA\TTSV\FPY\NHRMKKYL KTGREDIANLADEFKIDHL\VPDPP GCHYDQLIEINLSELKPHINGPF TPDLAHPVAEVGKVAEKGWP LDIRVDALACQS\LAFAA\WVQ CGCEEHGAWSQMAWA
19220	49588	A	19332	117	2603	GQHCLLPWGVPFPFLKKALGV RQ*\HVASVLCQRARVAMSHFE PNEYIHYDLLEKNINIVRKRLNR PL\TLSE\KIVYGHLDPPASQEIE RGKSYLRLRPIDRVAMQDATA Q\MAMLQFISSGLSKVAVP\STI HCDHLK\EPQVGGEKD\LRRAK DINQE\VNFLATAGAKYGVGF WKPGSGIIH\QILENYCVPWLF *LGPDFH\TPNGGOL\GGG\ICIGSC GWPNAWEWNGLGIPWELKCP QVIGV\KLTGSLSGWSSPKDVIL KVAGILTVKGGTGAIVEY\HGP VDSISCTGMATICNMGAEIGAT TSVFPY\NHRMKKYLSTK\GRE\D IANLADEFKV\H\LPDPG\CHY EPTELK\INLSEL\KPHIQWGPFTP DRGSPCWQEV\GKVGREGKGW PL\DIRGGS*LVA\TNFKLWKI GRSA\VAKQALAHG\LKCKSQ FTITPGFPRQ\IRATE\VRDGYAQ ILRD\LG\GIVL\ANACG\PCIGQW DIRKDK\RMGEKNT\VT\SYNRN FTGRN\NDP\NPE\THA\FT\SP\PE\VT ALAIAGT\K\VN\PE\TD*PDGAR MGKKFQAWRF\PD\AD*VFPKG EF*PRGRD\TYQ\IPPK\DS\SG\QH VGT*APRSQRLQLLDPFDKWD GKDLED\Q\ILIKVKGKCTTDHIS AAGPWLK\FRG\HLDNIPN\NHLL IGA\NIENGKANSVG\NAVTQEF GPAP*QLAR\YYQETLASRLGW
19221	49589	B	19333	1	1311	

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19222	49590	A	19334	2	1390	PRVRPRVRARPTKMSALGSLSPVLWGQLF\AVDGSNDVTDIA DDIGCPKPP IAHGYVIEHSVRY QCKNYYKLRTEGDDGVYTL/NTI EKQWIKLRLFGD\KLP*IVEADD GCPKPPEIAHGYVIEHSVRYQCK NYYKLRLTEGDDGVYTLNEKQ WINKAVGDKLPECEAVCGV\KPK NPVANP\ VQDGPVGHLUDCQRS FFPWARLKDGFPHH*SSTHQGP RWIQLNQWLA*PRLKNNLLSLN H\SENCQQRKD CPYF\HFMWG KKQLVGD*GRLFLQP\ .TPRVD IGL\IKLQTEGCS*LRRVMPICL PSKGLWQK*GRVGLCFLAGGR NAQF*NLLTHLKVCPCCPVA*P KTQCHKAIYERPSNKSPrKRKN TRKKPL*GVQAPILK*NTPFLCL AMS*RYPKERHPAYG\QNAGAS ALCPFHRPLEEDTPGMP\TGI\ S FDKSICAVA\ EYGVYV\KVT\SI\  DWVQKTA
19223	49591	A	19335	65	665	GVRGFWAGTMASRAGPRAAG TDGSDFQHRRERVAMHYQMSVT LKYEIKKLIY\HVLVIWAAA\WLL R*AVGHPEALV\DMIRWPCPIQ WE\YPVFC*AF\PLSLLG\PSFP\PR NNIRLTWVL\YHESSMGIFFSIG SIHFIGQHGDPW\HSSFYRHG KAYRFLFGFSAV\SIMYLV\LVLA VQVHAW\SLYYSKLLDSWVH QHTGEEA
19224	49592	A	19336	65	665	GVRGFWAGTMASRAGPRAAG TDGSDFQHRRERVAMHYQMSVT LKYEIKKLIY\HVLVIWAAA\WLL R*AVGHPEALV\DMIRWPCPIQ WE\YPVFC*AF\PLSLLG\PSFP\PR NNIRLTWVL\YHESSMGIFFSIG SIHFIGQHGDPW\HSSFYRHG KAYRFLFGFSAV\SIMYLV\LVLA VQVHAW\SLYYSKLLDSWVH QHTGEEA

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19225	49593	A	19337	71	1265	RCSKSLRMSTFFSDTAWICLAV PTVLCRTVFCTYKKSSQGLWS WMVCLAGLCAVCLLILSPFWG LILFS\SCFLMHLYLSQ\ELLPV DQKAVLPTGGDCGLDHALSKY LDELGFTVFGAVLNVENGPGAE LRRTCSPLRSVLQMDITKPVQIK D\AYSKVAAMLHDRLWAAIN NAGVLFGPVTDGELLMTDYQR CMVVNFFGTVEVTKTFLPLR* SKGRLVNVTSMGGGAPMERLA SYGSSKAAVTMFSSVMRLELSK WGIKVASIQP/GEGFLTNIAGTS DKW\EKLIEKDILGPPPLRVRQE DYGQDYILAQRNFLLIINSLAS KDFSPVLR\DIQQAILAKSPFAY YTPGKGA\YLWICLAHYLPIGY DYFAKRHFGQDKPMRPLRMP NYKKKAT
19226	49594	A	19338	1	861	
19227	49595	A	19339	248	930	DVHQLGNMAVIHSHLWEGLQE KFLKCEPKVLGVVQILTALMSL SMGITMMCMASNTYKG*PLFP CISGYTIWGSVMFIISGSLISAAG I*NTKGLVRGSLGMNITSSVLA ASGILINTFSLAFYYISITPYCNY YQQPPN*LSMGTMSHLKGWV MGMVLLSVLEFCIAVSLSAFG M*SALLVPPGGGCVNSAITFT WAETASSTTLNEGLRGTORFNR QMLPEIYA
19228	49596	A	19340	167	1164	RNLRLPSSALAGVAPSHREPRV RTISQTDRRKDA/PDPAARRDRVE LAPAYTSPPRCSANVGTSRRL RALCPARVRAPIRLPPLPSSPLG SEEQRKVPAAARMRPRAGAG RSTLPWLPA\T/WPGLPSLPLYL* ICGGINNSY*R*RKGEQFE*RNSS *DYRYLPSSPASPVN\ERQPNE NGPDDEKEKDRPERPSPLDTSP LDPPAVSDIAGKMSDEFSLADA LPEHSPAKTSASYPDHMVLPTD PAAAGPLGPWGSMSSGPWVPG MGGQYPTPNM\YPSPGPVPP PPQASGAAPPVPGTVPLGA GPPAPY\PAPIGSYPTPGLYPTPS NPF

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19229	49597	A	19341	2	716	SDPSPLLDPTAVSDIAKGKMSDE FSLADALPEHSPAKTSAVSNK PGQPQQGWPGSNPWNPNPSAPSS VPSGLPPSATPSTVPGPAPTGM YPSVPTGPPPGPAPPPSGPSC PPPGGPYPAVTVPGPPTGPYPT PNMPFPPLPRPYGAPTDAAAG PLGPWGSMSSGPWAPGMGGQ YPTPNMPVPSGPVYPAPPPPQAP GAST/LFHGAPFPPGAWGPPA YPAPTGSYPTPGTLS*FPPGAW GPPAPYPAVTGSYPTPGTLS
19230	49598	B	19342	54	178	
19231	49599	A	19343	3	249	RHKGSPSPHQTQEPSWLHPVDP ALGPQVELPASLVLCARTQPL GGR*DWV/PGTAGQESRAAP VPASAPPSTPRGRGGRI
19232	49600	A	19344	2	504	WAPVPRPEPPRRAPPAPQRPVP STTQGLRSAGA/PAPGLAGSYP CSPGVVNAPIDSLYLATFMGIR VKRPPNR/PLCEQ*SFYHLGAGE *PGKSRVPPIPQFQSP/GDPTVVR VPRR*SVPPTSCATPRSWCCSD TPGHPGLSPEQLPQPGPAAELP GGVVRPSTPPCPAL
19233	49601	A	19345	3	335	
19234	49602	A	19346	2	447	CACTPQPLGGRWDWAPWSRG RRSSGRLRLHNRNRRRGKAQA WRAAVPRPAPREGS*PGPRPAA PSAGPPSPRPQGTAGQAPRAA PVPAAPRLPQPHLPAS*GSSLRSP AQKGAPTVQ/PVG*RAPQVPPK WEPRQRERRARAVRTA
19235	49603	A	19347	108	729	QHAGSPQSPRLLSAPPPLPGLPL WWHLRSPSAPPPLHCGSPFLGW RLEPTPSACREVVWRERHKWEP G/PACGACGPAGVPGGRG/PWW APHSEHPSAGPAGP/PMGNLAP GPVAAEGVLSPPAVPAHRRCAR FLAGP*L/PFRGRAWDLQAM PEPPTPPWAPV/PAEPP*RAPPP APQRPVPSPPKGQAQDWQAAPP AAPVRDPLGEASWAPE

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19236	49604	A	19348	1	816	MWESLTLSRDFLNGFDQNADS GIDNKVQVEVASDEDDELVGN WNKERENPFSGEKLKPAEICIS YKEPNANHQDNGENVARACQ RPLQHPLPSQAQPRRKQRFPQ PGSGPTWDLVPCIPGAP/RLD*K GPRKPKSWYSEGQRYESPFGIP LGSDLFPTNALLLKPYKLPPSR PRDYCGRAAFPRGRVRDLQPA MPEPTTPWAPVPRPEPPR*APP AP/PAPSPIDHPRAAECEHTAQD WQAAAPPAPVRDPLGEASWAP ESGGDVESLYV
19237	49605	B	19349	4	669	
19238	49606	B	19350	1	930	
19239	49607	A	19351	170	444	
19240	49608	B	19352	1	1122	
19241	49609	A	19353	1628	3591	KGLRLKLCSFVQLRFSIRNFRGL ILTYWKKEFEIVGVWPRLEPTPL ACREWRERREREPGLRAALA GQLEFRVGVLGLAGPSLGAAGQ PCWPVIRDLAPGPVAEGLVG PPAVPAHRRCAFGFLTEP*LPSRG AGLGTCSPPCLSLPPTPWAPVPRP KPPQRAPPAP/PAPSPIDHPRAE ECERRAHDWQTAPPAALVPDP LGEASWAPESGISDEYITPMFSF YKSIGELKMTQEYALLTAIVIL SPA WATERHPVFKRERKKPSN CLEGVIAAAELAVGLPWNLG KFHTDGTSAGLOGIAPNSVGP GQPAPEWM/WGWERLLTDQDK TQGSASFCTATFQDAQKQLLQ ARFIHLSGLWEQQDGLWLSNW LSLKGQIGGGPALTEPLRLSVNR GTWPPKLRDARRRSAGRADRR APTGRVLPGSPGAGPQTTTPPPY DWSLRNRRRPAATDPEAQAAA AAAAVGQGRVGPQAQIEPSCRPA GRSDPPAPGPEAEVCVWSRRLRE PVRSafaWLRQSRALIGSWGR QGDVAPAFTCPPNAERGATGV RGGWGCWCGRAQLGRRDPAA TRPALNPERYQSPKMSQGLERP HVRNWGIELETLRDAFRPQPSV WRTARGEAGKRKGRLVECLGS QRKVLEGVLLYAVTRGSFPNLF
19242	49610	B	19354	1	412	

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19243	49611	A	19355	951	1453	FQTQEWSLHLVDPTPGLQVEL PASPVPVCAHIPQPLGGRWDWP WSRGWCCSGRLGPHRSPWGSW EAQAWQAAQGPEPCPMDRQVRP GEKSSAVPVGQPG/SGHSVHPP QPLARVLSPPLPGASRAGRLLR VWGPSPSRRPPTPAGPQARHTA PVPARASPSTPPCKLR
19244	49612	A	19356	111	658	LPSRGAGLGTCSPPCLSLPPTPW APVRPEPPQGAPPAP/PAPSPID HPRAECERTARDWQAAAPAA LVRDPLGEASWAPESGSGEPTPS GPGVAGSGSTHTHALTHACTH AHTRAEPRLPFFFFPPLPPLSPP /PPAPLLPSKPFSLSTDRISSKSR QQKVPFGPDRPEPRGVAGSW NRITH
19245	49613	B	19357	1	552	
19246	49614	A	19358	1299	1813	AHFPRAGTGAACSCACWPAVG GGRGLGGPRTSSRPCWPRAK GDLAPGPAAAEGVLGPAAVPA HRRCARFLAGP*LPYHGAGLGT CSPPCLSLPPT/SGSCAPEPPRR APPAPRHPVPTTQGPPWETC LLSIYGNAMNDERAWSLEGFW VLPKPSDSWMTSLERTISFF
19247	49615	A	19359	380	905	WIPHWGCRWSCLPVLLRRAF LSPWVVDGTGRRGVGSGAGRG GSGRTGAHVGVGLRHGGLQV PSAPAPREGS*GPARNRAQPGGP ALLGDSVHPPQPLAQVLSPPFP GPAGLAGCSECRCPPSPRPPGTP AGPQAPHAAPVPARASPSTPPL VHLTNVDLRVKVKWAFFTLH
19248	49616	A	19360	1	1052	MGLAERCPLNHLTLTVSSVKCS FLLAHILSVAGACYGVLRGAPH TFPGITCPGCSQENNPIKKWAE DLNRHЛИQEDTQMANKHLKDA PHRYIIRELQVKPTMRYCHAPT GVAHQSTNTPNAGEDVEHQEL TFIADGSPVITRGHMDLVQTS SRTLGVRSTGWSACAEFSHY CLAKRLLQLKHGNGNNSGG NAECITRHCQKPLTGILSFLAL NKVKNTTRPFDRCHSEGSEKEPS FCVTCPRRPEVNQSPSPYMPQPG KSSTHLSVVLQRALEVGEQAF PPVE/PEGFAGLRHPLWL*V*GQ GSGP/SSPPCLSLPPTPWAVWP EPPRRAPPPAPQRPVWURPPKG

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19249	49617	A	19361	417	1092	KWCSKRTAFSFLQGGVGEA RAGTRAACGACGPAGVAGRRG LGGPPHSGQPSAAGPG/PVRLD APGPVAAEGVLGPPAVP/APPA LCSIS/PPGSCCLPAG/PRRLRTCP PCLSLPPPWPAPVRPKPPR*ATP PAPRRPVPS/T/NPRAEECGRTAR DWQAAPPAAPVRDPLGEASWA PESGGDVENLYVQLRDCKYTN QHPVSSSGFVNAPISTLYLVNL VGTWRIFMSS
19250	49618	B	19362	817	1596	
19251	49619	A	19363	350	644	
19252	49620	A	19364	60	1362	SRVEPRVRSASQDSSRSRDRNGPD GMEPEGVIESNWEIADS/FDD MNLSESLRGIYAYGFEEKPSAI QQRALPCIKGYDVIAQPQSGT GKTAATFAISLQIYELDLKATQ GLGS*APTR/RENLAQQIQKVVM ALGIDYMGASICHACIRGAPTC VAEVQKLQMEAPHIIVGVPGLG RVFDMLYRRLYI/SPKYIKMFV LDEA/DEM/LSRGFKGQIYGHIQ KAQAAPRVVLLSATMPFD/VL EVTKFKMRGPH/IRILVRKEELT L/EGIRQ/FYINVEREEWRDLTL CDLYETPDPSFQASHLPSSTTRR KVDWPHPRRMHALRFPWESAQ HEDMAQKERR/DVIMKEFRLAS SRVLIITDLLA/RGIDV/QQVSL SHQLNY/SFPITRENYIHR/IGR GGRFQ/RKGVPINMLTE/EKTKR NLEDIETFVYNTSIEEPLNVA
19253	49621	A	19365	911	1278	NCGIVISKHLVFTLA*MMCHFL ASLQRKGILKRSASV*AHSH/DP SFHMKIYNAQW/GHRT*HPAGG FAGPPPWGSVWGLAARTRENA PRPALPLPRPAPSGLAHGADGD SNTEKIQSRDNRKG
19254	49622	A	19366	26	743	ETSAADMPSVPAAE/PEYPKGIR AVLLGGPAGAGKGTQAPRLAEN FCVCHLATGDMRLRAMVASGSE LGKKLKATMDAGKLVSDEMV VELIEKNLETPLCKNGFLDDGF RTVRHAEMLDDLMVEKREKELI DSVDLNFSPIDSSLIRRITGRLIH PKSGRSYHEEFNPPKEPMKDDI TGEPLIIRRSDDNEKALKIQLRQA YHTQTTPLEYYRKRGHSAIDA SQTPDVVFASILAAFSKATS

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19255	49623	A	19367	40	1002	VASGTRTELQDRRFRDTSGDM FPSVPP*EPEYTKGIRTVLLWPP GAGKGTQ/SGETEV*MACSLGY IASNLQLHLNDSKAPALSAAIY CPRHPNWAENFCVCHLATGDM WRIAMVASG/SSELGKLEGNL WDGWGNWVE*WKWVSWSSF GEGILENPLVAKNGFL/DGPPS GPVKARQK^SPMDLMGEGGKE KLDFC^*FEFSIP^DSLL^IRRNHKE GLIPPPKKWAGSYPRREFQPLP KEPP^KMNTGGNPLRIRRSR^*M KRPLKIRPASPHTQTVTPLIEY YRKRGHSTTDASQTPDVVFASI LAAFSKATCKDLVVMFI
19256	49624	A	19368	793	1152	SGRKRRGGGGSVKQAPALTP GPPAPVFPPIPEAPAACAPHHIPGQ GNRRKCNFPVVCP^PKTASSCP/ EPLPPPPSLQR^*PCPCHPWHHLE FSFLDEVTFSFNKTFPKRLVSSK MLPLKVGH
19257	49625	A	19369	1	873	
19258	49626	B	19371	1	322	
19259	49627	B	19372	64	2250	
19260	49628	A	19373	20	368	CEARGGSGHGGRAERAGVCGG PAELLPKGSKKEEQRDYVFYLV GNYRLKEYEKALKYVRGLLQT EPQNQNQAKELERLIDKAMKKD GLVGM/AIVGGM/ALGVAGLA GLIGLA^VSKSKS
19261	49629	A	19374	3	492	
19262	49630	A	19375	62	570	GSRGQWPSEAVLNELVSVEDL LKFEKKFQSEKAAGSVSKSTQF EYAWCL^VRSKYNDDR^RKGIVL ^EELL^PKGSK^EE^QRGFTSFYL ARGGGTTRLQGITEKALKLRS GLLAAQEPQEPRPKETGNGLI DKA/L^*KDGRLGA^WPIVGGM ALGVLAGTCRSSSDFAVFQ

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met/Asp	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
19263	49631	A	19376	1	944	MACHILQAGSPGNI.VVVFQSKP EGLRTREPMMSVPVQVKGPST RKLMMSEDPLTLGNWHELRVS RTAKNGILQVDKQKIVEGMAE LQQVVGKNMDSGVPVVGPHGG GLTRTGYLLNPESLQQKAFERR QIQGCDKEKLACVGKQTLGTWP LSESPLSLTRLYCRRQLTQGSLR MSLNNAGVPGQTAPDQRSGEG VAAAPAGPGEEVVGREEEGEAAA GKRQCPQCQGSCLVDTSRPRLP KSQAQIPSSRSSPSSSEQQRGQ LPSVREHVEGGQGEERAPHCD GGGRVVLLASGLAWLGTENIMD LASSPKDDWGVAVPSRGCREPS TFTLVLVPSPIVRRACSGQPISP GGGQETHGADTSHLTNP*ICLL SKAFCCRDGSLSK*PVLVRPPC \PQALQPSPCSYLLAVALPEPP LSSAYPPVRFHSLLCIEHARAS
19264	49632	A	19377	1177	1603	WVSSFSSSSFSFSPPPPPPPPPPP PPSFLPPPPPPP/PP*DRARRCQQ TSIPLNKLNLINKLULLLSPRPD DREKFTPQPQSQARQREPIKGT SRRGEGLPICPTLSDLYFLHVFLCF SCLSSQIHIYILRLSTVLLVLIKNS
19265	49633	A	19378	1	896	FPFLLLPPPKMPKGKKAKGKKV APAPAFVRKQDAQE*WLNPLAF KKRP*DFRIGQ\DIQPKQRPPPL L*KWPRIYIRLQR\QRAILYKRL K\VPSTAIPVSPRALDPANQLS LLKLAHAKYRPRDKAQRSKQR\LLA RAEKAA\GKGDPRNQRD PPVLRARS*HPSPTLVEEQEQLS WVVA\HDVDISIELGLSFLA\AL CRKNNGSPYCIKGGKGQDILGR\LV HRKDLAPLVAFTQVN\SED KRRFWLKLVGSYQGPVN\YNDRY RYDEIRRHWGGNVLGPKSVAR AKLEKAKAK\ELATKLG
19266	49634	A	19379	3	491	AKEALDWEEGHQ*DQR*SRN SQLGICGGLRGFRGDRAASVFS R*AEKESVRQL*ARVPGALGVA ARANKHQRRR\WREGDSTQATN TVDRRATRGRPMEWWRATRVAD EEDGDRRRGDNRPQARTFPRPT SVRRAAGTNNSEGRRTNAGT NGGRGVDIYTVN

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19267	49635	A	19380	1	1501	MRRSTPGVLPAAVGGARVRRA VGLSGTGAEAGRAGAMVEKEE AGGGISEEEAAQYDRQIQLWGL EAQKRCHRMRKCALSTAPRTDK ETHPKVSLAQVTRSSASVMVY GAFEVIGQRQSSAKPRRSQSE SLGPEFQQLWEWLPASQHIMRSL LKKQDGMGQGQYRVSLEWEVG QLIFEEKVTP\EDPGAQFLIRT\Y GSVGRNRAEASLRAQFNPNP MV/DMLKVDTDED\EKPKESFFT QFDAVCLTCCSRDVIVKNDQIC HKNSIKFFT\GDVFGYHGYTFA NLGEHEFVEEKT\KVAKVSGV EDGPDTKRAKLDSSSETTMVKN KVFVCPVKF\ALDGWLADACDE MQMAALKRTTSDYILLQVLLK F/RTDKGRDPSS\DTYEEDSEL LLQINGNDVLDLSLGISPDLLPEDF VRYCF\SEMAPVCAVVGGILAQ EIVKALSSAGTLP\PTTNFFF WA*KGEWGLWECLGPQVNNS FGQPORCQLQAHLYSLFPFM
19268	49636	A	19381	2	411	PGTSQGVFSPHRLGGAVRSPCP PPQDSRQASAGGAESQLKQRG FPGE*GCRSPVSCAWPQNRMG* GPQHREAGAWSGE*KTPIWLK QERCNRPGPLLVTAEAAAPAPRP DGMAPGCGGIRCTPGRPRRLH SGPPSP
19269	49637	A	19382	165	309	
19270	49638	A	19383	1	825	LATQPEGAGRVPsiHPPQGGPEA ALQDLRTLMGSSRLHSKGESIG HNSSAGSSSQGP\HPRRKTAIL EKGGKQPHRMLPFPGLGSSPE PANAGSPDTWLCP\AAARVL* NPVKPRKGRSEPRSGWASQLPG GDSRLPLRPGTSQGVFSP/APAG *AGKLVLGVLSLSLKQRGFPGE *GCRSPVSCAWPQNRMGCRTP GPSPSTPAAGE*GSRPRRKPG RVQGLQRDGPTLTQEDALAA KRCPLPVTSVPQTPESTGAAA PGSQPVGAPPSR
19271	49639	A	19384	1	378	

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19272	49640	A	19385	381	1653	QRPRSGTFTMGRKSLYLLIVGIL IAYYIYTPLPDNVEEPWRMMWI NAHLKTIQNLATFVELLGHHP MDSFKVVGSDDEVPPITSDENV TVTETKFNNILVRYVVPKURKS *STKEGGLFYIPCGGWRRGSYS LIVYDLPSSWTVIRPGSSLVSN HJRLAT*FHPLQLGELYDAL R*FLRKVLAKYGCEP*GESGIS G\DSAGRGI*LSAVTQQLL\DDP  DVQDPNFKIQS*IYPLASASWM *VLPSEYQGKFKFSYFSKSLQIC RFWSEYFTTDRSLEVAKMLSRQ\  HVPVESSHILFKFINWSSILL*E GLLKGH\ VYNNPNEYSS\ELAK KYPGVLDVRAAPLLADDNKLRL GLP\ LTIVITCQYDLLRDRDGLM YVTRLRNTGVSG*LNNHVEG\  GFHGAFSFLGLKISHRLINQYIE
19273	49641	A	19386	3	667	DAWADAWVVPVSSEVAYLFGG CHTCGGLPVAHPMMPRGSRSR TSRMAPPASRAP\ QMRAAPRPA QVGQPPAAAPPSAVG\ SSAAAAP RQP\ GLMAQMATTAAAGVAVG AVGHTLGHAI\ TGAFSGRK\ P PARP\ HHFNQEASG\ TPPAQHSK QQRHPLQQCPYIEIQTVFWE FCPGTRGDIQAL\ CEGNEIVLK Q\ CRLANGFGPNEEVSTFGRD WKFSSHNLs
19274	49642	A	19387	81	1257	RHQSDQTVPRLSRPHVQSQKSS MAAAAKPNLNLVHGPGLDR LENYPIPEPGPNE\ VLLRMHSVG ICGSVDHV\ WEYLS\ RFGNFIVK KPMVLGHEASGT\ EVGSSVK AP\ NQGDRVAIEPGCSPEEN\ W NSC\ KMG\ RYNLSPS\ IFCATPPD DGNLRCRFYKHNAFCYKLPDN VTFEEGALIEPLSVGI\ HACRRGG VTLG\ HKVLVCGSWANRGWVT LLVAKAMGAAQV\ VVTDLSATR LSKAKEIGADLVQISKEPQE\  ARKVEGLLGCKPEVIECTGAE AS\ QAGIYATRSGGT\ LVVGL GSEMTTVPL\ HAAIREV\ DIKG VFRY\ CNTWASGGFSMLCVPKS V\ NVKPLVTHRVS\ WRKVLEA FETFKKGLGLKIMLKCDPSQN
19275	49643	A	19388	2	431	

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19276	49644	A	19389	2	326	ARGSTRLMESRVQHLY*CTRKELETPEVLQEWLDEEMLMLVHMPRFRIEDGFSLKQLQDMGLVVLDFSPEKSKLPGIVAEGRDDLYVSDAFHKAFLEVNEEGSEAAAS
19277	49645	A	19390	2	368	
19278	49646	A	19391	1	2123	MAQFSIVGMCLGLFNQSPTDGSGVQLFVIMNQVMAANLAETHAALCPPTSSGTSARFRGKQNQFSGGLPQITLSPLAQPCGRLAAMYSNVIGTVTSGKSLPSTSPLVPLLLSGFAPFLKGQLQNWTQTTQEGKSPSAAPASSQPQACPTDHVRE SALGACLSLPGEDGKJIKVYLLSLLIGFWDCVTCHGSPVDCITAKPDRDPMNPMCYRSPEKKAT EDEGESEQKIPPEATNRRVWELSKANSRFATTFFYQHLADSKNDNDNIFLSPLSIISTAFAMTKLGACNDTLQQLMEVFKFDTISEKTSQDHFFFAKLNCRLYRKANKSSKLVSANRLFGDKSLTFNETYQDISELVYGAKLQPLDFKENAEQSRAAINKWVSNKTEGRITDVPISEAINELTVLVLVNTIYFKVLRMALERPQGLPLALQLTPFFFWRDRSPERANGLPKATQGLWKSFKFSPENTRKELYKADGESCSASMMYQEGKFRYRRVAEGTQVLELPFKGDDITMVLILPKPEKSLAKVEKELTPEVLQEWLDEEMLMLVHMPRFRIEDGFSLKQLQDMGLVVLDFSPEKSKLPGIVAEGRDDLYVSDAFHKAFLEVNEEGSEAAASTAVVIAGRSLNPNPNRVTFKANRPFLVFIREVPLNTIIFMGRVANPCVNLSSEALAVLVVNLTLMKRTHGESLDFMERKRRPAESILL

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19279	49647	A	19392	9	1630	PALCPITLSSGTSARFRGKQFS GGLPQITLSPAQPQGRLAAMY SNVIGTVTSGKRKVYLLSLLD SFGDCVTCHG!SPV!DCTAKPRD IPMNP!MC!YRSPEKKATEDEGS EQK!PEATNNR!RVW!ELSKANF PLLLTTFLFSTWADSKD*H*LT FCSP!S!FQGFL!WTK!VGA!CD TLQQLM!EVFKF!D!T!S!EKT!SR SHFFFA!KLN!CRLVYRKANKSSK LVSANRLFGD!KSLTFN!ETYQ!DI SELVYGA!KLQAPGT!S!R!N!E!C SRVAA!NKW!V!S!N!K!T!E!R!H!R C!F!P!S!G!R!P!F!N!E!L!T!V!L GACWK!SKFSP!T!R!K!E!L!F!Y!K DG!E!S!C!S!A!S!M!D!V!T!R!E!G K!F!R!Y!S!G A!W!E!G!T!Q!V!L!V!V!C!P!F!K!G!D!D!T! M!V!L!I!P!K!P!*E!G!A!W!A!V!E!K!E!L!T! P!E!V!L!A!K!S!G!W!D!*F!W!R!E!M!M!L!V H!M!P!R!A!N!E!D!G!L!Q!V*!R!E!Q!P!A!K!N M!G!P!L!S!D!L!F!S!P!R!K!S!P!Q!T!P!G!V!A E!G!R!D!P!P!M!S!S!D!A!P!I!R!H!F!L!E!V E!E!G!S!E!A!A!C!K!Y!P!L!*L!P!G!R!S!L!N!P N!R!V!T!F!Q!G!Q!Q!A!F!P!W!F!I!R!V!P!L! N!T!I!Y!L!H!G!A!E!L!A!N!P!C!
19280	49648	A	19393	3	737	
19281	49649	A	19394	1	705	
19282	49650	A	19395	2	757	
19283	49651	A	19396	1	1764	
19284	49652	A	19397	1	710	MAWALLLLTLLTQDTGWSAQ ALTQPASVSGSPGQCSIT!C!TGT NN!DVG!S!Y!N!L!V!S!W!Y!Q!Q!P!G!K! PK!I!M!Y!E!V!S!K!R!P!S!G!V!S!N!R!F!G!S! S!G!N!T!A!S!L!T!I!G!L!Q!A!E!D!E!A!D!Y!Y C!C!S!Y!T!S!S!R!P!D!V!V!F!G!G!G!K!L!T!V! L!G!Q!P!K!A!A!P!S!V!T!L!F!P!P!S!S!E!E!L!Q!A! N!K!A!T!L!V!C!L!I!S!D!F!Y!P!G!A!V!T!V!A!W!K! A!D!S!S!P!V!K!A!G!V!E!T!T!P!S!K!Q!S!N!K! Y!A!A!S!Y!L!S!L!T!P!E!Q!W!K!H!R!S!Y!C! Q!V!T!H!E!G!S!T!V!E!K!T!V!A!P!A!E!C!S!
19285	49653	A	19398	1	679	
19286	49654	A	19399	1	743	
19287	49655	A	19400	2	736	
19288	49656	A	19401	2	718	

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19289	49657	A	19402	1	711	MAWALLFLTLTQGTTGSWAQS ALTQPASVSGSPGQSITISCTGSS SDVGGYNYVSWYQQHPGKAP KLIHYEGSKRPSRVYDRFGSM SANTASLTISGLQADDEADYYC CSFAGSSALRIFGSGRVIVIGQ PKANPTVTLFPSSSEELQANKA TLVCLISDFYPGA\VTVAWKAD GSPVKAG\VETTKPSKQSNNKY AAASSYLSLTPEQWKSRSYSCQ VTHEGSTVEKTVAPTECS
19290	49658	A	19403	3	720	
19291	49659	B	19404	1	711	
19292	49660	A	19405	105	858	RRQDGSQQSPA\WPAGALLLTLT HCAVPGSWAQS\VLTQPPSASG TPGQRT\TISCGSSNIG\NDVT WYQQVPGTAPKLL\MYSDNHRP SGVPDRFSGSKSG\TSASLGP\SV GLQSEDEADYYCGT\WGLAA^M VFMSSAGGTT\TTSQPKAAPS VTLFPSSSEELQANKA\TLVCLIS DFYPGA\VTVAWKAD\SSPVKAG \VETTTPSKQSNNKYAAASSYLSL TPEQWKSRSYSCQV\THEGST VEKTVAPTECS
19293	49661	B	19406	63	756	
19294	49662	A	19407	1	757	MAWPLLLLFLSHCTGSLSQAV LTQPSLSASPGTSASLT\TCLRS DINVGSPFIY\WYQQKPGSP\QF LLRYKSDSDNQQGSGVPSR\SG SKDASANAGILLISGLQAEDEA DYYCSSYVGTNNFGV\LFGG\GT \KLTRP\GQPKACPPR\VT\FPHP PSEEA\SKPNK\ATLVC\I\SDFLP GKP\QLPWKA\*QPPSLAGVET P\PH\PPTRSNNKYAAASSY\LSLTP EQWKSRSYSCQV\THEGSTVE KTVAPTECS
19295	49663	A	19408	1	224	YISLPAGV\SLAC\CTLYG\ISWQF DPCC\KYYQVEYDAYKL\*RLPLH TLTCSR\TRDNRV\FRSPHSVRQ QSLGRCLA

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19296	49664	A	19409	235	955	ESTVQSVFCHRVPARTSSQTA LPVLLGLLGFVSGPLNLPEPSV IVNGELVGPQTCLHGMEIYN GIENAQDQF*VTELGAGP*EGP VTSYIVIEPTRIGDETARWITVG NCLHHTAVLAGTALLLHPGLR CTLRFIPHIIISPAPLGVVL\SLACC NLYGISWQFEPFACK*QVEVR TPNKLRLPLHTLTLLPPRVVLLV RKDDDLHHRKRL\HNPITGTGPPLV YCVKVIYELYAVMIFK
19297	49665	A	19410	1	764	MRLIGIFACPWKGKLADEFDLKI EKQRNQGRLLGFKLQLHLPFTE MEKMGDDRKHTRAPRQAER RRSGRVSFQPPLQPLDVTLLPG ATRENCNCPRASRGRPSRSPISHCQ ETQQPGRSDCTIRGVLSSIPAA RPLRKGSGFPTVCEKRPEQQQQ PALGPAGPAAVPAPAASRTQW GSRPCCGAGARRYWWRGLLL CNLISPLDPGSPGSGRWSAGA LSRPADSCPWWPRAGA*RRG AAAEGANSPSRCGASRPAEEQS GAFAGPLPSSPS*RAPGAEV
19298	49666	A	19411	209	536	TRSSCVTLVC*LAMVSLRVARP HGVPGTMFGKRKKRVEISAPSN F/EHRVHTGFDQHEQKFTGLPR QWQSLIIE/SARRPKPLVDPACI TSIQPGAPKEVCSPRASGTRS
19299	49667	A	19412	124	1983	
19300	49668	A	19413	424	1582	PPWAAVHGDRPHRVPGTMFGK RK/KRVEISAPSNFEHRVH/TGF DQHEQKFTGLPRQW/QLSIEES ARRPKPLVDP/ACITSIQPGAPK WGETGSWPPF/RHLPEG*HGPI PGCQREPORVSHEQ/FRAALQL VVDPGDPRS/YLDNFNIKIGEGST GIVCTPPSGKLVAVKKM/DLRK QQRRELLFNERPWQCP*HP/RR* EAQVPLPVLQALSV/LIHAQGVI HRDIKSDSL/LTHD/GQVSKEVP RRKSLVGTPTY/WMAPELISRLP YGPEVSPGWLGCPA VDSVRCH FQLQRWREMPGSPSGHSQCNGA LDKEEGQRPSTSHTGSLQWGSLG VERTLRVNMYECVHACNSFYL VNKLFFQKDSTQEASVTMVPDP DKDGKNRASQKRKAHSQGARR

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19301	49669	A	19414	488	707	TCGEGLSWTRPLPTASSLQV^H* SLSAGERPYLCDYPDCGKAFVQ SGQLKTHQLRHTGEKPFVCSEN GVNLVF
19302	49670	A	19415	16	454	GPAGRCPADCSEEKEGSPA/GD SGRPPSCT^*PWKGLPVMAILPG EAPVPGWPEPDAGGPLWR WGSPSPCAALHRPISGTTPPGR ALSGPGLERAKQRSPRVPAPR AAPHGHPTHCLPIPAGPRAKD HPAYGPPASCHHILAAAS
19303	49671	A	19416	166	1191	TAGSLVLAARGT^GPPPRARK* GPAGRCPADCSEEKEGSPAETP GTTPPGRALSGPGLERAKQRSP RVSPAPRAAPIGHPTHCLPIA GPRPAKDHP^PTHQKPPRTEGS TGGHCCGPPFLIPNTSMLTVYP SGPVMPAGFTLSPSDTRPSLLN GQEVLRKMNQAVQYIQLCDY!! PTCQLATTVLCVSMSLTVFA VSYMVELLLLQNAQVHQLVLQ NWMLKALPPALQDPPHVPPRV PRAARTRLPAV

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19304	49672	A	19417	1	2481	MRSGDLKFGKSAAWPSGQKEK LVFRGKIEEGLEYLHKKKPSAN SQDNKEASKAFHGQLQQPLLS QALGPDRREEWFPGQAPWPHCC VHPQDTAGCIPVVPAPAMAQR CTGTAWVTASEVAPSILDCFHIV LSQQVYRIRHPTSSLHPQYQGKA TRHTTPAVSMRAAGAEPCKA TGADWPKTLGAQPSHPCTMDV GQGFKKDDSGAALAPMAALM GWAGIECLWLFHTEGVNCWP WDLGEKNGLLGQPRGPAAVCS LRTLLPASQQPQLLRLPWLKDA QVQLGSLLQRVQAIGLCGFYIV LSQFIDPSKASYPPWVKNSRHS TAAQPMRAAAAGAEHKATGA ELPKALGAQPSGPCVLDVGQGF KKNDFGAVGLNNWPAGFWNV MGTCKSRLCFVLLSGKSSFRV EVLTQCLDSHTLEYQFYNREV AFEDVLESSQTGLVVQKPQTDRL LTKRGRGEATRNLRLGVLP SMP RSLLPSTAQPTAWKCORQGPSPY THQDMALIPSPTARCLSPAKEP KQEEVGEKSLLPDPTLPLTDPR LTGSTEQAHAEGLAALMSALR VSHLQGRGGVTVLVDSQLGV AVSSTQFNKGPSYRLLADVQN RLLPKYDSQKEAELRSWIKGFT GLSIRPDFQKGLKDGIILCTLVN KLQPGSVPKINASV*NWH*LEN LSNFLKAMVSYGMNPVDFEA

SEQ ID NO: NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
19305	49673	A	19418	1	1299	MHQEDLRAWYLDLGLPSPHQNE TTDVSVYERFSLTADATYPKQA KQWDFPFLRVSTAQPTAWKCQ RAPSPTYTHQDTALIPSPSTARWL SPEKEPKQGEVGEKSSLDPDPTLP LTDPLRTGSTEQKKDLAAGPVG SALRRRPPAVSSTQFNKGPSYR LLADVNRLLPKYDQSKEAEAL RSWIKGFTGLSIRPDFQKGLKD GILCLTVNKLQPGSVPKINASV *NWH*LENLSNLFKAMVSYGM /NPVDFEANDLFESGNNMQR VSLLALAGKAKTKGLRSGVDIR DKYSKKQNFDTTMKASQCVI RLQITNKCASQSGMTAYGTRR HLYDPKRNRLPPMDNSTISLQM GTNKYASQVGMTAPQTQRHIIY DTNLGIDKCENSMSLKMGYT QVANHSGQVFGRLRQIYEPKY QPGGPVAHGAPSAGNCPGPGE
19306	49674	A	19419	135	290	HREEESKSSVFLNPRGVQGTGV GDHRLMIILGRGRAVLKSE*AAG PRGGRHES
19307	49675	A	19420	92	1058	KGQYLNPNRNGKGGPEPPFEPPV PPASRSRMDAQNLKDLAQLRPA GPRGMGTALKULLGAGAVAY GVRESVFNVEGGHRAIFFNRI GGVQQDTIVLAEGFHFRIPWF QYPH/IIYDIRAKTSKKSPPLQGS KDLQMVNISPAKCWSRPNAQE LS*ACTSRLGLGLTRER/RCIPLSI VNEVLK/AVVVAKFNCNLTAF QRAPGYSLLDSAGSLTERAKGL SSLIL\DDVGQSQQLSFSRPSYT AVAEAK\QVAQQEAQR\QAFQ\I VEKAQ\QORQK\IQLQGRG\GR GLPKMGLGEA\LSKNP\GYIKTSQ RFEPAEII\LRRIAHHRNP
19308	49676	A	19421	3	861	DDDSWEPVHPGCCDFICQWSEE SGLWSTAEVWRERRGRPEGLC EGARGTARVPGGRGPPIQSGQ PVPPAPGS*GA\PGPAAVEGVP GPPAVPPASAALEFSRGFSCLPR CHLVVTKIGKQEDDVSIKRKNR PDYWPAPEPVAGCEGSDQEJV KPNATLEKHFLEGTGPRSPSC LSWPSSPHAAADPAMVPETPE PDRPQLTKKFCEARVMAGTS NVLGQTLKPSRTGGTSWSWV YLLTANRLPPFDVKRKGGGGSSI KPRPHYDHRLLQDFKEQVIIHF

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19309	49677	A	19422	808	923	
19310	49678	A	19423	1	339	
19311	49679	A	19424	1	621	
19312	49680	A	19425	3	1836	MAA VEEA AEPVTVVAAVGPK AKDEEEEEEPLPPCEA/LRWAP VLWRGPWAWATAFLEEATAEEP GAAPGSPPDSDPDRTLRRLRAER RRLDS/LLALSSDFAQVQFRLR QVVRGAPAEQQRLLRELEDFAL LKG/IDILGYEGPGDPA SDEGD GLPGDRPRLRGEDQSEQEKGQER LETOREKQKELI LQLKTLQQLDDL ETFAYQEGSYDSDL PQSVVLERQ RVIIDELIKKLDMLNLEDISSL TEELRQRVDAAVAQIVNPARV KEQLVEQLKTQIRDLEMFINFIQ DEVGSPLQTGGGHCECKAGGK TGNGCSRTGSSRTPPGNSRTKA EDVTKVRKTLGLHLMRRA LAVL QIFAVTRL VLPQARSLQPCGRG SRLTETTLPC* R/ELEASVDRVK QLALTAEPHDHVITSANLQDLS L*GKDELTM AVRKELTVAVRD LLAHGLYASSPGMSLGMATIA* LLPAFSSVPEAMHPRELFVKYY HAKNGRAYVESPARKLSQTFA LPVTTGTVVTPKQSLLTAIHMV LTEHDPF KRSADSELKALVCM ALNEHRLVCWMNLICKSGSLIE PHYQPWSYMAHTGFESALNL SRLSSLKFSLPVDLAVRQLKNIK
19313	49681	A	19426	366	477	
19314	49682	A	19427	3	432	WNSR DAGYEF DICFTSVHLYAI RTLWTVLDAIDQMWLPPVRT WRLNERHYGGLTGLNKAETAA KHGEAQVKIWRRSYDVPPPM EPDHPFYSNISKDRRYADLTED QLPSCESLKDTIARALFWNEEI VPQIKEGK\RVLIA

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met/Asp	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
19315	49683	A	19428	1	890	MRTRTRPRGEHSLSAFSSCVDKISRVCKSFGLELENSIQLTWAEREQSICLVAAGHVLVSSSSGMRNWCHARRHAAYKQVLRHGEVAWNLENRFGGWYDANLNPGDDEEAKRWEQALPDAGYEFIDC/FKRTIRTLWTVPDADLQMWLPVNVSNDKDRYADLTEDQLPSCNSLKDTLARALPFWNEEIVPQIKEGKWSDHCLGALVIPVKDGCNLHGDVTTVSSLTPEERALEEPLNRPTNA/P*HQEG*CWESHOKPVPFQTLGCLCEFSRGASRRKQARVVFERSNLCSRISGGEGF
19316	49684	A	19429	1	443	RALPFWNEEIIIPQIKEGKRVLIAHGNSSGAIVKHLEGLESEEAIMVNLPTGIPIVYELDKNLKPIKMQFLGDEETVRKAMEAVALVCVLESPLALFHGSEMPPLGPVQVYLSLISESCSSCLTPLHGSSVHLSITVLNPFSIV
19317	49685	A	19430	24	1039	AVLALLRGRRGGLLRNLLIPVGAASPARQWPYPYKLVLGRHGESAQNLENRFSGWYDADLSPA GHEEAKRGGQALRDAFYEFDCFTSVHLYAIRTLWTVLEMPLEMPL\SEMWLPPVVRTWRLNLERHYWG S*PGLN*KQKLAHKHGLRPLRK\WRRRSYD\WPPPP\MEPDHPFVY SNISKDRYADLTEDQLPSC\ESLKDTIARALPFWNEEIVPQIKEGKRVLIAAHGNSSLQGHCSRLL EGLFEEAIHGSNLNLPDLVFPLSIELDKNFESELSSPMQFLG\DEETVRKAMEAVACPGQGPSEGRG RILSPGCTLPCPVFVPSHLLAHVTLDHICKTS
19318	49686	A	19431	86	431	VYVSTMSLSCPASELAVRQRWSSQFDHPPGPLQPRPV*EMLL*PTLDLQPVVPPAVAILSWKP SALTISSQIVTPGLKTRSFTRKT FMKIWNHRQKYQKTMVLVMFPRYPSL
19319	49687	A	19432	599	900	ATWLFIISPITTTCTQLSKTLLVPLNFLEKQYLTFLLFLEFPTFLSLFFRHTEDHLMRSGCLKVCSCISPLS/PLPPSSSHVRHLPPLFAMIVSFLRAPQKLSR
19320	49688	A	19433	210	341	HFRKIFITVFQKLKLVEYNLLSGHSTQQSHPGGTVLL*DLVCPVV

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19321	49689	A	19434	239	464	SPKGGGPNPSHGTGFHTRPCEE TTKQALCEEHGCLFHAGGLS PKRESAKGDKGGASVHVCHI S*SPCS*LGP
19322	49690	B	19435	1	838	
19323	49691	C	19436	80	443	
19324	49692	A	19437	1	775	
19325	49693	A	19438	209	469	
19326	49694	A	19439	304	375	NVGE*SERHPCYD*TPREVCPPS P
19327	49695	A	19440	879	1188	
19328	49696	A	19441	615	917	ATWLFSIPTTTTCQLSKTLLVPL NFLEKQYLTFLFLFLEPFTSLLF RHTEDHLMRSGLCKVCSISPLS/ PLPPSSSHVRHLLTPSPFAMIVS FLRAPQKLRS
19329	49697	A	19442	674	1554	GQMASSSVSLQQGVQPAADPG WVTAGASLTRA WAAGVQGDG PGTESSIASRRVRLRGMTRTL LWACVLLWVCILLGLCPAVG PVSSVGPVSYCGPVPYCQGPYPA VGCPA VGPVCCGPVSYCGPV VPCGPVSCCGPVSCCGAVVSCC GPVSSVGPVSC/VLGLCPAVGP VSI*CGP*PAVGLCPAVGPVPC CGPYPV/SVGPVCCGPVSCCGPV SCCWACVLLGLCPA VGPVSS/ VGPVCCGPVPCCGPVSCCGPV SVVGPVSCCGPVSCCGPVSCC DHSSHSLLTFTML
19330	49698	A	19443	4688	4824	

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19331	49699	A	19444	1	2274	MLKPLMGGGAHRRAAAGARK WDGTAIAASTSGLEV.LWVTTSR SKTVESVGLAKPQHNDARMN LAIALTAARYGAATAN^MEVV SLLKKTDPQTGKVRSGARCK DVLTQEFDVRAKCVINATGPF TDSVRKMDDKDAAAICQPSAG VHIVMPGYYSPESMGILLDPATS DGRVIFFLPWQKMTIAGTTDP TDVTHHPIPSEEDINII^LNEVRN YLSCDVEVRGGDVLAWSGIR PLVTDPKSADTQSISRNHVVDIS ESGLITIAGGKWT^YRSMAEDT INA^AVKTHNLKAGPSRTVGLFL QGGKDWSPTLYIRLVQD^YGLE SEVAQHLAA^TYGDKA^FEVAKM ASVTGKRWP^IVGVRLVSEFPYI EAEV^KYG^IKEYAC/DCCG^YDFT SYSPGLS/EMSRQRKPY^PGLL N*/CGRELNWDDYKK^QEQLET ARKFLYYEMGYKSRSEQLTD^R SEISLLPSDIDRYKRRCHKF^DAD QRG^MTV^VEVQRV^LESINVQM DENTL^HEILNEVDLN^KNGQVEL NEFLQLMSAIQKGRV^SGSRLAI LMKTAEE^NLDRRV^IPVDRSCG GLYFCVRNWWV^GL^LTD^FKNE AADPSGVKLQ^TFTV^SVTARKGS VDPKNSGA^QLASP^SGRTGAA GGAACQS^RALRLHSSAL^GW^SM GLG^A^VEHGA^V^LIGEARAA^QEP MEGVGGSG^MAGR^SQV^LPRG
19332	49700	B	19445	439	1542	
19333	49701	A	19446	2	418	CLSLPPTP^WAPVR^PEPPRR/CAT PCSTAPSPID^HPR^AEECERTVQD WRAAPP^A^APVRD^PLET^GK^I^DQE IH^KYNT^PGFTG^CLS^R^VQFNQIAP LKAALR^Q^T^N^A^S^A^H^V^H^I^G^E^L^V ESNC^G^A^S^P^L^T^L^S^P^M^S^A^T^D^P^W^H LD^H^L^D^S
19334	49702	A	19447	111	215	GTC^WELE^*RKGK^PI^W^GEIKAS CRNLHKLQ^GAKC
19335	49703	A	19448	740	959	DLY^PHI^L^S^W^Q^S^R^N^A^A^R^K^R^K^S^* RG^Q^R^P^I^A^I^S^*G^R^I^S^Q^K^Q^Q^N^V^N T^S^T^P^S^H^C^P^R^L^P^Y^E^C^R^P^L^L^H^G^A^Q^S^ H^R^P^P^K^G
19336	49704	B	19449	260	508	

SEQ ID NO: NO:	SEQ ID NO: of peptide sequence	Met #	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
19337	49705	A	19450	11	490	RLSTSPPDGAGLARSRGSGHTG AAGGAACQSRTMRSHSSALGW SMGLGAPLQRH*INSSGGSLWV DKESFPVPSALNFSPLGRKSSPC SKVLYMPNPVSHSMIPSGERS MDTNGSCWYLTCSLSAPGRD TRIRKVFSQGRLLVTLMSIPSV GHSTA
19338	49706	A	19451	42	263	SGVSPMSFNTFTSAPAFNRSWT TCLCPK*HARCRGVQPKLDDLL PLQLMSAITSFLAMVSNSCLTSS ALPFLA
19339	49707	A	19452	662	1564	GSRICSFQTSGHPECPQCWHW RQNHSIIQPHKAAYTKTTIH PPNRSNSCSIWCKLQLKLYMCG P*GRSFNFSANLHQPKQKGHSGE RPF <del>E</del> KNKGRAILLKSHRVHTQE MPFPCSKVGKGVLVSSGLFQH QAIHNEKPCRSAAMYGDMFHTQ QGHFKCIDYGEAFSPKDTPGQH QIHTGEKPYVCTECEKTCTRSS NLIQHKPKGGLSLLVLSPTSGN ALFSTLSQLTQLLLTFDVRSDA TFFRKGSGRHQLWLALPEDAR ARVTSVSGTRRRDHGGARGVV CLIHGCVPDTRSSPDVW
19340	49708	A	19453	1	1167	MIREQKVKEVYICAAGKKSHM HLWHNGEKYNRLGRKDRKMT HEGWLIKIPHPGRKYYKASGLH WEQMKHMGGRGKVHLEFTEM YVAGRRGEVKDEVLEPMSLTE VYIPTENDREVWRERRRLRAPGL CAALEQQLEFRVGVGLAGSAL EAAGOPCWPRAGRARDLQPM PEPPPASVGSCAARSLRSAAP CSTAPSPIGHPRAEECERTAQD WQAAPPAAPVRDPLGEASWAP ESVMWPPLDSRQSEEVSVSKRH MDATDKIKFPWLKEKRTIEFGE AAGYVCHRRYKDMPEHEKMG EAAKKVHWVQMRSSRARDLQP AMPEPPTHSKGSCAARASPT/T HHPLLHDAQSHRPPKGRLRSGAT WRGTGRLQHLQPQCGIHWVKP AGLLSLL
19341	49709	B	19454	118	559	

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19342	49710	A	19455	26	813	LSHYLACSLRLPGSRIRSALI PSIMLNYTSPGLPGRHSKSEN LDDTARRSPGMAGPGCPPLPGG VPDVRAAYGAPTAQRPRVGW PPGGRWPRGARGARSFLKKPFR GTPTQVARGAWQCPPPP-TVIEK *PWIHPCGRFQGRRHEEKGGRE LGHSKSPPPRRSHYPAEKGEE ERKEREESSCAGLRRAHEHA QQQSLPGEELPAPGDPGPRCVRG GQGRSRMGPCS*SLAQHPPVCT RGKREKQERRATNKPVRGAPK
19343	49711	A	19456	497	756	TWLKSGISFPPALFTIAKWTW*P KCPSMIDWIKKMW/HIYTMEY YAAIEKDEFMYFAGTWMTLDT VILSKLSQEQKTKHMRMFSLISGS
19344	49712	A	19457	100	819	EWSSVRRILVEKRALRRHPQC LCFRMKTILSNQTVDHSQLNV DITLKGTQ*SCKGPRGT\RRRD FNHIKCGTSALLGKEQQRGFR VDIKWWGNRKGNWATRSGLF GSHVQDHDPRGVTGGASGYKD EGPVYASPSPHPTV\IPGRNGSS LLKSRNFLGEKYIPQGFRMK\TR VLLCSVSQSPEKMKLIE\GND\I ELVFKFQRALIQQ\ATTVKNKG IRKFFGWVSMSLEKGTVQPLI
19345	49713	C	19458	395	574	
19346	49714	A	19459	1	1476	
19347	49715	A	19460	2	323	
19348	49716	A	19461	539	711	HRPFQDRKAGECLLHEYEDLV PIRDTLRLPGGGRYLPRAKHVA PSEPDGFWLVLG*FYC*FCHSP ALLSGFCLAVNVYRERSV
19349	49717	A	19462	66	2873	SARTISYDYYQNWNGRDGGPRSS GGGYGGGPAGGGHGGNRGSGR GGGGGGGGRG/WQGPASRAPE RPRNRHVVREKTGAEEEQGSWR GKREL/LVHMDERREQIVQVL DSGQAENG*RVRTTDFRFAPE DHGYGTTEVSTKNTPCSENKL/G HPGKEVDKSRKKNV/SESGTDH ILTRDSEYLLQNEPDGTLDQK LLEDLQKKKNNDLRYIEMQELV NLIDNHQVTVISGETGCGKTTQ VTQFILDNYIERGKGS

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19350	49718	A	19463	1	2112	FRKTTRRLRKVKGRATGCARF RKWLRLQHGLRTLGLCNHTSR MTRCRWSAESESDGDEEEEGPIV LGRRQKALGKKNRSADFNPDFV FTEKEGTYDGSWALADVMSPL MKKRAATTLHEKIEKARKRRK TEDKEAKSGKLEKEKEAKEAGE PKEQEDLQENDEEGSEDEASET DYSSADENIL.TKADTLKVKDRR EEEERERTGSRRJF*RCIS/ATMKT SSFQDMNLSRPLL.KAITAMGFK QPTPIQKACIPVGLLKGKICA/C AAPGTGKTPPFALPVLERLYIP SPGSSL/TRVLVLVPTRELMQ VHSVTRQLAQFCNITTCLAVGG LDVKSQEAAALRAAPDILATPG R1JDHFLNCPSFHLSIIIEVILDE ADRMILDEYFEEQMKKEIIRMCSH HRQTMLFSATMTDEVKDLASV SLKNPVRIFVNSNTDVAFLRLQ EVIRNRPNREGDREAIVAALLT RTFTDHVMLFTQTKKQAHRMH ILLGLVLGVQVGEHLHGQLSQTQ RLEALRRFKDEQIDILVATDVA ARGLDIEGVKTVINFTMPNTIK HYVHRVGRRTARAGRGRSVSL VGEDERKMLKEIVKAAKAPVK ARILPQDVILKFRDKIEKMEKD VYAVIQLLEAEEKEMQSQEAEQI NTAKRLLKEKGKEAVVQEPERS WFQTKERKKEKIAKALQEFDL ALRGKKKRKKFMKDAKKKG
19351	49719	A	19464	354	446	RQHAH*ESSPLPNLTYPGTQILR KAAGTSA
19352	49720	A	19465	42	388	
19353	49721	A	19466	177	497	
19354	49722	A	19467	271	773	TAMSSEEGKLFVGGLNFNTDE QALEDHFSSFGPISEVVVVVKDR ETQRSGFGFITFTNPENHASSC Q*RSQ*TGEVSWNGRQIPLLDH AGKSCSGEPRGRWALGPMGVG SQLILEVVGQDQIYGSGRYYDS RPGGGYGYGYGRSRDYNGRNQG IGYDRYSGGNYRDNYDN
19355	49723	A	19468	2	414	GRVGPBRRAGGRASAAGDPA RGGAAPKMSQTAMSETYDFLF KFLVIGNAGTGKSCLLHQFIEK K/WSVTRTSYYRGAAGALLVYDI TSRETTYNALTNWLTDAEMLAS QNIVIILCGNKKDLDADREVTFL LEASRFAQEN

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19356	49724	A	19469	397	445	GHRGAHRPRTLRSVVVRRAHR CSYSGIWD/TAGPDRFRSVTRSY H*GRPGALLVYDITARETYNAL TNWLTDARMLASQNVIVILCGN KKDLDADREVTFLEASRFAQE NELMFLETSALTGENVEEAFVQ CARKIILNKIESERMGSIQYGD AALRQLRSPPRAQAPNAQECG
19357	49725	A	19470	2	559	
19358	49726	A	19471	1	483	
19359	49727	A	19472	95	352	RKATKMATIWA SGTPKQPCPR ELLAQERRQTRTRYNQ*DQ*QE RRSRQRIMGVGCLHMLRSEKA PQQRSFAHCTPKSSRPSARLT
19360	49728	B	19473	247	1364	
19361	49729	A	19474	422	877	CHTQTQ*QHTP*QPTPIDMAPTS HARMPFHHTHFLTQILTIVSRSP DPG/PHGGKVPTRIPIPPAQPVPG PSTL PSSFLGPPRFPSPVPGP GGENRKPFSTSPP*A*GFPGPPSG P*AGGEG/PPVVRGRGA TPSPTP SPACGPLKCWWHLIKN
19362	49730	A	19475	168	522	LALHPTRLIPATDDEVITVTED KINAPH*KQPVNNEVFPAPGLF AKAIALANVNIGSLICNVAGGP CCQPAAGGCTQPGGSCPLHCWL LPA*GRRKWEAKKEGFRGSFD* LTWGFGSF
19363	49731	A	19476	1	328	
19364	49732	A	19477	1	1204	MASRLLLNNNGAKMPILGLGTW KGSILRVGFSSREPPPYRGQP LMGGPPVRLGPSPGRPKRFINAR GRRGKWAQSTGGPRAQGTGWS RRQQVTEA/VKVAIDVGYRH DCAHVVQNENEVGVIAQEKLR EQVVKREE\LFIVSKLWCYHE ERGLV\KG\ACQEDTSSDLKL\D LPGPLTLIHWPPTGFPGKEFFPL DESGNVGPSPDTTHISDTWA\AME KLVDEGLVKAIGISNFNHLQVE MILNKP\IGLYKP\AVNQ\NECHP YLTOEKLQYQCSKIVVTAYS PLGLS*TGPWPKP\EDPS\ILLEDP RIOGGGSQPKHNK\TTA\QVLIRG SPCKRNLV\VIP\KSVTPERVAEN FKWVFDFELS\SGYDPP*LSLPT RNWRV\WWCPCWSCT\SHKDYP LPMKEVLKA
19365	49733	C	19478	300	489	

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19366	49734	A	19479	243	471	CDHLQVSRPRPATVPVVEWKRS EMDSKEEEKEKKEKKEKRRR *RRRGKEEEEERRRRRKRRRK RGRKK*IKKRV
19367	49735	A	19480	1	365	MGLYKDLDTRYLFYLVPGY LTQIELEVIAKDSAKPVGTPRV GLKLEMGIYLSGHLDKFIFAMP FKIKDILSLKKEEEK/ERRRRR RRKEEEDEEEEEEEEEERRRR RKRRRKKKRKKKID*KKEEEKE EEECEECEKKKKMKKRRKKK KKKKGGGGKGGERRRGRKK
19368	49736	A	19481	96	508	PAGSLVCPNQCSSARLFLSSFFCS SAVMSASPAVGKRGWAEALTGS FLPKPPLKTLGSGREDR*GQVW WLTPVIPALWEAEVGGSLEGQE FETSLGNMVKPLLYWLGNSGW LWKLGRRLWQLLWLQDDWPT RGSHILVL
19369	49737	A	19482	3	1013	SRPSWGTHWNEYARRLTLAPS WPLP*GHPVSPSLRVSCL/PHY ESVLEKKKGPCDRDYKFWAGL QGLTIYFVNSNRDFQHVEKLNL GAFEKLTDEIPWGSSRDPGTHF SLILRNQEIKFKVETLECREMW KGFLITVVELRVPTDLTL\PGH LYMMSEVLAKEEARRALETPS CFLKVSRLLEAQLLLE\RYPECGN LLLRLPSGDGARQRVGHHAAADA QRDA/PWFRHYKVEAGRGPKY VIRCGTAVLHLPWTTVNYF VSHTKKALVPFLLDEDYEKVL GYVEADKENGENVWVAPSAPG PGPSPLHKVPPSRCQPASSQDKL PPLPPLRNPGREIT

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19370	49738	A	19483	63	1496	LISAMACAVRPLAISVY\SEKGESS GKNVTLPAVFKAPIRPDI\NFG SHPNLRKNNRQPV\CWQGN*AG HQTSAE\SGWYWPRAVGSKFP R\VRGGGTHR\SGQGC\LETM C\RGGRNV\LHPTKTLGR\RRWHRR SSTQPKKRIRPSGSAPGCPQLP ALGHGLKGHLY\GKFPE\TSFW* VER*KLKG*QEEP\REAVFAPLR KLKRPGNDI\QKGSMASSAK*RA GQKAKLRKPV\ARI\PAAGAC\CI\ YNEDNGY\SFKA\U\RKHPWGLL MLNC*GKLEHF*KLAPLVGHV G\RF\FLH\GLGLESALREV*DDLY\G TWR*SHFPLQGVNLP\IFSPWI\K \M\N\NTDS*AESLKSP\IPE\REPLRA PR\KKIHSQSS*RRNPL\KE\I\I\ LKA*TPFAKAHAAG\TPFFGQAR N\HKL\RV\DKAAAAAA\ANLQA NSDEKAAVAGKKP\VGKKGK KAAVG\VKKQK\PLV\GKAAA TKKPAPEKKP\AEKKP\T\TEEK\P AA
19371	49739	A	19484	3	730	KRLPKMAEVQVL\ DGRG\ H LG\RLAA\I\VA\ QVLLGRK\VV V\VARCEG\IN\U\ISANF\YRN\RLKY LGFSP\PGMNTN\PSR\RL\TTSG APSR\JF\WRT\ VRGMLP\PPQ\N\PSG GQGR\LLDRLQ\GV*RA\SP\PPY\GQ EKSGM\VV\PAALKVV\RLK\PT\ KFCL\W\GRL\I\A\PEVG\W\KY\QAV TAPP\G\ERG\K\RAK\A\H\YR\KKK QLMR\I\RK\Q\ARE\ET\W\RK\K\ID\ Y\TEV\LK\T\H\GL\PL\SP\I\K\TV\N\SS KKKKK\RAAA
19372	49740	A	19485	1	660	PTPRTRGR\I\TRK\ST\PMK\GLGA RYREY\KVV\GRCL\PT\PQ\N\ATRG PLLP\AC\I\I\FA\PN\H\VV\AK\VP\AF W*LC\ILS*KKM\KK\FF\GK\IV\Y\L WGK\VF*EG\SP\LR\I\VERT\G\DL\GL R\LL\T\PR\ER\A\PH\N\I\VT\G\Y\RG\* PTAGC\G\ST\Q\LL\I\TRD\N\G\VAR\HR R\PEAH\H\H\RF\MEG\WEG\DR\G\PC K\I\PP\G\GL\VK\A\SS\N\DS\K\IK\V\SR\W PH\RV\LA\AF\RN\K\AR\FT\T\K\RP\NT

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19373	49741	A	19486	51	471	EAGRLPGNILLDSIMACGLVAS NLNLKPGECRLVRGEVADAK/ S*VLPARCVHGILSDRLVGQWG WSWPRWPHAPLPPSFVLNLG KDSNNLCLHFNPRLNAHGDN TIVCNSKDGGAWGTEQREAVF PFQPGSVAEVCI
19374	49742	A	19487	59	527	ETQSWPCGLVAISNLNFNTLES CLRFPKPSWLPAIKSFCR*NLG QRPPPTWCLHFQPSASTAHGGS ARHASLCNSQGTAGHEGGPTQ REAVFPFQ\PGKCCRGVAFTFR RANLNRSSLPDGITEFQVSPNGF NL\EA\IN\YMAA\DGGLSRSKCV AFD
19375	49743	A	19488	2	440	KQQCRDTGDEVVCSFCVGYQL LSDGVSCEDVNECITGSHSRAF GESCINTVGSFRQC\RISSCATG YELTEDNSCKDTLGSFRCRPL QCKSGFIQDALGNCIDINECLSI SAP\CPIGVTC\INTEGSYKCQKN VP\NCGPLVNLKE
19376	49744	A	19489	2	2061	
19377	49745	A	19490	2	2120	
19378	49746	B	19491	63	255	

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19379	49747	A	19492	2	1941	PPPMERAAPSRRVPLPLLLGG LALLAAGVDADVLLEACCADG HRMATHQKDCLSPYATESKEC RMVQEQQCCHSQLEELHATGGS LANEQDRCATPHGDNASLJEAT FVKRCCCHCCLGRAAQAAQGS CEYSLMVGVYQCGQVFQACCVK SQETGDLDVGGLQETDKIIEVE EEQI^EDPYLNDRCRGGGPCKQS CRDTGDEVVCSCSFVGYQLLSD GVSCEDVNNECITGSHSCLRGIES CINTVGSFRCQRNSSCGTGYE LTEDNSCKD^DECESG^IHNCLP DFICQNTLGSFRCRPLQCKSGF ITRML^GNLLLDI^QWSVLSIQLP RCPIGD^HGI^TEGFYNVPEGT CPNCGPLGYHLQRGRGTRCVID V^DECAPPCLSPVGK^HRCVE LFPGSPLAECKDGV^TIFDG^SR DVLFDVQRSCQRLPRGACC^GH K^CTENTLGSYLCSCSVGFRLS VDGRSCEDINECSSSPCKPGSVA NVYGSYQCY^CRIRG^PASAVI GWEFTCERTFDGV^AALPHRGH TFWFLTAGI^QTSWGSFPVAACP SSGLTGWAPNGPATCQD^DEL C^LGIHNCFH^STEDLVSN^PAG FRCLGLSSCPENYRRSAAT^S^G NSCMRAIGAGWEKEKGKLAGS
19380	49748	B	19493	123	237	
19381	49749	A	19494	285	456	VINKRLVCTRLLRRKWSCLQPH RMM^VQAGSRGSQPKYHRHE MGWTGHTDTPPHRL
19382	49750	A	19495	383	693	NFLPAQPCLSAPPSS^S/RSLLDNS PLNCKAFHSSSHLLKLECSE NSPGPLL^QPGGTCLGACPGCFS FSPGISAGKPLSKAASPPVCTGS GAETSTPPSPLR
19383	49751	B	19496	28	236	

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19384	49752	A	19497	1	927	PAAPQVAGRLGLGCPPLHLHV AVVSAMPLLLRCVPRVLGSSV AGLRAAAPASPFQQLQPAQRL CTRPFGLLSVRAGSERRPGGLLRP RGPCACGSGCGSLHTDGDKAF VDFLSDEIKEERKIQKHKTLK\^ MSGGWELELNGTEAKLVRKVA GEKIPVPFNINNSIPP\^TDFGEEE TLARARRFEDREPELTSLPKFV VEVIKND*WQERPLVLDVHYP EDEVGQEDEAESDIFS\^REVSFQ SITGESEWKDTNYTLNPDWSFT GPLYD\^HLMGFP*PNRGVDNTF A\^DELVELSTAPRSPGVPLPFP
19385	49753	A	19498	3	342	LDTNL PANRVPAGLEKRLCAA AASILGKPADRNVTVRPGLA MALS\^STEPCAQLSIS\^IGVGT ARDNRRHIGAPFFGFS\^PRELALG QDRILRFPPL\^ESWQNKGIRTGM TFL
19386	49754	A	19499	3	520	SSARAVSVPLPAMPFLEDTNL PANRSARGGWRKRLAAAAS\^I LGKPA\^DRVNVDRYAGGFAIGA "AGST\^EPCA\^QLS\^ISSIRRQWGT AED\^NRSHSAHFF*VSSPRELSP GARDRIILFRFPPL\^ESWADWAR *GTVIDDFMIWGT\^EGFQGHLVN LAASFQKRSSWAEVKGLG
19387	49755	A	19500	7	355	
19388	49756	B	19501	172	479	

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19389	49757	A	19502	1	1656	LEDPDSSSRPRRAGSGHSASFP PPLEQLWRQVKTLNPKAEVAR AQAAALAVNISAAQLQDVLR NLGPKGTMKMLVSGAGDIKLT KIDGNVLVLRNCKFQHPTASLV AKVSNKPQE*YNLVDTGDFLIV LINWESLLQQAIDLYIS EGLHPR ITTEG FPEGAKEKAQLFLEEVK SREMDRETLIDVARTSLAKTV HAE LA DVL TEA VVD SILA IKKQ DEPUDLFM/VSIMEMHKHSESET TSLRGLVLDHGARHPDMKKA WARDAYI LTCNV SLEY EKTEV SGF FYKSAEEREKLVK AERKF EDRVKKIIE LKRVCGDSDK VVINQKGIDPFSLDALSKEGIV LRRAKRRNMERLTLAGCGW/G PLNSFDDLS PDCCLGHAGL VY YTLGEVEKFTIEKCNINPRSVTL LIKGPNAHTSRLRQWQ*GDG L*GAVKNAIDDGCVVPG/AGA VGSGQWAGSPGFKHKPSC*RA RAQLGSPKHL DDAFAH YPKV CFRNSGFLTFQGNIKLKLKFAE SESGIQLVGVDP*TPGEPNWW ARSKAVWG
19390	49758	A	19503	2	424	EGPVMAAPPNP GPATLG GPG PDP DLGRPLH EFLH IRV PAPR PRG APLHRRGLRGRH VRA VR QRR REP EGAAGA VDRAGGAGV L C RDRESEGP LTD*P P EAD RAP LLQPERGRFSHPLP L TCA P SII FPVAERWG
19391	49759	A	19504	3	174	
19392	49760	A	19505	2	153	LPLH EFLH IRV PAPR PRG APLH RRGLRGRH VAH V*PSEGP D P ARL LQPERG
19393	49761	A	19506	3	354	EDGRHGAPNPPATLG GPG PDP DLGGLP H EFLH IRV PAPR PRG APLHRRGLRGRH VRA VR QRR REP KNGAAGA VDRAGGAGV L C GPGDTEYE GP LTD*PSEGP DPA RLLQPERGR

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19394	49762	A	19507	3	1246	GSTHASARMAVMA PRTLPPAT LGGPGPDPLGGPLH EGFILHI RVPAPRPGAPLHRRGLRGRHA VRAVVRQRRREP EDGAAGARG* EARKGPE* LGRG\NTESEGPTHR LDPSEPGDPARLLQ P\*G RFTP FQIMYGC\DVGS DGA FSSAGYP QERLTNGKD YIALNEV DLR SWT AADMAA QITKRK WETPPMRRR SLRAYLDGTC VEW LRRY LENG KETLQR\TDP P\KTHMTHHPIS*P *RPL*RCW\AL\AF YPCGDH\*P WQR DGED QTQGHG SLL ETRPA GAGVTFQK W ASMV VPS GOEQR YT\CHVQQ* RVL PKPL TLKM\W EPSSQAHPSI RGA SFAG PWFSL GSL*ITGA\AVGR CW* C\*RKEQLR WRRGER*KKEG AYSQ GCKASD QCPGASD VSLH SFSV KVL RQ LAL
19395	49763	A	19508	1	392	
19396	49764	A	19509	1	220	
19397	49765	A	19510	3	500	
19398	49766	B	19511	28	134	
19399	49767	A	19512	1	1662	MAASVV C RAATAGA QVLLRA RRSP ALL RTP ALR STAT FAQ AL QF V PET QV SLL\DN GLR VASE Q SS QPT CT VGV VD VGS R FET\EK NNG IAG YF LE\H LAF KGT KNR P GSA LEERR WRA WG A HLN AY ST RE HTA YY IKA LAK EL PKA VEL LG D IV QNC SLED FTD* GRN DV IL R EM QEN DAS\MR D VCN YL HATA FQ G ITPL A QALE GPSE NV R KLS R A DLT EY LST H\QGP SKW C WAA AGRE WE HQ QL FRT FQA E GT SV GIP W TYA EAD VPT L TPC R FT GSE IN R HR D D ALP FAH VAI AV EG PGW A SPDN V A LO V A N A NG H\Y DCT\Y GGG V H LSS P L AS G A VANK L C QSF QTF SIC Y A E VT GLL GA H FV C D R M K I D D M M F V L QG Q W M R L C T S A T E S D\VR D G K N I L R N A L V SH LD GTT P V C E D I G R S L L T Y G R R I P L A E W E S R I A E V D A S V V R E I C S K Y I Y D Q C P A V A G Y G R S L G L P H L C S R T A A Q L T E Q P V K A P S S P O S P G C Q Q G V L A Q K T C P S S S L T A C Q G A F I N T L H P S G P I E Q L P D Y N R I R S G M F W I R F

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19400	49768	A	19513	2	1693	AQSTLARRNRADCSWKMAASV VCRAATAGAQVLLRARRSPAL LRTPALRSTATFAQALQFVVPET QVSULLDNGLRLVA^SEQSSQPTC TVGVWIDVGSRFETEKN/DSGA GYFLEHLAFKGTKNPALAVPW EKEVESMG AHL^NA^YSTREHT AYY^KALSKDLPKAVGALGDI VQNCSLEDSQIEKRDVILREM QENDASMRDVVFNYLHATFAQ G^TPLAQ^A VEGPSENVRKLSTA DFTRYL^STHYKAPESVLPQTEG VRTEQLL^DL^ARNHRVHIP^*TY AEGAL^P^TITPCRFTGSEIRHP^D^ ALPFAH^V^A^A^VEGP^G^WPAPD N^VALQ^V^GNA^I^G^H^D^C^T^F^G^ GVHLS^SPLG^SGACGPTKLCQS F^Q^T^L^S^I^C^Y^A^E^D^G^L^C^W^H^T^L^F^C^ DRMK^I^D^D^M^M^F^V^L^A^G^H^W^M^R^ L^C^T^S^A^I^T^R^S^E^V^A^R^G^Q^K^N^P^Q^K^ M^P^L^G^I^S^*^D^G^N^Y^S^L^C^V^E^D^I^T^P^A^A^ L^L^T^L^W^A^R^N^P^P^G^L^K^W^E^S^R^I^A^G^ G^G^F^Q^V^V^V^R^*^D^L^A^P^R^Y^I^Y^G^P^C^P^ A^V^A^G^Y^W^P^H^S^M^L^P^D^Y^N^R^I^P^ A^C^F^W^V^A^F^R^A^G^K^P^M^V^K^Q^K^G^R^ G^G^G^L^W^S^P^P^P^Q^T^Q^H^F^R^L^L^T^C^C^
19401	49769	A	19514	46	422	
19402	49770	A	19515	568	1567	GPWAANGVVLA^F^P^P^C^L^G^S^P^P^ H^L^A^P^Q^K^A^V^P^P^K^W^G^I^S^S^F^H^ H^I^Y^V^G^G^V^A^F^C^G^R^I^F^L^S^T^D^ K^R^R^A^G^G^S^G^L^M^S^Q^E^E^K^H^L^S^G^ K^I^R^S^Q^I^M^D^D^H^A^R^P^Y^L^T^M^S^N^P^ C^W^A^G^A^L^G^P^Q^E^S^K^C^S^R^G^R^L^L^H^R^ A^F^P^S^L^V^T^L^L^A^Q^A^T^T^G^L^L^S^C^ Q^Q^Q^G^A^G^W^D^K^L^D^S^H^R^P^R^N^L^A^A^ W^E^E^P^C^G^M^E^A^F^P^K^P^S^Q^S^L^V^E^A^I^ A^Q^L^A^T^P^G^L^L^D^C^K^A^A^C^P^W^G^A^P^C^ P^R^G^P^I^M^Q^N^A^T^K^V^I^G^N^M^T^E^D^H^V^ D^A^P^G^S^R^N^A^E^P^P^*^K^V^Y^P^P^I^L^K^G^S^F^ P^/^E^K^N^L^R^H^L^K^N^T^M^E^I^E^W^K^A^F^ N^W^M^H^H^W^U^L^L^F^E^L^S^K^Q^S^L^W^E^Q^/^ Q^S^P^L^D^A^P^K^/^E^N^S^L^E^L^D^P^S^G^S^G^ G^V^T^K^Q^D^L^G^P^V^P^M^
19403	49771	B	19516	1	1428	

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19404	49772	A	19517	1	2293	MARSEAAAAGPGPGPPGLAAR ERRGGRGCVRGCERASVRVWS VALRRARAPARPYVARCRRV RRPARVAIGCGGVSSPAGVSGC ARVSPERPRLCVWALSARHG GAVCRAAGPGDLSKRGLTSHPP AFPLHHGSRTLLGPLSPPPAAL PFLLLIWAGHLVAS/ACPGRCIC QNV/SPTLTMLCAKTGLLFVPP/ SIDRRVVELRLTDNFRRRHFAN MTSLV/QLTLSRNTIGQVAAGA F/VDLRLRALHLDNSNRLAGC/ GGDQLRGLGNLRLHI/VGNNQI RRVESAAFD/DLLSTVEDLLDS YNNLEA/LPWEAVGQMVNLT LT/LDHNLIDHIAEGTFVQLQSW ARAQAAHPLTVSFGGNPLHCN CE/LLWLRRLTREDDLETASP N/NLTDRYFWSIPEEESCTRQR FCG*ASLVAAELTSNSVLRW/S TQRPVPGIRMYQVQYN/SSVDD SLVYRKYSLSTYMNPTR/MIPST SQTFLVNDLAAGRAYDLCVLA VYDDGATALPATRVVGCVQFT TAGDPAPCRPLRAHFLGGTMII AIGGVIVASVLVFIVLLMIRYKV YGDGDSSRKVGSRSLPRVSHV CSQTNAGTGAA/AGPGPAGPG PLRGAARGGVP/WLPPPSPSRPR PWRPR/LASAEPEVVLGRSLGG SATSLCLPSEETSGEESRAAVG PRRSRSGALEPPTSAPPTLALVP
19405	49773	B	19518	97	255	

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19406	49774	A	19519	1321	1728	EHAHDRLHHAHYVQATLVR ASLREAVVGSPTDAWLQQRATA RSSASLLLARNRPATSVWLPRAG GFIAGTGRERRGSEGWEGG GAGGTGAGLSAHSQTSAECS/CGGSAGRGRCLLSSAATPPQLQP RPAPPTAGLVQPRQVPTAPPRA SAGNEHHQGWSGRL*KSLAAA RVGEAPGKLPKPRDFRKQSNGA LARASLRVSAQPGTCSSSAAAF PPLGPAPLAAPARSCDESGPRQP DGRGGFPVGQQQRGA/ESEPCA AATRRPWVNRRR/TSRREARTS VACT*CAWCRSRSCACSHSPWS SASSSSAAICSSSPRA*STSS*RT GGRLRRWRWSWGPDTDPYAP AATAPTPAHFASP/ACAPHYQR LGEANLSESIISLD/CRPGKKRP VSPPSESPHAWQSEESAQTLN SAESGKKRAIRAQNFG/RLLL'T WNAGRPTVRRPFSTRRWAKLW GQVERAGRGETQRH*SPCDRKS DLLKATQQTHGVSQIRVRVRSPL FSLLPPCPRKGGANGKIPNCKR ARFKKGFFVFCLEIQMFE
19407	49775	A	19520	192	447	
19408	49776	A	19521	1	591	
19409	49777	A	19522	281	421	
19410	49778	A	19523	174	512	
19411	49779	B	19524	67	1166	
19412	49780	A	19525	1	1620	MGAKDGRLLSESSQGLSSCGSLVPCVSKSRLLMKPTVRLDKE TVSTVDGAPTDLAQLPTVLKQ PCCSVMASQFVNKLQEEVICP ICLDILQKPVTDGHNFCLKCI TQIGETSCGFFKCPPLCKTSVRK NAIRFNSSLRNLEVKIQLQASE VQSKRKEATCPRHQEMFHYFC EDDGKFLCFVCRESKDHKSHN VSLIEEAQNYQQQIOEQIQVQL QQKEKETVQVKAQGVHRVDV FTDQVEHEKQRLTEFELLHQV LEEEKNFLSRIYWLGHETEA GKHYVASTE/PTVERSQEAH*FP VCLLASYDEISGGQGASSQDTKT FDVALSEELHAALTSAHPDLILS QDEIVTLNLASQGGSQKRGNPR RFYRRGFLEVEPLTGFVELHSS GSQCQALIESGSREDLPCPNK
19413	49781	A	19526	203	359	

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19414	49782	A	19527	135	466	DPAGSSAASMSSAAGLCA!TPP /GLLSLGLLLLPLVVAFASAEA\ EEDGDLQCLCVKTLPGSVPGH IHQLGG*FKGRDPHCPCTP**A TVEGMGRKILLGTWQAPLLQ
19415	49783	A	19528	46	468	TGPTHASAAILVPRSLHCKMPGE ATETVPATEQELPQPQAEQGSG TESDS/GKSPASDTYIVFGEAKIE DLSQQAQLAEEAKFKVQGEAV SNIQENTQTPTVQEESEEEVDE TGVEVKDIELVMSQANVSRAK AVRALKNN
19416	49784	A	19529	337	509	ISQQLVVLAGINLRSWLPQKL CKYLKQDVLTALDLSVEPF C PFDHLVVALEEEGPAL*GHPA SDTYIVFGEAKIEDLSQQAQLA AAEKFKVQGEAVSNIQENTQT P TVQEESEEEVDETGVEVKDI E LVMSQANVSRAKAVRALKNNS NDIVNAIMELTM
19417	49785	A	19530	91	1019	GEALLGHRVPTRWPASGQK GVCGWCPGKSTLQGLRCGPTIR ACRDGSSCSVEGRGRVRLV LG TASQDPKEKMPGEATEVPVA T EQGVAASPRAETGSGETSDISD ESVPELEEQDSHPGQPHNKAQ AGRQQSEIDEDPVSKAKQSRN* KEGPGRAMSQTGVFGQVTGVT KEFTMRKSKNILLCHPPKPDVY QGAPASRYFTIVFGGSPRSEDL S PSKHNLASCLRSKQFQGEAVS N IQENTQTPTVQEESEEEVDE TGVEVKDIE\LVMSQANVSRA KAVPSPEERTSNDIVNAIMVS
19418	49786	A	19531	1	261	MWGHFHSHPGTGQARYTDT S GSPIPLIMHVNRGRHSEIPVLER NLLHFRMDAST*NLMGSSLME AILKNQFRHVSLAVSFAFSGEK
19419	49787	A	19532	277	349	
19420	49788	A	19533	792	1014	

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19421	49789	A	19534	849	1752	GESRGWERRKCVRPLSSYATHL SVCDCDHGNVREGADPAGGAG *L*GARQQQHTHKKPATAKQR GEDREKKRETKEERLGGQE NERDERGRKEPRNRRGTRKRE AEKGRRR/ESSEGKREKEGEEER QERQKRAREKRRGRRGARRRG REKKKTQRPRTQAQRPPLKKIK DYTHHTQTPTQHQHHTHTKH KQPHTNTTVFLFFFLLAKEHR RAARKQHEPERGRGGGSKA KIKHTSIAAAADRRHDPRTQRD TRRKEGRRAQS GTKHGRTAHT EAGGGIPVHSTS RVRQVILLQPP
19422	49790	A	19535	139	470	
19423	49791	A	19536	2	83	
19424	49792	A	19537	32	434	NRRKGA\GPV FQRAT*KH/RV*R AGLRAVDF\ERHGYKIGIVKDKI IHNPRR/GAPLA KV VFRDPYRFK KRTEFLIAAEIHTGQFVYCGK KAQLNIGNV/LP/VGTMPEGTV CCLEEPRLCRRKRTSAEGLNKV CVYAT
19425	49793	A	19538	10	443	
19426	49794	A	19539	63	376	
19427	49795	A	19540	170	368	
19428	49796	A	19541	175	427	
19429	49797	A	19542	1727	2262	
19430	49798	A	19543	131	596	
19431	49799	A	19544	695	1337	GFGTQGERRRQCRLLRTQPLG ASSATQKTPALPPTPVKAEQSC TLLSPRTPGHLQPRLLDPPSW AVLIRG\QRKGAGGSVRRATL HGK/GAVRLLR RWISPERHGY IKG\IVKDI\IHRPRSRAPPLRQR WFFRDSIYRF*ER\TELFVIAARG AFHTGPSFVYCRQERPSFNIGQ WCSPVGHHCLEGYNSCCLPWK EETLET CGKAGPGAFKGN
19432	49800	A	19545	1	813	
19433	49801	A	19546	227	381	
19434	49802	A	19547	135	740	PQPLPPPTS SMARHVFLTGPPGV GKTTLIIHKASEVLKSSGVPVDG FYTEEVRQGGRRI GFDVTVT VVR HPGGLLSR VGLEPPP/RENVNAE LGSYVVDLTSFWSSWALTRLE GM*ADCCQWAQGQ RVCVIDEE LGKMEALSVK\PSFKAVRQTLS YPRDIPSL/VHKSQVPKGKPLAL VEEIRNRKDVKVNVTQ\ENRN HLLARYS

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19435	49803	C	19548	251	574	
19436	49804	A	19549	2	450	
19437	49805	B	19550	721	3048	
19438	49806	A	19551	3	396	
19439	49807	A	19552	2	450	
19440	49808	A	19553	2	1152	GPPLHCTRAAGIRHEAPLAG LCRAADAGLCSAGWGFVKK KNKAY FKR YQVKF*KTPERV KRDYYARKR LVIQDKNKYNTP KYARMIVRVTNRDINLSRLLYA PV*RGDMDSLQR* LTELAKI LVVEGLALTNLPAALFVPGPA CLAPQAFQLQ*VLAMDKDLLLEG PSWS*LGDEYNV ESIDGQP GA FTCYL ADALARTT TGKVF G APEGA VGGLSNPHSSKRFGL/ YVYPLHSTQTDSPGMDFSEKQR NFnARSTSGKHIMGQNC LQDY  A LL*WERKMKDAYKK QFSQY IK NSVTPDMM EEMYK KAHA AIRE NPVLWKR RPKERSLKR GWNRSQNVPLLKKDRVA QR KASFLQSSRSLGLES TPA FP
19441	49809	A	19554	3	991	LTSRGVGSCAVMLLVRA AWLRPTGSQGLS SLAEEARA TENPEQV VASEGLPEPVLRKVEL PVPTHRP RVHAWIESLRGFEHE RVC LVDLHPDV FANAPRLDILH QDAMLQKNF RISYAKTKTRA V GGGGKPLAERHWAGPA WQHPLS ALARRRCCP WPPG T SYYYMLPMKV RALGLK VALTV KLAQDDLHIMDSL* LPT GDPQ L* PELAH HYRRWGS VLLV THEEMPQSIR EATSR LKT FNL  PAVGLNVHSMLKH QTLV LTP TVAFL EDKLL WQDSRLQTPLY PFSLAPYSDF P RPLPHATQGP A ATPYHC
19442	49810	A	19555	31	305	
19443	49811	A	19556	213	541	DGGPAAH TPGAARGELSPVG SGGYF RPSHLRC WLNL CISVPL SSAKD LLHPS SEE V RNP MKN RLVQSPNSYFMDV K C PGEETV CCIGESTGP QQLENV VV LAVSY

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19444	49812	A	19557	164	591	DINSRDRSGPRA TRIDGS GEGDKMAAQLRRH QGRG RASSP RFA K DILLHPSPEEEK RKKHKKR L\ VQSPNSVY F MGVVKCPGICFKFT TVF*AMA QT VVLCVG/CAAPLF LCQPTGEKARL TEGC SFRRKH A LKATLSQD EWE TILQ
19445	49813	A	19558	362	916	GGRCTM ARTKADWP ANRTGG KAPKEANW LTKSPLRKSAALY LEGSKKPHRYR\PGTVAPP\NLD GYQKST\ELLIRLKLPFQ\RRLVRE IAQGLLKQDSRFQ\SA AIGCFG RQV RAYL VWPFLK D TNLCA\IH AKR VTIYAKKT FQLST P AYRG EPCFKDPLMDGETFH S QKKKK KISL P VIGSSER
19446	49814	A	19559	849	1261	DGHIAGGPC S*GWPRP DPA PKSQ PTMSSGSEPEK LPPA PRPQHYCS PAEVSGP RFAVG KIKA LNQQAFT E RRLH TSLCPV PAAL TVP SPESL PQPQI F PGLAPATH TLYSKAWA GATV S R P GAIL GAGLYWGLVR ETAS
19447	49815	A	19560	3	1852	
19448	49816	A	19561	362	1298	QGGRNV RHP SPLL A WGSDLIV KPHWLH WLLDLN HARLS ALFA AAGARLP SHIP A P SAG S R L L L L L L G G C R A C L L F F P E M A N R G P S Y GLS R E V Q E \KIE Q K Y D A D L E N K L V D W I I L Q C A E D I E H P P P G R A H F Q K W L M D G R V L C \K L \I N R L Y P P G T R S P Y P R F S E S K D G F L G R W E QISQFVLKA\AET YG V R T T D I F S R R W F L W E G K D M A A C A E G P *L ALGSV A V T K D D G C Y R G E P S W F H R K A Q Q N R R G F S E E Q L R Q G Q N V I G L Q M G S N K G A S P G G P *T G Y R E C P R Q I H V R T R H P A P W L E R T N V S T P W S F T K K K

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, !=possible nucleotide insertion)
19449	49817	A	19562	3	2518	AAGEWPQRPRAAVAAAGAAA QRQLPGSRQVAAGAPQPAGGG DPSQRPPGAELIKVQVYVSGE LVPLARASVVDVFGNRTLAAAG TTDSEGVATLPLSYRGLTWWLV TAARPGFLTNSPVPWRVDKLPL YASVSLYLLPERPATLILYEDLV HILLGSPGARSQPLVQFQRRAA RLPVSTYSQWLASLTPASTQQ EMRAFPCLPGH*G!SSSGNGSW LELMPLTAVSVHLLTNGNTEVPS LSGPIHLSLPVPSERALTVGTSI PAWRFDPKSGLWVRNGTGVIR KEGRQLYWTFVSPQLGYWVA AMASPTAGLVITTSQ!QD!GTYH T!FLLTILAALALLV!LLCLLIY YCRRRCLKPRQQHRKLQLSGPS DGNKRDQATSMSQLHLICGGP LEPAPSGDPEAPPGPPLHSAFSS SRDLASSRDDFRTKPRSA!RPA AAEPMSGARGGESAGLHKGARSA EGPGGLEPGLEEHRRGPMSGAAA FLHEPPSPPPFDHYLGHKGAA EGKTPDFLSSQSVDQLARPPSL GQAGQL!FCGS!DH!LKD!NVYRN VMPTLV!PAHYVRLGEGAAA GVGDEAPPEGTAPGP!PARFPQ PDPQRPMQPGHSGP!GEGGGG GGE!WGAGRAAPVSGSVTIPV LFNESTMQLN!GELQALTEKK LLELGVKPHPRAWFVSLDGRS NSQVRHSY!D!LQAGGGARSTD
19450	49818	A	19563	206	1126	LESGSHIYAFSHESLLHVASAS V*TSFSDFATSVCHSP!HCQLH HALIPHGKGECSVSG!IVATGF GATGFLGRCVVNHLGRVGSQIP QAIAQVSKEAEVGKF!HVAH!LN VNIKSSRYLRKKAVGEKAVR DTFPEAIIVKLLDIFGREDRFLN YFANMCWFGA!PLVSL!GWKA KQPVYVVDVSKGIVNAVKDPD ANGKTFAVFGPNRYL!LFDLVK YIFAVAHSKGWVARD!FEISPFE SWT!TRDKVERI!H!D!MTL!HLP SLEDLG!QATPLEK!AIEVRLH HTYCWLSAEI!EDV!KLA!TVNI

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met/Asp	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, =possible nucleotide insertion)
19451	49819	A	19564	196	553	KLSSEFFLTHSINTAIRGNLFV NRVTEVTRSGGNELGSFCLLAI KFTLLSFLGTGTRRLLPALRPRR LQQRGSHGLAGRLFTLWILHA GCHARGEELLEPDTC*SLCRAR KPRLSTLK
19452	49820	A	19565	1	505	ATEDPGVAMGRRPARCYRYCK NKPYPKSRFCRGVPDAKIRJFDL GRKKAKVDEFPLCGHMVSDEY EQLSSEALEAARICANKYMKVKS CGKDGFIHRVRLHPFHIVRINK MLSCAGAD/RIHISKWKWGFTKF NADEFEDMVAEKRLIPDGCVG KYIPSRGPLDKWRLAHS
19453	49821	A	19567	6	904	AQLSSLAVALLLVLTFRPSVLVFR SDSLFFVAATEDPGVAMGRRP AIRCYRYCKTKP/YPKSRFCRG CPLMPRIRIFDU.GRKKGKKWN EFPLLCP/HMVSDEYEQLSSESP GRLPRICPKNKYMVKSCGKDGF/ HISRVRLLHP/FHIVRIHKMLSCA GADKAPKQACRGAFWKSPKGN LLARGSQLAQVIMSIRTKLQN KEHVI*GPAARPSFKFPPGRQKII HISKKWGFTKFQC*WNLKDM VAEKRVHPHMACGGQSTSPSR GPL\DK\WRLPLHEGLPNVAA HPLNTPPIKFLLPWSKKKKKK
19454	49822	C	19568	346	471	
19455	49823	A	19569	1495	2780	EGLHLFCDLLDGPGVQVAGG FDSFSSILASFTYWHDEPNSTML LSTFRDINLGMMIIKKSAVCFSR LGSETTWEMPANLRPSEGART RTELSPQTSPSRAHLAWRGRGG LGAVPRRRLSRRSLSK*P\RSL* AEAPAGAPVRRCRPAAPP\PPR SRCGPSTPPPPSPGA\PRRRRPP CSEHNKLSPPPPSLLRPAAPSP RPAPRSPSRRRRRRHPRPAD RREPLASATRVRPLPPPPPR*PP SSCPRRGGRRFLAPWLAPAG APRRAPCSRAARSRRAGASGAR VGDPAGAGRGWRRRAAGRP* APERRPPPLPAVCEVSGGPLRA SFADSVPGVRRRPPGGLGTPLSS SGV*PRNERGVETTSWGGSE GAPGSGEGGNLFPAPQVIVARS GEGTVVPRFPVCQLRDSAVLLC LFD
19456	49824	A	19570	178	256	

SEQ ID NO: NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, !=possible nucleotide insertion)
19457	49825	A	19571	622	1726	QGSGRTMMRMLVPASVGLLET GPPGDPSLSHPLSGDVTLPED QISTVQKLAISDHKDIHSSVSRV GKAIDRNFDEICGVVSDAVW DAREQQQILQMAIVEHLYQQ GMLSVAEELCQESTLNVDLDF KQPFLELNRILEHQDQLGPA LEWAVSHRQRLLELNSSLEFKL HRLHFIIRLLAGGPAKQLEALSY AIRHFQPFARLHQREIQVMMGS LVVYLRLGLEKSPYCHLLDSD WAEICETFTRDACSLGLSVEESP LSVSFASGCVALPVLMNIKAVI EQRQCTGVWNHKDELPIEIELAS *SAWYHSVFACPILRQQTSDSN PPIKLGICGHVISRDALNKLNGG KLKCRCYCPMEQNPAKGKTH
19458	49826	B	19573	271	392	
19459	49827	B	19574	58	296	
19460	49828	A	19575	215	861	QLPAESVRTRGPAKAAQARAGG PPGPWHCSYKWRAPWSSLGTT GWPDMEGETTAAAPASRENSA DCSAGEI.RGPGIKELWISPQIQ VTATSS*MGRDFVLAT*EKVSH VDS*/QPRSLQRIDPRVAGPAQ AKQGTPRAQASRESLSRPTAA V\QPSGPQHPVTSGS*KGLAG KTSMGRKGLPWARGWAPWSL EAQNP\PTRLCDLFITGEDFDD DV
19461	49829	A	19576	65	782	SSSSSAIQRKPRWVLYKYIQL WRKKQSDVMRFLLRVRCWQIY RQL\SAHHRAPRPTP\PDKVARRL GYKAKQGYVIVRIRVRRGGIRK RPSFLKGATYQGQSPVHSWVFN QLKSFASE/VLSVPFARGRRSLG RHICGGLLEEFLNFFNWVWVER FPHYQFLKVIPHLIPFP*KLFR N\NDTQI.IHQNQVHKH\EMRG \LTSARPEKSRGGLGKGHKFHHTI GG/SLRRATWRRRNTLQLHRY R
19462	49830	A	19577	1	179	QEDYLRELLTTMGDR\FTDEEV DELYREAPIDQKGG/MFNYIEFT RILKHGAKDKDGLKEL

SEQ ID NO: NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, + =possible nucleotide insertion)
19463	49831	A	19578	144	722	KKGLNHHHVQEQQNTRPRRSQ PQRATSN\VFAMFD\QSQIQEFK EAFNMIIDPQDQDFHPRGKICND MLASLG\KNPT*WSILDAMMNE \APGPPSNTFPWPHHGFGEEV* MATRS*KMVIRKCPULTCFE*KK PLGTIGEDY\LRRELLTTHIGIGF TDEEVDELYREAPI*+KRGISITS EFTRILK\HGAKDKDD
19464	49832	A	19579	3	429	VACLREHK\QRCE RATRSLLREL LQVRARVQLQGSELRQLQQEA RPAAOAPEKEAPEFSGLQNOM QALDKRLVEVREALTRLRRRQ VQQEAEERRGAEQE/DRPQTQAA DRLAAGGAGP GGGLRRPAEE PRGQOPEGPGGGQN
19465	49833	A	19580	1	2454	RFPAGVAPRRAMANVSKVSW SGRRDDEEAAPLLRTARPQG GTPLLNGAGPGAAARQSPRSALF RVGHMSSVKLDDELLEP\DMDF PPHPFPKEIPHNEKLLSLKYESL DYDSENQFLFEEERRINHTAF RTVEIKRWVICALIGILTGLVAC FIDIVVENLAGLKYRVIKGNIKD FTEKGGGLSFLLLWATLNAFF LVGSVIVAFIEPVAAAGSGIPQIK CFLNGVKIPHVVRLKTLVIVKS GVILSVVGGLAGVGKEGPMIHSG SVIAAGISQGRSSSLKRDFKIFE YLRRDTEKRDFVSAGAAAAGVS AAFGAPVGGVLFSLLEEGASFV NQFLTWRIFFASFMISTFTLNFVL SIYHGNMWDLSSPGLINFGRFD SEKMAYTIEHPVFIAMGVVGG VLGAVFNALNYWLTMRIRYI HRPCLQVIEAVLVAATVATVAF VLIYSSRDCQPLQGGSMSYPLQ LFCADGEYNSMAAAFFNTPEKS VVSLFHDPFGSYNPLTLGLFTL VYFFLACWTYGLTVSAGVFIPS LLIGAAWGRLFQGILSYLTGAAT WADPGKYALMGAAAGLQGIV RMTLSSLTVIMMEATSNVTYGFP IMLVLMFTAIVGDVIEFLYDM HIQLQSVFELHWEAPVTSLSLT AREVMSTPVTLRREKVGIVV DVLSDTASNHNNGPVVVEHADD TQPARLQGLILRSQQLIVLLKHK
19466	49834	B	19581	508	4413	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met/Asp	SEQ ID NO: in USIN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
19467	49835	A	19582	8	331	EVTACWQSSQPSLTLSASSAWASTLAALEEPFSPPHLHSESPFLWPRIELGPSAACAPVPPPEPPPORVPPPAP*RPVPSSTTQGLRSVGAWCRTGRQLHLIIPGVGSTG
19468	49836	A	19583	831	1121	
19469	49837	C	19584	1	1524	
19470	49838	A	19585	270	578	RFSKSPPDGSAQLAAPSGSRTGAAGGAACQSRAVRPHSSALGWSMGLGAMEQGAVLVGEAWATQQPTVGGRRLHGGLQVPSAPRGGS*GPAKSHSSCWPRC
19471	49839	A	19586	2	298	
19472	49840	B	19587	113	515	
19473	49841	A	19588	1	569	MLPDRLRSPVVAHHRCRASGNYHSGRHSPAPAWRVTLTGWLDRSSRIHRSIAFKDYSKKGKEERTHIKGMCSELLPSG/EARLQAGFRSEAADLRGECYSS*RQCGPKELRSPAGFTQWIPHGYRWSCLSVPRPAPALLSPWVVDGTCRGCGAGGAHRRGGSGRSGAHGGGGRLRHGGLQVPSAPREGS
19474	49842	C	19589	1	1200	
19475	49843	A	19590	511	846	ARHRVLIQVFTIPELDIKVLHVPTRLRSPASFTQWIPHWGCRWSCLPVPRRVPALSPWVVDGTTGGCGAGGGAHRRGGWGCTGAHGGGRLRHGGLQVASAPREGS*GPARN
19476	49844	A	19591	9	481	QQPLREKPSAGDHPAKNANRWRPSPTRYPVES*NWMPMSLHLIQKSIQDGLKT*TLDLKP*KL*KKT*ALPFT*ARTSCLKHQKQWQQKTKLTNGI*LN*RASA/PAKETKI/SSEQATYKMGFNFHNLF*QRANIQNLP*TQRDLQEKNKQPHOK
19477	49845	A	19592	1	3339	MSVRKDVEKLEPSDIVCGNVQCYSCMETNLTVSQKVKHEVTVGREGATKPNRMKGKEGRSGSLLGEGLDFKDESMVMSSEQGSSKDGEKRRGKAQRWKWPMQGICRQLGVAKSMEGYQSRRDQQGRGVSDKWPQVCAKKPEFYPTAQVWANFSVTSCQSVTITQLCHGLRRLEISPARNAMHLPDPPGQKQNLSPKVNDIITDISSSGASA GKFQVISKSDISEVLLQDMAGHSSKDDPNEYGGWKSPPRRC
19478	49846	B	19593	1	631	

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19479	49847	A	19594	71	208	PCPKHCSKFPMPCEPLVGWSWH* LQE*SHGPSRFLC*KQPQDLQ
19480	49848	A	19595	138	650	AWAQLPSALGSTRVSPPPSARS QPPWRRRHKCWRRLRNCKE/L DEDAVASADFSSLMLSEEKEEL KAEVLVQLEDEITTLRQVLSAER KAS/ELR*NKNSA*T*/CNELKPE LQQKLA*HAD*HCLQEDT*YAE SRRAKGNCSFQQRWNNGHQQEY RRHELLHSPFHKYACYETKVG
19481	49849	A	19596	1	1222	MRADGTAQKDPFATDKQLPEL LIQHCWDGLAVCGGSTVGV LPFILHGSWVRPVAASFPPLPDN LHDSAEPAIILLEPTQMMRNQK TNAGTMTKQISSTLPKNHHTSS PAMDPNKEEIHDLLKEFSLRV ELIREGPEKGKAQCEEIQKKDT KVKGEIFKEVDSLKKQLNQE NLETLLFEVLNALESLSNRIEQVE ERNSEREDKVFELTQSNKDKA QRIRKYEPSSLQEVWDVYKLPLK RIISFPNEEENSKSLENIFGRRIK EHFHISIARDLDIQIQQEEQTTPGK LIVKRSLPRHIVIMRAPTPMDHP RAEECGRRARDWQAPPAPV RDPLGEASWAPDSEGRK\WNTS KHQRNKLRLTRHL*EL*HSSRGS VASFLKSVRPRTHQFQTQSGYP KLRWRKES
19482	49850	A	19597	381	598	
19483	49851	A	19598	1	1906	
19484	49852	A	19599	493	589	
19485	49853	A	19600	60	261	
19486	49854	A	19601	1423	1831	PRRSANVNLPPIPQLATLSPGPW EERKSVGSPTSPPPPLRRLSA APGISGGAWPEPGAWSLD*TAS PAGAPVQRPAGNG/PSALDASH ARALYLQRIPRVTWTPASQPA PLGPFLPLIPPAASHRQPSSFFR RHR

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met cod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, !=possible nucleotide insertion)
19487	49855	A	19602	1	1535	MEEKTNVQLPPGQTEQHVEIHI MNFCSKNHHRITPEKPKELTDP FKEAACCKLYEIDKKLYRMA EWIKIHKPSICCLQETHLTHKDS HKLKVSIIFKDLAVRFSEEEWR LLEEGQREFFYRDVMRENYETL VSVEPGRAVGGGSHADEGQEP AGCGAVSPGPGAAEGDPRVLV WRSQGRYQPRERGRGASLD GERASPEAA/DGKRALPLSPRPA QLPSRKYQPAAPPQ/PTPTDSSCS SGPTGDGVQGSPLPIRISPGNSP L/PRPHIQLSEGNPCAWAPAPRDI PKLLATSP*PGHVQANQSRPGA WEPALGRSDQRACSASGSAELC ERWPQOAP/APPEEPPAPSPHPA APTGIPGFWESCGECPGAA/PGKG SAPKPSPLHCLESALRGIL/MEGP CASPANEAPAPAPAPARASA A/AEGEDPRPEPELWKPLPQER DRLPSCKPPVPLSPCPGTTPAGS SGGSPGE\APGEQSPGTAAASV Q/VSPAHWPCFS/SPVRYSSGSLP GFSAGEKAQG
19488	49856	C	19603	4	150	
19489	49857	A	19604	148	448	RTRDWSLFLLMFGCVRSFFLLV GLWSCWLRLSEAADLRGECYSS *GGASGVVRSSWWVRLTSFR SETGFTQWIPHWGCRWCSLPLPV RCAPALLSPVVNG
19490	49858	A	19605	136	439	LVHFTEC*LVRLQTLARHSTDW CIYKSLARQKSSPSPHSTQEVQL ASPLTGRQEDCSEPRASPLHSSL GPTERDSICVAASSVRWTRPGA RFS
19491	49859	A	19606	2	399	SKLQKLKRSLSFKTKSLRSKSA DNFFQRTNTSEDMKLQAHMVAE ISPSSPLPAPGSLTSTPARLVCI QVARLMPFRNTSSRSPLFC/RCL QPHDSSGLFLRPARPRAHREER NNSSRVALRAVTLTTERLQLHS

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met/Asp	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, ^=possible nucleotide insertion)
19492	49860	A	19607	1	1262	MPLSYAYKNAETLAGRHTSSW MSRGAYQRRNTRAAGRPEECT DRNWHAGRTRRIWLGQLEERC SDVFGVSVFWVRGLAGSGAK LQFTFTSVTAHRGSKDQKSEQ KQDLLQKAKEQTIHNVKGDP ELPLLAPAACFYSLICPRPPPHIL LIGPFYRELIGPFYRELIGRQLRP GEKSSTAA/VWPRC^AA/RLPGA G/WTAPSAGPAEPTPTWNSRWP ASATRPGSRRRLSLHTSPQAE GAGSGLSOPRKGLPQCSGRLKR SSSAARVGVARQRRRERASEG/ WPACCHILSVLPFCGFGLEA/ISS SPEQTDEHQNCPADIKVMRLA GQPTNARGAANRAQPLHSTVS SHLKAVIFKIQTQQKNSHFPPL FLEMITSLATGRLRPSWVDYA RPALSVSVSRFSLLTSLELLV ETLGECGLL
19493	49861	C	19608	173	394	
19494	49862	A	19609	1	924	
19495	49863	A	19610	3	689	EVQEELEGPVRGAPHQLHQGP VEHLEAPHQIHKGKKVIYFNY LSELHEHLKYDQLVIPPVFLRVT MRSSRACTRAGRRLPPRHRR GPRCPHSSLASVCNTSKTKIKA NSSPLC^GSO*RT*ERKACAPRA CSGDPPACRPSARSRGSTT/KGK PVNFDDYGDIHIPAVILKTFLRE LPQLLTQFQAYEQILGITC/GGE QPACHSLPPDLTEPPRAQLRRPP LPHGLPACG
19496	49864	A	19611	1749	2411	APSLCLVSEHSAPGPQRELPQPPL TFQAYEQILGITC/GSCP/AQGW GAWSADAQPOLLARRPPLPHGL PACGEWGRGELGVKPSGLPSH AGPAWGHQVRTVCATAHQD CISPEGAVEEEIVGG*GC\TEGQ SQRVLQIWPSSQGVSSLSALVPL N\MPTELLIEYYEKIFSTP\EA PG EHGLAPWEQGSRAAPLQEAVP RTQATGLTKPTLPPSPLMAARR

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met/bnd	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, -=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
19497	49865	A	19612	883	2164	EHRRPMRAQASHEGHRHPMRAQASHEGHRPMRGTGVP*G QMSHEGYRRPMRVQASHENTGVP*G VQASHEGRTGIP*EHRCPM RTQVSHEGTGV*ECRRPMRTQ IGPMRGTV*EHRCPMRGTV* P*EAQASHEGHRPMRGTGIP* GAQASHEGHRCPMRGTGVP*G HRRP/DENTGV*GHRPMRAQASH/REHRCP/DEGHRRSP*GHR PMRAQASHENTGV*GAQAS HENTGV*GHRPMRGTV*G HENTGV*GHRPMRGTV*G HEGTGV*EHRRPMRGTV*E FRRPMRGTV*GHRPMRAQASHENTGV*GNR/PYHEGTGV* ECRRPMRTQASHEGTV*EHR CPMRAQASHEGHRHPMSTQAS HEGHRRPMRTQASHEGHRHPM RTQASHEGTVASHEGHRPMRTQ QVSHEGTGV*EFRRPM/PGHG HPMRTQASHEGHRPMRVQAS HENTGV*GJRHPMRGTV*G HRCPMRGTV*GYRHPMRTQ ASHEGYR/PSHEGTGIP*EHRC MRTQVSHEGTGV*ECRRPM TQVSHEGTGV*GHRPMRTQ VSHERRHPMRTQASHEGTV P*EHRCPM/MGHRRPMRTQASH EGTV*EHRPMRGTV*EH RRPMRAQESHENTGV*GAQA SHENTGV*GHRPMRAQASH
19498	49866	A	19613	1	552	VPQDSLQLAGQATPEIPLGL QLHTVLVQEIQELIEAQTRAPGE CAEVRALPAPAAEPEPAWEEAP PERALELEGAPAKDQNTNEELPE TA/PYC/EPLALTLELKAWLERE VGGRRGDQHSPSQLPCP*SW ARWQTCRQAGHLAWPPVPRC REALSIH*NHSPAAAGPFLILLIV YLCAGGA
19499	49867	A	19614	443	991	VDSRPLNTRLMLRTSGRRWTP RPQVDTGP*VNNKTQ*AIRQP/C GYSQPQVQDSLQLAGQATP EIPLGLQLHTVLVQEIQE/RH*G TDTCWSMCRSKSTASTSRWS Q/RPAWEEAPPER/GTGAAGGSSS QGPDQRGAA*NHGGAGEH*KK AGRKSSEERYACCSRQPPP DAGPQLGIQAVCP
19500	49868	A	19615	16	450	

SEQ ID NO: NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, !=possible nucleotide insertion)
19501	49869	A	19616	2	477	PRVRSGHSMDMRVPAQLLGLL LLWLRLGANCDIQVTQSPDSL SVGDKVTITCRASQGNSGLSW YQQKPGQAPTLLIYAASSLQSG VPSRPSGSQGTDFTLTISLQPE DVATYYCLQDYTTPTFTVLQAIT KTPQR!RDV*VCTVLATPPGVIN WL
19502	49870	A	19617	2	675	LPLSSA LPTESGSHLPPSGIMA RPSDPLVVKPQRSSKREPKKVHP GTQSDR!YVKIKR!NW!AENPRG! ID!NVRV!R!RFVKGQDLDAPTLG YG!SNKKTKAHACPSGFREVPG VIINVQGSWEVACLMLQONLY CCRGSVHNVFLPRNRQSPSWG KELAQLGLSGVHPTPLARA!AQ! KEN*VRQLMCNKSYCAEIAHN VSSKNRKA!VERAAQLAIRVTN PNAR!RSEENE
19503	49871	A	19618	2	527	VWAANMPSRLRKTVRKLT!GHG AATGHGPHPRPSTRKAPPGPR* MPGGPAI!HPPGSNFRQNTHPQA YFGKVG*!KHYP!KRN!QSFL PPTVNL!DKLWTLVQ*NRHRVK CLPKNKTGAAPHHMLVRSGY LQSSGERGKLPKASLFFVEGPK FFSRRSLREEGL!RGVW!GGPVSL
19504	49872	A	19619	45	233	
19505	49873	C	19620	95	154	
19506	49874	A	19621	2	241	
19507	49875	A	19622	63	320	RQWGNRLVTA/WSFFSWLSDC EGPGYGTIAEVGQLWGIMAKD LLRHSLASEELALNQNLTCHDQ FAQSTRSSARACGSIFCSTTQGS
19508	49876	A	19623	2309	2560	RNREARFYMTTPNFTETK/R/WF HERVCALE RERERERERERERER RDNHRLVGDISQLKKELDQYL QAIISDLED CNGKRLI!QILEA

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met codon	SEQ ID NO: in USNN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, <=possible nucleotide insertion)
19509	49877	A	19624	4994	7008	QWQQKPKLTNDNLKFIWNQKR DRIAKTILSQKNKAGGITLPDFK LYYKATVTKTAWYWYQNRHI DQWNRTEPSETIPHIYNHNLNFD KPDKNKKWKGKDSLNFNKWCWE NWLAICRKLKLDPFLTPYTKIN SRWIKHLNVRPKTIKILEENLGN TIQDIGMGKDFMTKTPKAIATK PN*QMGSNILNGQKLEAPPLKT GTRQGCPPLSPPLFNIVLEVLR AIRQEKEIKGIGLGKEEVKLSLIS ADDMIVYLENPIVSAQNLLKLS NFSKVSGYKINVQKSQAFLYTN NRQTESQIMSELPTIASKRKY LGIQLTRDVVKDLFKENYKPLLK EIKEDTNWKWNMPCSWVGRINI VKMAILPKVIYRFNAIPIKLPMMA FFTELEKTTLKFIWNQKRARIA KSILSQKNKAGGITLPNFELYVY KATVTKTAWYWYQNRYIDQW NRTEPSEITPHIYNYLIFDKPGK NKQWGKDSLNFNKWCWENWLA ICRLQLDPFLTPYTKINSRWIK DLNVRPKTIKTLLEEDLGITIIDI GMGKDFMSKTPKAMATDKDID KWDLILKLKSFCATAKETTIRVNR QPTKWEKIFATYSFDKGLISRIY NELQQIYKKKTNNPIKKWAKD MNRHFSKEDIYAAKKHMKKYS SSLAIREMQIKTTMRYHLPVRA MATIKNSGNNRQ

SEQ ID NO: NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, ^=possible nucleotide insertion)
19510	49878	A	19625	1	764	GSSEKRKFKTGNQKLSMEVEK NQQMRSLSLYQQRVEGSKCAV RRKGGSPPKAFLAAAEKFLN VPVMSASHEQLVLTGDPNKT LPGSKSRLSGTDSPRACSTFPIW ATKIVTEMQVQLFAACRVQLIK HPRPSAARTAMEVLESGEQGV LQWDRKLSELSEPGDGEALMY HTACQGHEEQVWEEEALQLGL RSGILLNHWKRQLVGGAGILRS AQLHSPYHHWQMISLVSPSPAV MAVMENDDCIMVLCKVMD PNHILDAISEHQIPLSEDQWFSE CALWTSKAYENLVERHILGPHC RPTLETLGISEDDIDIHNPYLD PGVAGLGSRRNVKERGWLSEM KKEGDIFMKIQQ*AICTSGPAAE GLPPPTPVPHVDRPCGT*GP/PP SPGSDDSSPACGPTAACRPARSP APPWRCGPRWAEDVLLTGLCK QQIAEPAFRLQFWWP1

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met/Asp	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, ^=possible nucleotide insertion)
19511	49879	A	19626	1	1430	MNGTAEGQHPWVHSTFNGEPQ SLSSSVRVKNQGPRDQAEALGFQ GNGSTVPAAQARTIARARGSGS GGGDAHQGGGAGAGPQATKR TARLLARGLRRAALRPDGRGV LGAGAGSSQRGGGRRKMETH ISCLFPELLAMIFGYLDVRDKG RAAQVCTAWRDAAYHKSVWR GVEAKLHLRRANPSLFPSSLQAR GIRRVQILSLRRRLSYVIQGMAN IESLNLSCGYNLTNDNLGHAFV QEIGSLRALNLSLCKQITDSSLG RIAQYLGKLEVLELGGCSNITN TGLLLIAWGLQRLKSLNLRSCR HLSDVGIGHLAGMTRSAEGLP GPGAAHATGLPFEAHRSFSKAHL PRADGPEAPQPQLLWGNLGRW PPAPVAHGQPAHAQCPACPDNI SDTGIMHLAMGSLRLSGLDVSF CDKVGTDQSLAYIAQGLDGLKS LSLC\$/RRGLRRAALRPDGRGV LGAGAGSSQRGGGRRKMETH ISCLFPELLAMIFGYLDVRDKG RAAQVCTAWRDAAYHKSVWR GVEAKLHLRRANPSLFPSSLQAR GIRRVQILSLRRRLSYVIQGMAN IESLNLSCGYNLTNDNLGHAF/R AGDRLPALSQPEPLQADH*QP GPHSPVPQGP/ARCWSWEVAAT SPTLAFCSSPGVCSASRALTSAA AATFRMWDRAPGRHDAQRGG GLPGPGAAHATGLPEAHRFS
19512	49880	A	19627	293	1520	TTMDGSHSAALKLQLPPTSS SAVSEASFSYKENLIGALLAIFG HLVVSIALNLQKYCHIRLAGSK DPRAYFKTKTWWLGLFLMLLG ELGVFASYAFAPLSLIVPLSAVS VIASAIIGIIKEWKPKDFLRR YVLSFVGCGLAVRGTYLLVTF APNSHEKMTGENVTRHLVSWP FLLYMLVEIILFCLLLKYFYKEKN ANNIVVILLVALLGSMTVVTV KAVAGMLVLSIQGNLQLDYPIF YVMFVCMVATAVYQAAFLSQ ASQMYDSSLIASVGYIISTTIAIT AGAIFYLDFIGEDVLHICMFAL GCLIAFLGVFLITRNRKPKIPFEP YISM DAMPGMQNMMHDGMTV QPELKASFSYGALENNDNISEIY APATLPVMQEEHGSRSASGVPY RVLEIHKKE

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, ^=possible nucleotide insertion)
19513	49881	A	19628	751	2034	VSSSPTLSGCMQRKEYRIPKKLTNMPFLGSQPSLLALRSCHPTGRTCSA/SQVALFCLAARHVSQIGALLAIFGHLVVSIALNLQVSFHIIRLAGSKDPRAYFKTKTWWLGLFLMILLGELGVFASYAFAPLSLIVPLSAVSVIGKTIIGHIFIKEKWPKDFLSKFVLSFVGCGGLAVGTYLLVTFAPNSHEKMTGENVTRHLVSWILFCCLLLYFYKEKNNANIVIVLLVALLGKLTVTVTKAVAGMLVLSIQGNQLDYPIFYVMFVCMVATAVYQAA*VSQASQMYDSSLIASVGYILSTTIAITA GKGFYLDFIGEDVHLICMFALG*VLAFLGVFLITRNRKKPPIPFEPIYISMDAMPGKVNMMHDKGMTVQPELKASFSYGALENNDNISEIYAPATLPVMQEEHGSRSASGPVY
19514	49882	A	19629	19	933	QSARPSLKRARSQRGRPLPSRALVFLFLFFFFFFNFLPHTQPSAHKDMTTNAGPLHPYWPKQHRLDNFVPNDRPTWAYTGLQGLFSVTGGRLSWTTWAVVQGRAPGL\PIGDFGRATVPCCVWLLQWCQFIIHLVIEGLVPFSNYERPCFGDQSLLYSQLW\KEYCQGETARYILGVTNFTVCM\ETITTSFA\WGEPSFLWWVIV\FLI\QHPL\RFIL\QLVVSVGQIYG\DVLYFL*RATPTDFQHGKPGPTPLLPGFSVFHEMPLWLVPAPGSPLCLDA/V*KHPQLMPQSNAWNAKGPQPKSKK
19515	49883	C	19630	113	257	
19516	49884	A	19631	143	330	HHGPVPFPGLIS*HSLHCPCTPGGKNVFFFCEYFLKLAGIETTNCSDAKRGKKVCLIPR
19517	49885	A	19632	3	432	
19518	49886	C	19633	112	192	
19519	49887	A	19634	1	4410	MARPLALPLTGMSAPGSSLTTIPHTPSHPRSPTPDTVSHPRSPSTPDTVSHPRSRPSTPDTVPTPVTYTRHRVPPTLTVYTRHRVPPTLPVYTRHRCPHTHAPGLHQQTMCPTHAPGLHQTCPCTHAGLHQTPSHPRSPSTPDTVSHPRSRSTPDTVPTPVLPVYTRHRVPPTLTVYTRHRVPPTLPVYTRHRCPHTHAPGLHQTMCPCTPRSRSLPDTVPPTLPVYTRHRVPPTLPVYTRHRPHTAQLRHQTPSHPRSR

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met/Asp	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
19520	49888	A	19635	1	444	
19521	49889	A	19636	3	1017	SSRPVRPRPAARLSAMSSSTQFN KGPSYGLUSA\WVKNRL\SKYD PKAE\ELRTW\IEGLTGLSIGPD FQKGW\KDG\TIL\CTLMNKLQP G\SV\PKINRSMQN\WHLQLENLS NFIK\AMVSYGMNP\VDLFEAN DLFESGNMT\QVQVSSL\ALGG KRPKTKGA\EGGL\DIGV\KYSE KQERNFDDATMKAGQCV\GUL QMGTNKCASQSGMTAYGTRR HLYDPKNHILPPMDHSTISLQM GT\NKCASQVG\MTA\PGTRRHI YEYQAGNPTSCDNFSMSLQ\QM GYTQGAQTQSGQVF\GPGRPDI *TPSTCPQGT\IADGAPSGT\GD\CPDPGEVPEYPPYYQ\IEEAGY
19522	49890	A	19637	1	479	MQGLRVSHSTFYTLIPEV\TENP HRLDFHWFLSAQLERVASGTL KKKESPRPKV\LGSA\RW\DLPV\PPGWCNSTALQ\SPRS\SDQV\SE RGMEA\FFLPMPMSE\VASVCCRF SPWTSQKPOL\TS\DRKLQGKR *WFSTGVWAS*DHS*ERRCSQC PKTTCW
19523	49891	A	19638	2	501	FVPEERSSETALQRC\SLPPGRRA APDPGLQGLRG\LSLGG\SELES RKAKLRAAEGLRRKTTEINQRD TADRC\TRGH\SPGES\PPKPSAF SL\LSVPRSGKLRL\FSRREPA AN\SHRLRRHREKKCFHPPFTL NLIASGTSLEGGGVAP\TWSTGR SQRALPSTL
19524	49892	A	19639	1	1122	RFLILNHAVF\YEYQDIFV\ASFP\SI FFNIHC\RGEGEREKG\FA\GKDRT PPPSTLLCGSGH\LP\PLASRRP\PR PRCACCLPGGP\LS\SSA\LEAG\Y WRFPKL\SG\KRS\HTP\WV\WPQ\Q PLPNPSPGK\WV\WAS\SEALQ\GT RA\RGIAELTH\LLR\LP\ARRG\TQ RPA\PGH\RA\GASP\QFRE\ASSRG PGLR\PR\PG\RT\REL\GP\K\RRV\WA TAASW\PRG\TEPC\AAA\RRRRR RR\AR\GEL\SP\RT\WSS\DT\TESTF ALSCDPS\PRHQS\VP\KG\RV\GSC KG\KL\ANKG\FFC\PT\W\QR\PI\RV\AS VDM\ELL\HFV\PK\RA\LP\G\FT\IA\SF LSSA\PL\CP\WY\SG\SN\W\LR\N\PL K\PR\LA\LF\Q\RS\AA\PR\L\H\FS\GA SL\QV\GERR\Q\J\RD\FR\VS\AGA

SEQ ID NO: NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
19525	49893	A	19640	14	618	GNENVKSGRKTSLSFVLSDFT ASSALLASDSSRWMSLQSASEC \PGRAAGSGPGYG*PVSEVTGG PLSAHTHSSL*TSQRGCPGPIPE HHGAGPFP*GPGLKDVSGRGG NGCWGRRKPAHIMGGGLGPAT PLQFPPRPSPPPPPLGPQ\PPPPP SPPLGPASSPP/CLPHRPPPPPPP PSRCVTAPCVTAPGPAGTAA RRH
19526	49894	B	19641	42	121	
19527	49895	A	19642	1	153	
19528	49896	A	19643	104	355	
19529	49897	A	19644	459	988	DPRTMNLAISIA\LLTVLQVSR GQKVTS\LT\TA\CLVDQSLRLDCR HENTSS\SPSKYEFSL\TRETKKH \WLFGTVGVPEHTVYRSRTNTS KYNMEGPLTYSAFH*ARTRGT QVLQFHQFQGALSP\I\FLSRNVIT VVQRTNWKVCEGI\SSLLAQNNTS WL\LRLLLSLSLLQ\ATDFMSL
19530	49898	A	19645	1	950	
19531	49899	B	19646	55	1459	
19532	49900	A	19647	1	165	
19533	49901	A	19648	183	700	PNGNQP\PRETPQR\ISRGIGQLGT AVASSGGSRSLPRSASAEPQAQG AAARRAA\PGPAGRCAARGAG AGSARLLP\APAH\APPEQGRR/ SRTARSRAAPQPPPSSQPSQSQL GPRPSQGA\QRRGPSSPGPRAG CRA\*EALTPRLWRS\RTPSSR GLGPHVRGGIFSPK\IPT
19534	49902	B	19649	71	264	
19535	49903	A	19650	3	810	GVSPCWPGWSRTPDFGSNPKCP PIRASPGAE\QLALSSTVTTPYW GILVTA\VFPH\GLR\PRQCRQDH PAGRQGP\GPGEVPEIL\GQSGCT DRTWSKAGGR\TQAPGPRSRAG RRVSGQEIRAPG\PLGCRHGG/V GAPWTPEAASPLTATE\PSCPH/L QAPCGY\MP\LSVSPR\RYRGPA GDQKV\MLKFKAFCL\DYWQF LCLQPLH\GAY\KRDSDLMTW\I GLLPEV\TGAAGT\TSPN\VHTSGR FFRACVFCPV\HTLVKKEPHPGQ QEII\MEPS\WPWSP

SEQ ID NO: NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
19536	49904	A	19651	258	1378	REILSLDRLPGATPNQALSAEA ACPKGQTSLLCGAMGIQGLAK LIADVAPSAIRENDIKSYFGRK VAIDASMSIYHFLIAVRQGGDV LQNEEGETTSHLMGMFYRTIR MK\ENGIKPI/YKSGELAKCSEL RVAEAEKQLQQAAQAAEQVV EKFTKWLVKVTKQHNDKCKH LLSLMGIPLYLDAPIEAEASCAA VKAGKVVYPVATEDMDCFTFGS PVLMQHLTASSDYCKSIWSGP KRAVDLQKHKHSIEEIVQLRDPN KYPLPENRLHKEAYQLFLEPEV LGPESEVELKWSEPNNEEELVKFV CGEKQFSEERIHSGVKRLTEK GGGERPGRP/DWTQPGRASPTKR PDHQEDQHTRSRSSEGSHE\GWL
19537	49905	A	19652	1040	2322	LPACPPASTPASTMSIMVTQKS YKVST/SRWSSGPQAFCGNCSYA RGPGACISSLSSRVGSSIFRGL GGSYGGASGMGSITAVTVNQS LLSPLNLEVEPNIQAVCTQEKT LNNKFASSIDKVQFLEQQNKML ET/ESY\NSLKQQLETLGLERLK LEAELGNMPGLVEDFKNKYED EINKRTEMENEFVLIRQYVDEA YMNKVELESCLEGLTTEEINLLG QLYEEEIQKLQSQILDTSVVL MNNHSLSLMDMSIIAEVKAQYEE MANHSQAEAESMYQIKYEEELQ TLAGKHGDDLRRHAKTEI/S/EM NQNGAKQDMA/*QLHEYQELT NIRLALDIKITIYRKLLGEESQL ESGMQNMNIHMKTTSGYAGGL SSAYEGLTSPSLSYGLGSSFGSG MGSISFSHTSFTRAIVVKKIEHD GKLVSESSDVLPK

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19538	49906	A	19653	1040	2322	LPACPPASTPASTMSIMVTQKS YKVST/SRWSSGPQAFGNCSY RGPGACISLSFSRVGSSIFRGV GGSYGGASGMSITAVTVNQS LLSPLNLEVEPNIQAVCTQEKV LNNKFASSIDKVQFLEQQNKM ET/ESYINSLKQQLETLGLERLK LEAELGNMPGLVEDFKNKYED EINKRTEMEFVLRQYVDEA YMNKVELESCLEGLTEEINLLG QLYEEEIQKLQSQILDTSVVL MNNSHSLDMDSIIAEVKAQYEE MANHSQAEAEQSMYQIKYEEQL TLAGKHGDDLRRHAKTEI/SEM NQNGAKQDMA/*QLHEYQELT NIRLALDIKITIYRKLLEGEESQL ESGMQNMNIHMKTTSGYAGGL SSAYEGLTSPSLSYGLGSSFGSG MGGSISFSHTSFTRAIVVKKIEHD GKLVSESSDVLPK
19539	49907	A	19654	152	207	
19540	49908	B	19655	75	402	
19541	49909	B	19656	1	2319	
19542	49910	B	19657	1	1341	
19543	49911	A	19658	198	1118	LHAPNSLHHHLPRDLI*LLPLPL QHRVSDPGLHSALRPMEEHRA QS*QPSAPEDA VQA*WGHGGH SPGPDRAGCHHCRGDQERVST HHVLPVCHHPDDAYGGCGAG WNPDL/PQQMRSHWMSPKIRPA NWTRTSWWALPQAPGLSPGAQ SWPSFVPRTTPTPGTTCTPTPSW *SWRSTSRTSSSLNPFTESLKNS LRTSKPFGWSQSAMA TPCPLLP PASRVELWPETW\PLGQGHATS SQWKCVPERKL*QGGEAGGEQ LGREPKPSPPSSFLTGQRQEKP EEYCSLLVPLQYFGSRGTHADL LHG

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met cod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
19544	49912	A	19659	1	2707	MPGPHPASASCPPRLFTP RRRAF CPLRICAPLAAAFCPPRFLPHT RRR AFLLLCRRGFLLPPCLGGG LAAAFFPHPPLPFLRPHRRGFLP HRRRGFLPPRLGFLPAAAFYPP PPRVFAARRGVPPSPRFLFARRA FCHTPPAAAFPSAA AACFCPTA DTAFC TLAALAFCRRGFLLPPRC RGFLPLRHRRSFLPHRRRGFLPT AAFCHRGFLLAATFYPPRLFAP RCHGFLPPCRSDFFAAACFRCR RRGFLPLSPLFAPAAAVFCPRH RGFLLPRLFAPVTAAFCHRDFL PPPPRIFVPAATALRAGAADS AASSTGV LARAALRGPCGLHRV ALPVEAMGEKEGGGGDAA ATEGGTGAAASRALQQCQQLQ KLIVFIGSLCGLCTKCAVSNDL TQQEIQTPEPAKPAKPAQSOTRQ PSQSPSHPASQASQTSQPAKQPA SQASQPAKPAKPPSQPSQPSH R ASQASQATQPERPASQPSQASEPS QPSLPASQASQDRQPAKPAKPD SHPRQPSQP/YQPSQPASQASQA SQPAKPSRQPSQPROPSQLASQ ASQSTQPLKPAKSPVQQSQPSQ PASPDSQASQASQATQPAKPAK PPSQAAQPAKPAKPPSQPAQCQP PSQRAKPAKPARQPSQPSQSSPP ASQPSQACQPSQPGSQAQASQ AAKPGMPAKPARQPSQPSQPS QARHASQAIQPAKPAQ*PSQTS

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met cod	SEQ ID NO: in USNN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
19545	49913	A	19660	1223	2286	RQCFKATEQPPA\HHPSSQPSRQ PSSQPIIYPSIICGRKSGIOPKFQ LNG\*MVNG\*MDEISRERHEWP CNYQVRPKAGEKQPGAEANRE TRPEGGTP/RGERGRQGPATRR QKSTPTEAGPSDLEKQIARQEAP AGTDEIERQQ\*RPH\*AP\*KIPVE WVNGEWLNGRMPGDHEWQC NYQPAIQPAIQPANQLSIHNLW TQFRHSTKIPVEWVNGEWLNG RMPGKHHEWQCNYQPAIQPAI QPANQLSIHNLWTQFRHSTKIP VEWVNGEWLNGRMPEDHHEW QCNYQPAIQPAIQPASQLSIHNL MWTFQFRHSGQIPVEWVNGSRL HGRQQGIFMHGNATSSHSPSIQ PAIQPAIQPANQLSIHNLWTQFR HSTKIPVEWVNGEWLNGRMQR NIMNGNATISHSPSIQPAIQPAIQ PVNHLISIHNLTQFRHSTKIPV EWVNGEWLNGRMPGKHNHEW QCNYQPAIQPAIQPANQLSIHNL WTQFRHSTKIPVEWVNGEWLNG RMPGDHHEWQCNYQIAQML QSRTAASHSPSIQPAIQAAIQS ATHLSPNLWTQVRHSTKIPVE WVNGEWLNGRMPGRDMNGH ATIRYGPKPEKNNRAPRQTEKQ GQKGAAHQRREGKARAGNEETE KYRSRRAIRPRKTDASRSSRGH RRNRKAAASAATLGPIEDTNQNK LHVRDTGLEVKAISIQPGTLM
19546	49914	A	19661	39	599	GASPNNQQNRPALARQAPPQ/G /PPGEPERPLPSGHGEPCCRHR PPPFPQPP/AGTQKPLLQGPGGG *PAENAPTAALGSPAPRPGCQA APPPRSGAGRPDLPTLAGPRPAP A\PPPSAAPPPPSGAPSR/PAAG QRQLSGVSSGPGLWW\*VGRG RGLPAFAQIAQHGVQGRRRTP AGRKPRSPAGPR
19547	49915	A	19662	39	599	GASPNNQQNRPALARQAPPQ/G /PPGEPERPLPSGHGEPCCRHR PPPFPQPP/AGTQKPLLQGPGGG *PAENAPTAALGSPAPRPGCQA APPPRSGAGRPDLPTLAGPRPAP A\PPPSAAPPPPSGAPSR/PAAG QRQLSGVSSGPGLWW\*VGRG RGLPAFAQIAQHGVQGRRRTP AGRKPRSPAGPR

SEQ ID NO: NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USNN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, V=possible nucleotide insertion)
19548	49916	A	19663	1	379	YFPHTAIRYPPHLNRQDPLKDL VSLACDPASQQPGPLNGSQLK MPSHCLSAQMLAPPPLGIPRLA LPPATKAATTSEGGATSTPTSP/S PGIWDSKGLLPSPLLHRPRNPR GQHSRPPAHVFGGKLE
19549	49917	A	19664	3	285	
19550	49918	A	19665	2	1556	RLEFPGRRFRSAPAPAGPAPPA APGMYSSPLCLTQDEFHPFIEAL LPHVRAFAYTWFNLQARKRKY FKKHEKRMKDEERAVKDELL GEKPEVKQKWAWSRLLAALKLRKD IRPECREDFVLSITGKKAPGCVL SNPDQKGKMRIDCLRQADKV WRLDLVMVILFKGIPLESTDGE RLVKAACQCGHPVLCVQPHHIG VAVKELDLYLAYFVRERDAEQ SGSPRTGMGSDQEDSKPITLV TDFQESFVTSGVFSVTELIQVSR TPVVTGTGPNSLGEQVQGHLAY DLNPASTGLRRTLPSSTSSGSKR HKSGSMEEDVDTSPGQGDYYTS PSSPTSSRNWTEDEMGGISSPV KKTEMDKSPFNSPSPQDSPRLSS FTQHHRPVIAVHSGIARSPHPSS ALHFPTTSILPQTASTYFPHTAIR YPPHLNPQDPLKDLVSLACDPA SQQPGPSWYLG*QRSSSLAPSPS SQESQGAACQAPGPRFRWKIRV NKNTPADSQPGQKDTHRRTH SGGKEKTAE
19551	49919	A	19666	1	477	
19552	49920	A	19667	1	440	WTQDM/EGGISS/PVKKTEMAK SPFNNSPSPQDSPLSSFTQHHRP VIAVHSGIARSPHPSSALHFPTT SILPQTASTYFPHTAIR/YPPHL NPQDPLKIDLVS\ACDPISQQP GP/SYSPDTPSANR\SFVGLQPR DPAGIYQAQSWYLG

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met	SEQ ID NO: in USNN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, + =possible nucleotide insertion)
19553	49921	A	19668	2	1963	CPTGFEGHGPCCRRTPTGRVSVTRCRRAWGSLRVSVCGPRAQLQAEVLVQEQQGGVCLCIVIMP LTPGRTPRLPRGRALCNGRRGVWGGGGSPRGLLPAQAPGDPEVCKFRFLDRCFPPYAGPSDSLRLGRAVGPSASALLTSLRSLQLQDEFHFPFIEALLPHVRAFAFTWFLNLQARKRKYFVKHKEKRMKSDERAVKDELLGEKPEVKQKWA S RLLAKLRLKDIRECREDFVLSITGKKAPGCVLSNPDQKGKMRRI D\CFRQADKVWRLDLVMVILFKGIPPLESTDGERLVKAACQCGHPVL/CALKPQHIGVAVK/ENLDLYLAYFVRERDA*QSGSPRTGMGSDQEDSKPITLDTTDFQESFVTSGVFSTELIQVSRTPVVTGTPNFSLGELHAHLAYDLKPASAGLTRTLSSTFSSGNKRYKAGSMEEYVDSTPWGDD*T+PSSPTSSRNWTEDMEGGISSLVVKTEMDKSPFNSPSPQDSPLRSSFTQHHRPVIAVHSGIARSHPHSSALHFPT\TSI LTPDGPSPTFPHTAIRYPPHLNPQDPLKDLVSLACDPA\SQQP\GP LNGSQLKMPSPHCLSAQMLAPPPPGLPRLALPPATKPATTSEG GATSPSPSYSPPDTS PANRFSVGLGPRDPAGIYQAQSWYLG
19554	49922	A	19669	332	551	ESWLGRGHQPPP\GLFHSKPSSGTAVLPAWRPPSPGPAGDDASPSPS*AGPGAGANPGA*QRSASGEKGS
19555	49923	A	19670	1614	1673	
19556	49924	A	19671	72	227	EEFPMGHTA*WSCEKRATILQI QEW*IQQLAPCAWQS SHRST RAHES SHG
19557	49925	C	19672	1	604	
19558	49926	A	19673	653	889	VYPQTNWKQNTGTRVIAALFTMAAKGENK*PSMGEW\IKQMWSIHTMERHAAIKRIEAQVYATM*MKLKSMILLERNQT

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19559	49927	A	19674	75	1619	EVSI PAQTMWTADEIAQLCYEH YGIRLPKKGKPEPSHETLLA AVVKIQSPAIDKACDTPDKPVQ VTKEVVSMTGTKCIGQSK/M* RKNGDIL\NDSHA\EVIA\RRSFQ RYLLHQLQLAATLKEDESFIVPG TQKGVVWKLRRD\LINVFFSHT PCGDASIIPMLEFEDQPCCPVFR NWANNSSEVASSN\LEAPGNER KCEDPDPSPVTKKMRL\EPGTA REVTNGAAAHQSFGKQKSGPIS PGIHSCDLTVEGLATVTRIAPGS AKVTDVYRTGAKCVPGEAGDS GKPGAA\FHQVG\LLR\VKPGRC DRTRSMSCSDKMARWTVLGC QGALLMHLLEPIYLSAVVIGK CPYSQEAMQRA\LIGRCQKV S\ALPKGFGVQELKILQSDLLFEQ SRS\AVQAKRADSPGR\LVPCG\A AISWSA\VP\EQLDVTANGFPQG TTKKITIGSLQARSQISQKVELFRS FQKLLSRIARDKWP\HSLRVQKL DTYQEYKEAASSYQEAWSTL KQVFGSWIRNPPDYHQFK
19560	49928	C	19675	45	140	
19561	49929	A	19676	3	354	AKIKTGYK\REH\INLGCMDMFDI VGPSIRGALV\LG\YEGWLAGYQ MNFETAKSRVTQSNF\AVG\YKT DEFQLHTNVLLNLERTCFLTG PTPTPPPLSWLPGT\TFSLTWAM TGRY\TINSQ
19562	49930	A	19677	1	983	AARSAPLPGSAPCLRVAAPAVA ASEPAATSSSEQKMAVPTYADL GKSARDVFTKGYGFG\LIKLDLK TKSENGLEFTSSGSANTETTKV TGSLET\KRYWTEYGLT\TEKW NTDNTLGTEITV\EDQL\ARGT* SLTFDSSFSPNT\GK\KNAIKIT GYKREH\INLGCMDMFDIAGPSI RGALV\LG\YEGWLAGYQMNF* DCKIPE*PQSNFWQLANKT\DEF QASR*M*ND\GTEFGGSIYQKV NKK\LETAVNLPWTAGNSNTR FEIAAKYQ\VD\PU\DACFS\GKVN SS\ILG\G\Y\T\QTLKPG\IKL\TLSAL \LDGK\N\WNA\GGH\K\LG\LEF QA

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19563	49931	A	19678	551	831	CHPSSIVLCAPASLSDHQWPPP ALCPSSRPQ/PCALPWGSTLSSR PQPCTHPSGIEA*LCLPLVSQL G*LPVLPAPQHLVPPCPSTCPMT LKLF
19564	49932	A	19679	47	980	VCQYCTARMADFGISAGQFVA VVWDKSSPVEALKGLVDKLQA LTGNEGRVSVENIKQLLQLCLVP GSTTLLHSA\ EILA\ E ARLRRPGG C FLKEPVETAVDNNNSKVKTAS KLVCSALTLS\ GLVVEKELQREP LTPEEVQSVREHLGHESDNLLF VQITGKKPNFEVGSSMQLKLSI TKKSSPSVKPAVDPA\ AAK\ WT LSANDMEDDSMDLJDSDELLDP EDLKPPDPASLRA\ ASCCEGKK RKACKNCTCGLAEELEKEKS EQMSSQPKSACGNCYRGAMP GCASCPTYLGMPAFKPGIEKVLLS DSNLHDA
19565	49933	A	19680	29	1270	FPPWP\ AVFQVCQYCTARMADF GISAGQFVA\ VWDKSSP\ EAL KG\ VDKLQAF/TPGNEGRVSV\  ENIKA\ AVAILPTKNPSFGHYFV Q/CLVPGKAPLWHS\ A\ DFWAG NPPGFLRPGWMFFF\ KEPVETA VR\ Q\ AKWKTASKLIC\ CSAL\ TLS GLV\ EKL\ KELQREPL\ TPEEVQSV REHLGHESDNLLFVQITGKKPN FEVGSSR\ QLKLSITKKSSPSVKP AVDPA\ AAK\ W\ TLSANDMEDD SMCIFCGCSLTHRWP\ LEHVVQV E/IMMDQPKRRTRVDT\ FFTPRT PKFPSRS\ PASHFSFIKQKT/TP VSLIALNTL\ QDL\ DSDELLDPE DLKKPDPSLRA\ ASCCEGKK KACKNCTCGLAEELEKEKS QMSSQPKSACGNCYLGDAFRC ASCPTYLGMPAFKPGIEKVLLSD
19566	49934	A	19681	3	405	QDFGTRALAAVQIKNNGGSWWC PPVSLAA\ AVGPRPQQLGRPVYRV APHGQVIGLSFAMWKTLT\ FFR GASPVGVSQAMLKCV\ A\ SPHH WRARRDPEFIA\ Y\ P\ H\ R\ IRT\ K\  FPWGUDGNHTQQYITPH\ VNPLS NLATED

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19567	49935	A	19682	2	450	VNKAGGLIYQLDSYAP/RAEAEKTFSYPLDLLKLHDERVLVAFGQRDGIRVGHAVLAINGMDVN GRYTADGKEVLEYLGNPANYPSVSIRFGRPLTSNEKLMLASMFHSIKFVVLADP\RQAGIDSSLRK IYEIYSDFALKNPVSYLEMP
19568	49936	A	19683	1	2034	
19569	49937	A	19684	202	453	RRLWRGSCPRCGGKARDGMG VRGR/YSEG/RERV*FGGPPRGS TWPLCGRWRRPARPSAHLRWS AMCPNTSDAAGACAAVRCG
19570	49938	A	19685	269	326	
19571	49939	B	19686	98	562	
19572	49940	A	19687	1	2223	
19573	49941	A	19688	374	1107	IPVSERQGSDWRFFSVYVNKA GGLIYQLDSYAPTGLRLEKTFIS YPLDLAGSS*HDERVLVAFGOR GRHPEWGHAVLAINGMDVN GRYTADG\KEVLEYLG*PLLNYP VSIRFGRPLTSNEKLMGLP CFHSLFAIGSQACLPGTREASR HLKILGRQDTFKLH\CYQTLTG IKFVVLADPRIQAG\IDSSLRKI YEIYSDFALKNPVSYLEMPIR CELFDQNLKLALAEVAKEAGTF
19574	49942	A	19689	119	288	ALHUNNSDVHQKLLPVQSLKKS *GRHRNNTCNQRVHA/SSTSRE FFTKLNKNDNLKPK
19575	49943	A	19690	92	317	KSVGPNFPLPSGNMNDN*M H*HPFSSVTQAFRLRVLQSIQR PL*TFNPGSSSLFSSI\GQSNFPL GVAVLRP
19576	49944	A	19691	27	389	NFKTLKNN*IYK*MCSQEIKILS *KLIRFWYEIHAFFPWAHGVVF CVAQEFCLPTVVLLPVPRLLIM KDMVRRLQELRHTEQVQRAYA LNCGEGATVSYEIQIRVLREFGL ADAAAELLQN

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19577	49945	A	19692	313	2255	KTPQVQQPFPRTQGAAGAGAP SGRSGERAAGRAGPSGGSGGG QDSAHAGEAYRVRGILLRKTFQ CLKDYFLTYYTSSKKVVPVKVPC RQVLTDIKCSLPRSSHNRARTV SNDFPRKCSRERCTHCMRPP GRRPPNGNMNSWKWPSGDESK WRRGEPGAVPEPEPLTGEERA AAAVGGGWPGVLAPVRTAVL VAAAAAEATAAVPAAAAAAGG ASGHCHNHPVMQGRNLSHRFLL PLHHSPYQFGTSSYSQQGYGCE SKLYSLDHGHEKPQDKKKRTS GLATLKKFIKRKSNRSADHA KQMRELLSGWDVRDVNALVE EYEGTSALKELSLQASLARPEA RTLQKDMADLYEYKYCTDVDL IQFETCFPVHRAILARCPFFK/I TAFFLTRVGRDNNGHQYSW Y*YAHVFCFVTLPLYRRVWEW EDSRFQNVDILVQLSEGIWEHQI PLM*DMRGTLI/DMCYYDVVL SFSSDSELVEAFGGNQNCLDEE LKAHKAVISARSPFFRNLLQRRI RTGEEITDRTLRTPTTRILDESIIP KKYATVILHCMYTDVVDLSVL HCSPSVGLSEVQALVAGKPN MTRAEEAMELYHIALFLEFN LAQGSCWEICPPNDEANQEQRS EGSRKWAPTREGSKGRSHASA
19578	49946	B	19693	4	3923	

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19579	49947	A	19694	1	2154	MEYYAAMKTEIMSFALTWIE LEAIVLCELTHVLSELMQKQKT KYHMLSGLGSPVPTFALWNFDV AQDFHIFIENARSSQCRGRPRM TGAGAGAPSGRSGERAAGRAG PSGGGGGGQDSAHAGEAYRVR GILLRKTFQCLKDYFTYYTSS KVVPVKVPCRQVLTIIDKCSLPR SSHRNARTVSNDPDKSCSRER CTHCMRPPGEGRPPNGNMNSW KWPSCDESKWRRGEPAVPEP EPLTGEERAAAAAVGGGWPGV LAPVRTAVLVAAAATAAVP AAAAAAAGGAGSHCNCNHPVMMQG RNLSHIRFLLPLHHSPYQFGTSS YSQQGYGCESKLYSLDHGHEK PQDKKKRTSGLATLKKKFIKRR KSNRSADHAKQMRELLSGWD VRDVNALVEEYEGTSALKELSL QASLARPEARTLQKDMADLYE YKYCTDVLIFQETCPVHRAI LAARCPFFK/ITAFFLTRVWGRD NNGHQYSWY*YAHVFCVTPL LYRRVW\KEDSRFQNVNDILVQL SEEFGTPNSLDVDMRGLFDY CYYDVVLSFSSDSELVEAFGGN QNCLDEELKAHKAVISARSPPF RNLLQRRIRTGEEITDRTLRTPT RIILDESIIPKKYA\TVLHCMYTD VVDLSVLHCSPSVGSLSEVQAL VAGKPNMTRAEEAMELYHAL FLEPNMLAQGSCWECIPPNEA
19580	49948	A	19695	1	163	
19581	49949	A	19696	1	207	
19582	49950	A	19697	1	579	PTRPGQAGSSSAMAAQRLAKR VLASKLQSPSRARG/PCAGSPGG LQK/RGHARVTVKYDRPQGSLQR RLDVEKWIQDPLEGLYRRIQEA DIMPMSRNIDELLE\LESEE\ERS RKIQGV/LRDS*KSCGKPVEDFI QELLAKLQQLHRQ\PGLRQPSPS HDGSLSPQ\DRARTASPLTLLA LFPGPPERRPALLCVLSCI
19583	49951	A	19698	2	151	PPSPPPPLPPPPPLPPAPSLPLSPF DLQPQPVLDLTLGV/LF*LCRKKI SVS
19584	49952	A	19699	2	310	

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19585	49953	A	19700	1	688	LTWMTTERVDFTALLPLEPPLPP GTLPQPSPTPPDLEAMASLLKK ELEQMEDFFLDAPLLPPSPPL PPPPLPPAPSLPLSLPSFDLPQPP VLDTLDLLAIVCRNEAGQE\EV G\MPPLPPPQQAPSFLLLP\QPSR WGPLTHIPGQPTRGGP\AKQKEE RPRNKSAAALKVTPSGKRARG\*S PWRRAKSQGLEGEFASLKER\A ESVEREIQYVKD\LLIEVYKARS QRTRSC
19586	49954	A	19701	3	902	AAMATPARPGEAEDAAERPLQ DEPAAAAGPGKGFRFLVRICFQ GDEGACPTRDVFVVGAILRSIG MDPSDIYAVIQIPGSREFDVFSR SAEKLAFLRVEEYKREQEDC WETFGGAGGEASPA*RRSSSS GTRRWWTWRTL*LGSATATCW PCIGESDRQVLDDL/LGSTNARS SCARGRAGSGTCGPPSSWGP G/CYSWYKGQPKTCFKCGSRTH MSGSTCQDRCFRCGEEGHLSPY CRKGIVCNLCGKRGHFAQCP KAVHNSVAAQLTGVAGHLNTR LPARVNTQASLSSLKCPKLLF
19587	49955	A	19702	1359	1981	QSPFNNDLPGVPVSA*LHSLPP HHPSKG*GVAKSPPVYPAGILL VCNNCAAYRKLLAEQTPSVRK WALRQRNEPLEVRLQRLERER TAIKKSRRDNETPEEREETDEQ RARRLQRDREAMRLKRNANETP EKRQARLIREREAKRLKRRLEK MD\MMRLAQFGQDPSAMAAL AAEMNFFQLPVNGVEL\DSQLL GKMAFE\EQNSSSLH
19588	49956	A	19703	1	1875	

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19589	49957	A	19704	1	673	MSAKDGTCTLQDCMYKDVQK DWPGYSEGQDQLLKRLVRAH NTQRQRQNERSDTRPCQRAAP RRFSHGTRRGTLPLASPRDARA PRTGHCRTRQRLDRTGCGFPPL TGAWAMLADWIHEGTPSRGRS DNDEPSAGSVGGLRQHGPGR APKLTTTKVAKALASPVLGQKIA ALCLGLTAQGLNIMDNPNGSLAI HVHPDSVLTRKTNPCHTHIWGFT QREPPLVANMSAKDGTCTLQD CMYKDVKQDWPGYSEGDDQQL LKRVLVRAHNTQRQRQNERSD TRPCQRAAPRRFSHTRRGTLP LASPDRARAPRTGHCRTRQRLD RTGGGFPLTGAWAMLADWIH EGTPSRRGRSDNDEPSAGSVGGL R/HAWPRTKSPKANNH*ESTG QPGAGPKNCSPVLAGYSPGPOH HQQPGLPGHTCP/SRTQCC*PGRP TPAPTSGVSLRGNPLWWP
19590	49958	A	19705	1088	2273	SPCLLTGGHLPADTSYRRAPAG IWQVPLWDEASQRKE*YQHQQ KKMSTQKPHPKDHNSPAREQ/ SSMENKFHELTEVGFRKITSLE KNINDLMEKNTARELREAYTS IKSRIDQAKESISEIEDQNLNEIKC EDKVREKRMKSNKQNFQEIWD YVKRPNLRLTGVPESDRENGTK LENTLQEIJQENFPNLARQANIQ IQEIJQTAQRQSSSRATPIHIIVR FAKFEIKEKMLRAAREKDISMR QKINKDIQDFNTVLDQVDLIHV YRTVHPKSSEYTFSAPHHTYC KTGHIIJGSKTLLSKCKRMEEIJTN TLSDYSIAKLELRRIKKTQNHHT TWKVNTLLVNEY

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19591	49959	A	19706	318	873	AYELTPEPSPLPVFPVSADGSTT HPLADKRKASPVPQEHHELPA RPVTQRLCTYPFPNITTASEFGP ATGFRARRSGRGSTVCCNPGCY PRARPEPEPRGTPPSVSAPRAAQ EAPARQRAAGPVLA/DTVP/SPAP RGKRDISPLFGNAHSAPKPSLD LWAPP^*AAGRGGPQQA*DVTE DTQQQQWSAMA VGGTAKWM AALGRFLVTVYVEVEGVKLQTF TVTTLTQSFKYSLSKYLLQQQPL LSSRTIYPTFYYSLSLLRNLRRAFK LNAAEAKPMSSPQNLVLFLCFL SLQMAAPPRLQTKGKQAAQCS STKSTFQRGRSLRGVSPTLSPTS QQPRNLDDQQLASEQGEVGEAP LCAVIQGVIPVLGRSRSRSEEHPP VSALPGLHRKRQRQDKTLEAGPVL ADTVFPRPHAGKGTFLRCLETL TTRAPNPRWTFLPLRKLQGA VAHSRPEI/RTHSVNPNRT
19592	49960	A	19707	1	690	DQDMTSSDIPVRLEGSLWLP*IF IGTFKA/FDKHMNLILCDCDEFR KIK*GVDCGGRRLEDGNGLSG WAKQ*SLVSMTVEGPPPDKVS QSRKP/CWRRGGPTVSQALC*IL YPSWGSHPAGS/RTCWASPGWG WRAIPTGEELGKGYHLLVAKIK DKGEGP*FSNPVPTWPWGSPT YGP/RTPSR*GAHKET/SAN**K MPASWINDEI*PPGM/PPP/GMRP PPPGMRGKCLQW

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19593	49961	A	19708	1	1348	MVFWARPRTLLLCAALGLGAL YTATPAPTVAKRQGQTAQALS SEGASPKPWVLRHGIEPCKQSY WEVRTEQSPGVSERKAAAPVRL GLEIKLPLSPWDKAPEGGGGCGH SFSRLKCSFMPVLKRAVVDLPAQ RSSPANGQTACSSGSLAPVLPD WEIPPSKGRQTPYATGEIRLAS DGCPSGFTKLPEEGTDSNLCCSA SSAESNNINININININKDAHGTK PSKGPOHQRSKLDKSMKTRKN HIIKNAENSKNLNASSPPKDHN SSTAKEQNWTNEFDELTEVG RRRVIANSSKLKEHVLTTQCKEA ENFEKILEELLTRITSLEKNINDL MELKNTAQEHREAYTTSINSQID QAEERISEIIEDKLNEIKREDKIR GKRIKRKNKKISLQEIWVYVVKRA NL*IAVVPPLNKITSPTSETLST STNMSRSTLSCLLSFSCPASCT ATSAALF
19594	49962	A	19709	718	1138	GGRAAEGSQPPVAEPRCSRGA RALPLPDTSWRQPS/APQAA* VELPASPASPFAVLLSKPRLSQN KPKSPFSVASP*HGDKRQPQPSR LI*IPHLSSRAPVHS/PLGWPSNR K/HKHLRPDTAHAPAEGPPLNY VRKQQKQS
19595	49963	A	19710	5	760	RAAACCGAAPGRKRCAAPGRKR CGPQRKRSLGPPTLGQRPQPS QQLRKPRRRRGSPGSLPKSSPLP SSTGKTGWTSTRGRSVRPVVTLS RCCPPGHPCSRAPSCATARAPL PT*PPTTAPCRASPPAPRPPRPR PPPGTRSPTSRGRCRWTSGAG TSRCWSWRAGPGTAPAAAGARS RPGAPGVSAAVPCAAACSWMT SAPEVRAASSPGTPSRSGGGRS HPPCSRGLPTTGPATTAAPEAPG CWSCRRLS
19596	49964	B	19711	180	300	
19597	49965	A	19712	249	700	RQDPVSGGQSCPASCPSLWAA ARVWLQG\PAPRAR*CPVCSSC PGPGAPEDTPEAGGCCCCGCR CLRTQEPPAPLQPPHPMAQTP REEVGRRGWTPGCPGTDPCWL GLRLLCPLWDPHRSGTRPWAQ VQRDTTETKAQRGLVRCQRC
19598	49966	C	19713	273	485	

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19599	49967	A	19714	35	779	VRPPSHVTADSGRSPLSLUTYPLPLQEPGDMAAAVPRAAFLSPLLPLLLGFLLLSAPHGGSGSLHTKGALPLDVTTFY/KDYGDKLNMELSEKYKLDKESYPVFYLFRDGFENPVPYTGAVKVGAIQRWLKGQGVYLGMPGCLPVYDALAGEFIRASGVEARQALLKQQQDNLSSVKETQKKWAEQYLKIMKGKILDQGEDFPASEMTRIARLIEKKNKRSCKKAVCDPFGFGGGREGRVNLLAVSPLWNIRG
19600	49968	A	19715	2	253	
19601	49969	A	19716	494	1443	LAVPRPA\YGRSPGSLLRIPVPGLHLLNLNVWSRGAAALHTKGALPLDVTTFYKVIPKSKFVLVKFDTQPYGEKQDEFKRAENASSV\DDLLV\AEVGISDYGDKLMN\ELSEKYKLDKESYPVFYLFRDGFEPHSSHTGGS*RLGAIQRWLKGKGKVYLGDGIELVCTV*LTPLAGEFIR\ASGVEARQAPLEAGAQDNLSKCERRLRKKW\AEQYLKIMKGKILDQGEDFP\ASEMTTESLGLIEKKNKMSDGKKEELQKSLN\ILTALPRRKGAERKGAVNAVCDPFRVWWEYGRGELTLAVSPLWNIRG
19602	49970	A	19717	286	332	HHHHHPHYHHHHHHPHYHHHHHPQVHHH\HHPHYDHRRHRQGDHHGQLQYDDDHQPCQCHQHDHLRCEHQHYI\Q\WLNINNLRASRYKPLLNIMLVFAAEIMIVLVALGLMVVVLELTVVVALTMVVIVRMMGGDIGDDGGGSGDDGGGSQDDMSKNDSIPTTTTTIPTTTTTITIRAEQFTILTWKPVVSSQKNTSSFR
19603	49971	C	19718	1	546	
19604	49972	A	19719	1	90	
19605	49973	B	19720	217	951	
19606	49974	B	19721	67	1708	
19607	49975	B	19722	218	3267	

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19608	49976	A	19723	1	634	LGRLSFPREPQDPGHR/AHPSSP PRPRPHARGRRGPRRH/YHD TGANRAPEV/RPPCPES/SPVGV AEPNGLRGQQQSPRSPGAPKG L*PTPPSASSSPKPREPSALGRPC CRCEESRFLEHRNSNPRVKDSR QARGRHAEFHGRTGVFERRRS RDHLPTHFPASVRWEKLSWCA RKNGLSQLRLCHGSQHFSGYSN RKVGTESLNQVWE
19609	49977	A	19724	3	1090	
19610	49978	A	19725	1	609	
19611	49979	A	19726	23	636	FSYLPGPSPHGTWGLWELQFK MRFGVCRHLMEDSMMDMVDSP LR/PQNYLFSCELKADKDDHIFK VDNDENEHQSLRTPTVSLGVF EITPPVLLWLKCGSGPVHISGQ HLVAVEEDAESDEEEEDVKKL RISGKTKTFMATTNGKEYKHYK! SSEKSLDNKYKTRTPGFQAFGF EDLHPWPLGSQAFYLSRVTTP VFLVRLLLDFD
19612	49980	A	19727	1	830	MEDSMMDMSPLRPQNYLFGC ELKADKDYHFKVDNDENEHQI SLRTVSLGAGAKDELHIVEAEA MNYEGSPIKVTLATLKMVSQPT VSLGGFEITPPVVLRLKCGSGPV HISGQHLVAVEEDAESDEEEED DVNRVLFMKP/KRQGQPAQYVR GFGVQLEIGSH*DPEQQF*RDSA QPSLATPSTPHLQLALLCSQGV LRLPLWGQRL*GLQQLLPPQHP EEHGVHVSPGQELHHQQGDPE PLPVLPATAEVL*SGHVQGVCEK RPKQEEEGGAQARVL
19613	49981	A	19728	1	684	
19614	49982	A	19729	3	535	DSVLRGCSLEQRSFISVRLLSYL SACRHMPMEDSMMDMSPLRPQ NYLFGCELKADKDYHFKVDND ENEHQSLRVTSLGAAGAKDEL HIVEAEAAMNYEGSPIKVTLATL KMVSQPTVSLGGFEITPPVVLR LKCGSGPVHISGQHLVVYRRK HQELQAMQMDCRALSTS*ASS APRPS
19615	49983	B	19730	1	2268	
19616	49984	A	19731	198	472	AHDIGCPEVSPLVLEVARDEGP AHRPRFSH*SSHCSHWGTSQRA APPCCPICIOTTW/PGAVTGLG G*PKTRSGPGKDRSSGAASSFP GGRV

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19617	49985	A	19732	92	2049	LTALPPAVSPGGHSSSSSRTIS GIT*ELQR/LLQAVVPGPWQED VADAEECAGRCPGLMDCRAFH YNVSSHGCQLL/PWTQHSPHTR LRHSGRCDFQEKGEWGYMPT LRNGLEENFCRNPDPGDPGGPW CHITDPAVRFQSCGIKSCRVAA CVWCNGEEYRGAVDRTESGRE CQRWDLQPHQPHQPFEPGKFLD QGLDDNYCRNPDGSEERPWCYT TDPQIEREFCDLPRCGSEAQPQR EATSVSCFRGKGEGYRGTANTT TAGVPCQRWDAQIPHQHRTPE KYACKDLRENFCRNPDGSEAP WCFTLRPGMRVGFCYQIRRCT DDVVRPQDCYHAGAEQYRGTVS KTRKGVQCQR/WSLE/TG*DYP ATTSLPLPPRFTFTSEPHAQLEE NFC/RDPDGDSHGPWCYTMDP RTPFDYCALRRCQDVQFEKCG KRVDRLDQRCSKLRVAGGHPG NSPWTVSRLRNWQGQHFCGGSL VKEQWILTARQCFSSCHMPLTG YEVWLGLTFQNPQHGEPGLQR VPVAKMLCGPSGSQLVLLKLE RYVDNLGGWTKCEIAGRGETK GTGNDTVLNVALLNVISNQEC NIKHRGHVRESEMCTEGLLAPV GACEGDYGGPLACFTHNCWVL KGIRIPNRVCARSRWPAVFRV

SEQ ID NO: NO:	SEQ ID NO: of peptide sequence	Met Ind	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *="Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
19618	49986	A	19733	2	2296	HSAGQRSPSNDQVLRGTELQH LLHAVVPGPWQEDVADAECA GRCGPLLSRAFHYNVSSHGCQ LLPWTQHSPHSRLWHSGRCDLF QEKGEWGYNPTLRLNGLEENFC RNPDGDPGGPWCHTTDPAVRF QSCGIKSCRVAACVWCNGEEY RGAVIDRTESGRECQRWDLQHP HQHPFEPGKFLDQGLDDNYCR NPDGSERPWCYTTDPQIERFC DLPRCGSEAQPRQEATSVSCFR GKGEGYRGTANTTTAGVPCQR WDAQIPHQHRFTPKEYAC/KVR WAGGRALGRAAAGETGG*SR A*GWRLAG*G*VERLLRDLREN FCWNLDGSEAPWCFTLRPGTR VGFCYQIRRCTDDVRPQDCYH GAGEQYRGTVISKTRKGVQCQ RWSAETPHKLQ*VPGAPGPAR ALTLGRHALMSGTRAWKWLR LSLPRFRSRSRLGSRLTSEPHAQ LEENFC/RDPDGDSHGPWCYTM DPRTPFDYCALRRCADDQPPSIL DPPPDQVQFEKCGKRVDRLDQ RRSKLRAVAGHGPNSPWTVSL RNR*GTTACLPQRGAEVVSSVV MPLAGANLSLPPEVLAARRWQV *HLSQESVPCPNSPLL*QQQHF CGGSLVKEQWILTARQCFFSICE PPLCLGTQSHPTPPFPQAS*QVS LGATD*ESQMT*QSFSPSHMPL TGYEVWLGTLFQNPQHGEPL

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met/Asp	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, ^=possible nucleotide deletion, !=possible nucleotide insertion)
19619	49987	A	19734	727	3012	PAPTHAHSAGQRSPNDFQVLR GTELQHLLHAVVPGPWQEDVA DAEECAGRCGQLPMDRAFHYN VSSHGCGQLLPWTQHSPHTRLRR SGRCDFQKKD^YVRTCIMNNNG VGYRGTMMATTVGGLPCQAWS HKFPNDHKYPTPLRNGLEENFC RNPDPGDPGGPWCYTTDPAVFR QSCGIKSCREAACVWCNGEEY RGAVDRTESGRECQRWDLQHP HQHPFEPGKFLDQGLDDNYCR NPDGSERPWCYTTDPQIEREFC DLPRCGSEAQPRQEATTVSCFR GKGEGYRGTANTT^AGVPCQR WDAQIPHQHRTPEKYACKDL RENFCRNPDGSEAPWCFTLRPG MRAAFCYQIRRCTDDVPRQDC YHGAGEQYRGTVSKTRKGVQC QRWSAETPHKPQFTFTSEPHAQ LEENFCRNPDGDSHGPWCYTM DPRTPFDYCALRRCADDQPPSIL DPPIDQVQFEKCGKRVDRLDQR CSKLRVAGGHPGNSPWTVSLR NWQGQHFVCGGSLVKEQWILT ARIQCFSSICHMLPTG^Y*GMVG ATFFQNPQHGEPSL^QRVQ*AK MLCGPSGSQLVLLKLERSVTL N/HRVWALIILP^PEWYVVPPGT KCEIAGWGETKGTO^NDTVVLN VALLNVISNQECNICKHRGRVRE SEMICTEGILLAPVGACEDSYG GPLACFT^HNCWV^LEGIPIPNR
19620	49988	A	19735	66	234	WCSAWHWSWLPHSPSGPAASYP PAACRSAPQWPDP*^R^CPRTHR RRSPWRAPWHCP
19621	49989	A	19736	3	500	GRGGGGVRRCARPAPGRPAA ARRRGDQRGGRLGR^HVPGKTF CCGICGRGFGFRRETLLKRHERIH TGEKPHQCPVCGKRFRESFHL KHHVVTTRPYKCELCGVF GYPQLSLTRHRQVHRLQLPCAL AGAAGLPSTQGTPGACCPGAS GTSAGPTDGLSYACSD

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19622	49990	A	19737	899	2348	GRRRGGGGRCWRCGQSGPERF SCATCGQSFKHSW/DLVTHKYV HMLLLLPPSCEAVAPRGWRRSC SCPECCRVC/ELSSAA/RSATAR CFRRRSPSHIAQAPGPQVQPQDW RSRPARIRLPVGPVGMPAFPTSA SGKAWPSLRSVSPHAFWKYHT SPPAMQPSGPLWASVPAcap* <sup>K</sup> NIPSPTIWQRQLAFLSGLGLPICWV ENHGPATSSQWLVSGRSPHLL S/RAEHPFSRPLPRWVATAERQ RRPSGKRTNPFPPASPPPGAG PEVSVPPAGALPGEALGPARDL WPCSSWT*AGLPALG/DTGGGE APAP/AAAEPSEDTLYQCDCG/ TFFASAA ALASHLEAHSGPATY GCGHCGALYAALAALEEHRRV SHGEGGGEEATAAAREREPE GEPPSGSGRKKIFGCSECEKL RSRDLERHVLVHTGEKPPFCL ECGKFFRJECYKLKRHRLLHGTE RPFPCCHICGKGFIITLSNLSRHLK LHRGMD
19623	49991	A	19738	2	358	
19624	49992	A	19739	635	2441	LKAIKRHPPFTIDWNVSCMPQ SPPPFKPAVGRPDETFHFDPEFT ARTPTGVCHSGSLYNAHHLFR GFSVASSLIQEPSQQDLHKVPV HPIVQVTVFACSGFTDGYEIKE DIGVGSSYVCKRCRVHKATDTE YAVKVRQAC*VSSLVFPAGTG APGIGEYGSGLVSIQCAQDSP HNLLPQRKVEKPSLSSILVGESRS HVDKGQEVDILEMGMEFFFFIE FLVSPLATG*CFPMARSPCMGC SLSVCTAL*GQPLQGNTPFKY QQVTWPQAKPPTATAVLSPETA NVTSPQEQTRECLLKDRWLYPV VRNSSTRGPSEEIEILLRYGQHP NIITLKDVSGPRATASLVMELM RGGEELLDRILRQRYFSEREASD VLCTITKTMDYLHSQGVGAMP GAAFNILYRDESGSPESIRVCDF GFAKQLRAGNGLLMTPCYTAN FVAPEVSIPLQLTQACDIWSLGI LLYTMAG*AVTSNRCHDTPEE ILARISGGKYALSGGNWDSISD AAKVSTCPVALDPHQRLTAM QVLKHPWVVNREYLSPQNLSR QDVHVLVKVPGAGAVRTEWWE WDLNRTPQAPRLEPVLSNLAQ

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met cod	SEQ ID NO: in USN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, + =possible nucleotide insertion)
19625	49993	A	19740	144	1143	REAGRGCSAGVGGRPRRRRRK GAASRARLPFSLSIMDPSLLRER ELFKKRALSTPVVEKRSASSEVS SSSSISKKKTKVE\HGGSGSK QNSDIISNGSFNLKA\LSGSSGIVY KFGVLAKV\VNYSMKDTGIQRGD THPLTLDE\LDDE\QHLDIGLQQ KQWLMT\ALVNNPKIEVIDGK YAFKPKYNVRDKKALLML\LD QHDQRGLGGILLEDIEALPNS QK\AVKAL\GDQIPICT*SGPVRR KILFFVNDKSCQFSVG'RIFRKL WEECQLVDSHGTEEK\EEYLE ADRVFSSHARES\GPKVKVGPYS RRKGKSPA\TRKKPTFLRTSLT NHLAWN
19626	49994	A	19741	677	1590	AHPHSRRTLERQARISGAGRR SSPNAANRGSAPPSSRLASFCT AGSAIGRPA*SPCSGPWTAVSA PRSPGPGRGGRPPSPGRRPCCS VFSGGASPPSSARVSSPGSCSAS PPAAPAAWSLRGCGCWPG/VW EVHVN\TGGDVAAPAAWGSR AACGPNLGCGSHPRAGRRAGH RCGHPWSPRPAPRPSCCGRSPR PGPPGASGCPRPAPRPTPASRS GRPCSWRARAAGWPRGWWG SSAGGCRRGSGRREWPCGTA RGSPAAGVSRWTAPRCRHRRS DASASGTPARFPGAGRKGRTL WQ

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, ~=possible nucleotide deletion, ^=possible nucleotide insertion)
19627	49995	A	19742	754	2179	SKMSRLEAKKPSLCKSEPLTTERVRTTSLVKRIVTSCYGPGRLKQLHNGFGGYVCTTSQSSALLSHLLVTHPILKILTASIQNHWSSFSDCGIIFTA1LCCNL1ENVQRQLGLTPITTVIRLNKHLLSLCISYKLSETCGCRIPVDFSSQTILLCLVRSILTSKPACMLTRKETEHVSALILRAFLLTIPENAEGHIIIGKSLIVPLKGQRVIDSTVLPGLIEMSEVQLMRLLPKKSTALKVALFCTTLSGDTS*PGEGETVVVSYGVSLENAVLDQLLNLGRQLISDHVDVLVLCQKVIIHPSLQFQLNMHPIIAIDRIGSDSD/VEPLDLKWTGTQPIGSLSICPNSYGSVKDVCATAKFGSKHFFHLIPNEATCSLLLCNRND TAWDELKLTCTQTAHVQLQTLKEPWALLGGGCTETHLAAYIRHKTHNDPESILKDDECTQTELQLIAEAFCSALESVVGSLEHDGG
19628	49996	A	19743	1	652	LMPKPGDRDTKKENFRPISLMNIAKILNKILANQIQQHIIKKLINHDQVGFIQPGMKGWFWNIHKSINVJHHIKRTNDKNHMISIDAGKAFNKIQQCFCMLKTLNKLNIHGIVYLKIIIRAYD/KPPANILNGEKLEAFPLKTGIRQG/CPLLRNIV/LEVLARAIROKEIKEIKGIQSGNEEVKLSLFADDMIVYLENPIVSAQNLLKLILISNFSKVSGYKISVQ
19629	49997	A	19744	1	834	MGDFNTPSLTLDRSTRQVKNDIQELNSALYQVLDIYIRTLHPKSEYYTFFSAPHHTYSKIDHIVGSKALLSKCKRTEIIITNCLSDHSAIKLELTIKKLTQNRSTTWKLNNLLLNDYWKYKQPSENKHYANKLENLEEMDKFLDTYTLPLRNQEEVESLNRPITRSEIEATNSLPI/ KKSPGPDGFTAEEFYQMLLEVLAIRQKEIKEIKGIQLVKEEVKLSLFADDMIVYLENPIVSAQNLLKLIGNFSKVSGYKI/NVQKSQAFLYTNNRQTESQIM
19630	49998	B	19745	1	1521	
19631	49999	B	19746	1	1461	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met cod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, !=possible nucleotide insertion)
19632	50000	A	19747	1	2347	MELKTKARELHDECTLSRFD QLEERVSVMEDEMNEMLPTK KSPGPDGFTAEFYQRYKEELVP FLLKLFQSIEKEGILPNSFYEPSII LIAKPGRDTTKKENFPISLMNI NAKILNKMLANQIQQHIKKLIIH HDQVGFIPGMQGWFNIRKSINV IQHINRTKDKNHNMIISIDAEKAF DKIQQHFMALKTLNKLVLLEVLA RAIRQEKEIKGIQLGKEEVKVSL FADDMMIVYLENPTVSAQNLKL IGNFSKVSGYKINVQKSQAFLY TNNRQTERQIMSELPTTIASKRI KYLGIQLTRDVKDLFKENNPKPL LKEVKEDTNEWKNIPCSWVGRI NIVKMAILPKVIVRFNAIPKLP MTFFTELEKTTLKFIWNQNPKAC IAKSISFSQKNKAGGITLPDFKLY YKATVTKTAWYWWQNRDIAQ WNRTEPSEIMLHIYNYLIFDKPE KNKQWKGDKDSLNFNKCWCENWLN AICRKVKLDPFLPTYTKMNSR WIKDLNVRPKTIKTLLEENLGIITI QDIGHVGKDFMSKTPKAMATKA KIDKWDLILKLKSFTCAKETTIRV NRQPTTWEKIFATYSSDKGLISR IYNELKQIYKKKTNNPFIKKWAK DVNRHFSKEDIYAAKKHMKKC SSSLAIREMQIKTTMRYHHTPV RMAIIKKSGNNRKIQ/GGIWCD RIL*R*TTCRVAKEIQSQL*RR/W KRLQRTLSIPVLDV*PPMF*AS
19633	50001	A	19748	1	1818	

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19634	50002	A	19749	1	1725	MELKTKARELREECRSLRSRCD QLEERPNLRLIGVPESDGENGT KLENTLQDIIQENFPNLAKQVN VQIQEIQRTPQRYSLRRATPRHII VRFTKVEMLKEKMLRAAREKGR VTLKGKPIRLTADLSAETLQAR REWGPIFNKLKEKNFQPRISYP KLSFISEGEIKSFTDKQMLRDFV TTRPALQELLKEALNMERNNR WFFEKINKIDRPLARVIKKRE KNQIDAICNDKEDITTPNTEIQT IREYYKHLYPNKLLENLEEMDT LDTVTFPRLNQEEVESLNTSITG SEIVAIIS/NSIPTKKS PGPDGSTA EFYQ^MLEVLARAIRQEKEIKGI QLGKEEVKLSSLFADDMIVYLEN PIVSAQNLKKLISNFNSKVSGYKI NVQKSQAFLYTNNRQTESQIMS ELPFTIASKRKCLGIQLTRDVK DLFKENYKPLLKEIKEDETNKW KNIPCSWVGRINIVKMAILPKV YRFNAIPIKLPMTFFTDLKTTL NFIWNQKRARITKSILSQKNKA GGITLPDFKLYYTATVTKTAW YWYQNRWYWYQNRDIDQWN RTEPSEITPHVYNYLIF

SEQ ID NO: NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USNN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
19635	50003	A	19750	1	1719	MHNTDGNRFLSHWGYRQALSI SKPASASLHPSSKTKPLGTQSKT VVAKRNREHGKKERSSPAME QSWMENDFDELREEGFRRSNY SELREDIQTGKEVENFEKNLE ECITRITNTEKCLKELMELKTK ARELREECRSLRSRCDQLEERR KQERSKIDTITSQKLEKQEQ THSKAGRQEITKIRAELEKIEET QKTLQKINESRSRWFFERINKIDR PLARLIKKKREKNQIDTIKNDK GDITTDPTEQTTIREYYKHYLA NKLENLEEMDTFLDTYTLPRLN QEEVESLNRPPITGEIVAJINSLP TKKSPGPDGFTAEFYQRYKEEL HINRAKDKNHIISIDAEKAFD KIQQPFMLKTLNKLVLEVLARA IHQKEIKGIQLGKEEVKLSLFA DDMIVYLENPIVSAQNLKLLS NFSKVSgyKINVQKSQAFLYTN NRQTESQIMSELPTIASKRIKY LGIQLTRDVKHLFKENYKPLLK EIKEDTNKWKNIPCSWW\GRUNI VKMAILPKVIYRFNAVPIKLPM TFFTELEKTTLKFIWNQKRACIA KSILSQKNKAGGITLP

SEQ ID NO: NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, !=possible nucleotide deletion, !=possible nucleotide insertion)
19636	50004	A	19751	2	2133	WRRYYQANGK*KNK/QKKAGV VILVSDKTDFKPTKIKRDKEGH YIMVKGSIQQEELTVLNLYAPN TGAPRPFMKQVLRDLQRDLDPH TTIMGDFTPLSTLDRSARQKV NKDIQELNSALHQADLINIYRIL HPKSTEYTFISAPHRTYSKIDHI VGRKALLRKYKRTEIITDCLSD HSAIKLELRIKKLTQNNSTTWK LNNNLLNDYWIHNKTKAEIKM CFETSENKDTTYQNLWDTCKA VCREKFIALNAHKRKQERSKID TLLSQLKE/LEKQEQTISKASRR KSRRNG*IPGHHIHPPKTKPGR* VPE*TNNRV*N*GNN*LTNQK KFRTRIHSQILPEHSAAGSSGQG NQAGERNKGY SIRKRGQSIVPV CR*HDCIFRKPHHLSPKSP*AVK QLQQLSLRIQNQRAKITSSPHQ* QTNREPNHE*TFIHNCFKENKIP RNPTYKGCEGPQGELOTTAQO NKRGHKQMEEHSMMLMDRKNQ YHENGHSAQGNL*IQCHPHQAT NDFLHRIKGKNYFKVHMEPKKSP HCQVNPKPEQSWRHAT*LQ TILQGYSNQNNSMVLVPKQTYRP MEKNRGLRNNNTLRLPSSL*QT *QKQEMGKGFP* *MVLGKLAS HM*KAETGSLPYTLYKN*FKM D*RLKC*T*NHKNLRRKPROYH SGHRHEQQLYV*NTKNSGNKS QN*QMGSN*TKEELLHSKRNYH
19637	50005	A	19752	1	1314	

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19638	50006	A	19753	1	1998	MVKGSIQQQEELTILHIYAPNTGAPRFIKQVQLSDLQRQLDSHTLIMGDFNTPLSTLDRSMRQKVNKDTQELNSALHQAAALIDITYRTFHPKSTEYTFPSA.PHHTYSKIDHIVGSKALLNKCCKRTEIITNYLSDHSAIKLELRINKNLTSRSTTWKLNNLLNDYWVHNEMKAEIKMFFETNEKDITTYQNLWDAKA/PLARLIKKKREKNQID/TIKNDKGDITTDPTIEQTTIREYYKHLYANKLENLEEMDTFLDTYTLPRLNQEVESELNRPITGEIVAINSLPTKKS PGPDGFTAEFYQRYKEELVPFLKLFLQSIEKEGILPNSFYEASII LIPKPGRDITTKKENFPRISLMNIDAKILNKILANRIQQHKKLJHH DQVGFIQPMQGWFNIRKINSINVIQHINRAKDKNHNMIISIDAEKAFDKIOPQPFMLKTLNKLVLEVLARAIRQEKDIKGIGQLGKEEVKLSFADDMIVYLENPIVSAQONLLKLISKFSKVSGYKIHVLKQSQAFLYTNNRQTESQIMRELPTIASKRKYLGQLT RDVKDLFKENYKPLNN EIKEDTNKWKNPICSWIGRINIMRRSSAPSGCHLCPPSLYLHSPNVELKQASFVAGFQWKLGITAPTQPRGVGDDFVTSTSPPSLDMFPRLKGAENSPHRSGRD
19639	50007	A	19754	1	3288	
19640	50008	A	19755	1	1293	
19641	50009	A	19756	264	490	VYLLIVLAVLYTNNRQTESQIMSELPFTIASKRKYLGQLT RDVKDLFKNYIPLKLEI*EDTSKWKSIPCSWI
19642	50010	A	19757	1	1845	
19643	50011	A	19758	1	3144	MGDFNTPLSTLDRSSRKVNKDTQELNSTLHHADLIDITYRTLHPKSTEYTFPSA.PHHTYSKIDHVVGSKALLSKCKRTEIITNCLSDHSAIKPELRINKLTLQRSTTWKLNNLLNDYWVHNKMKAEIKMFFETNEKDITTYQNLWDFTKAVSRGKFIALNAHKRKQKRCKIDTLASQLKEVEKQEQTHSKASRQQEITKIRAEKIEETQKTLQKINESRSWFLEIRINKIDRPLARLIKKKR EKNQIDVIKNDK
19644	50012	B	19759	1	1743	

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19645	50013	A	19760	1	1500	MGKKQSRKTENSKNQSASPPPE ECSSSPAMEQSWMENDFHELR EEGFRSNFSELKEDVRTHSKEA KNLEKRLDEWLTGITSVEKSLN DLMELKTMARELCDKCTFS KFHQLEERVSVTEDQMNEMKS WFFEKINKIDRLLARLIKKKRE KNQIEAIKNDKGDIITDPTEIQT TIREYYKHLYTNKLENLEEMDT FTGTYILPRLNQEEIESLNKPIT GSEIEAAINSLPTKKSPGPDGFTA EFYORYKEELLNFNIRKLNLQI INRTQDP*PPLVLSRIGRRVHQ YLENPVSAQNLKLKSNFSKV SGYKINVQKSQAFLYIKKRQTE SQIMSELPFTIASKRKYLGQLI RDVKDLFKENYKPLLNEIKEGT NKWKNIPCSWSIGRINIVKMAILP KVIYRFNAIPKLPMTFTTELEKI TLKFIWNQERACIATLSKKN KAGGIMLPDFKLYYKA/TVIKT AWDWYQNRYLDQWNRTEPEI TPHIYNHLIF
19646	50014	A	19761	1	3192	
19647	50015	B	19762	180	190	
19648	50016	A	19763	1	3212	MVKGSIQQEELTILNIYAPNTG ALRFIKQVLRDLQRDLDHSIIUM GDFHTPLSTLDRSTRQKVNDI QEINSALHQEDLIDIVRTLHPKS TEYTFSAPIHHTYSKIDHIIVGSK ALLSKCKRTEIJTNCLSDHSAIK LELRINKLTQNRSTTWKLNNLL LNDYWWHNEMKAIEKMFETN ENKDTTYQNLWDTFKAVCRGK FIALNAHKRKQERSKIDTLSQL KELEKQEQTSHSKASRRQEITKIR AELKEIETQ

SEQ ID NO: NO:	SEQ ID NO: of peptide sequence	Met hed	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, !=possible nucleotide insertion)
19649	50017	A	19764	1	2607	MTNHCFKRQFQKHEMLLKEDC EPGDSSFILGEQHWENMLCEPK QHPPQQGEGRAAGQANPILNT DVSPGAGAKESEEKIYQHLYNT YFKQKCMSCSGFTFSSYAMHW VHQAPGKGLEWVSAIGAGGGT YYADSVKGRFTISRDNAKNSLY LQMNSLRAEDMAVYYCARDTI DAYGDEKPTIVTRIRVLRKLR DTCHMGAEADRTFLSPIAQHPV CHVETHLGMQVANSSEEDELV WSKWDVDVKFILCCAKYHREQ LQESALDLKSLHCPSPASPALFL ATPSQPVLTTPGSAASSQGAE MGAHFLVQLVQSGAETRESFD PALPEMETQRTDEQCRAVHPGP QKERHGNMSPPLLMKGSSSPVP SGPGEEPSHREPVSFICGRCLLT LLLGDCWLWEGEGAWTQGDVLQ PSDRASFLAMGVNTTVQVGD LSGYFPNSVGKACKCREFHTLT PLAHTSSTTHETFPGAQCEVQL VESGGGLVQPGGLRLSCPDSG FTFSNHYMSWVRQAPGKGLEW ISYISGDGSYTNYADSVKGRFTI SRDNANNNSPYLQMNSLRAEDT AVYYCVKHTARGKLEKQEOTY SKASRQEITKIRAEKETETQK TLQKINESRSRWFEEKIKYIDRPL ARLIKKKREKNQIDAIAKNGKD ITTDPTEIQTTLREYYKHLAYN KLENLEGMDKFLDAYTLPLRN
19650	50018	A	19765	1	1251	
19651	50019	A	19766	1099	4113	
19652	50020	A	19767	1	2628	
19653	50021	B	19768	1	2970	
19654	50022	B	19769	1	4142	
19655	50023	A	19770	1	4091	MHIVVETALSASWQNKA KPPARVLLQVVPNVWFLV AVVWELYPSLDLMDRSIE CSSSPATEQS WTENDYD KLREEGFR RSNYSE LQEDIQTK GKDVEN FEKNLE ECITR ITNTQK CCLKE LMELKT KAR ELREE CRLS RSCD QLEER VSV MEDEM NEMK QEGKF REKRIK R NEQL QEJW D YV KRP NLRL IGV P ESDG ENGTK LKN TQDII QENF P NLA RQAK VQI QEIQ RMP QY S L TRAT PRH I V RFT KVE

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met/hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, ==possible nucleotide insertion)
19656	50024	A	19771	156	450	LQVEIYKTVKMHCIWHKQMVS SYFFYQKKNLSNFEELVFLKTA SGMFSTVGCHPTRCEFEKNN PDLYLKELLNLAEKKNGKVVA IGECGLDFDRLQ
19657	50025	A	19772	173	1009	LHGGNLQDSKDALHLAQTNG MFFSTVGVIHPTRCG*YFEKNNP DLYLKGVAKIFA EKTILKGKLW QLGEGLDLD RLQFCPKDQL KYFEKQFE LSEQTKLPMPLFLHC RNSHGWNLFDIMKRNRDRFCVG GVVHSFDGTKEAASSISLIDLDLY IGFNG/CASPENLEANLGRFWK S PSEKLMIA DAP WCGVKST HA GSKYI RTAFPS KKWESGH CLKDRNEPCHIIQLEIMSAVRD EDPLELANTLYNNTIKVFFSWN IGICLPLS IMYVKFHSTS
19658	50026	A	19773	16	1558	QEHLQRASPRLLQLLPPLPPPP PPAFGGSLSSLGSRMSRQV VRS SKFRHVFGQPAKADQ CYEDVR VSQTTWDSGFWC/SVNP*VLW ALICEASGGGAFLVPLPLGIWT LWDKNAPTCGCGHS/APVLDIA WCPHNNDN VIA SGSED CTVMV WEIPDGGLMLP REPVV TLEG HTKRVG IVAWHTTAQNVLLSA GCDNVIMVWDVGP GAAMLDT GPRGA/HPDANRYRGDWEP DGG LICTSCRDKVR IIEPRKGTVVA EKDRPHEGTRPVRAVFVSEGKI LTTGFSRMSERQVALWDTKHL EESPV/SLRKLHTRNGVPVAFFG P DTNIVYLRGKG SGP RVFEUT SEVAPFLHY SMFS SKESQRG  MGYMPKRGKVNK CEIAGFY KLHDGR/CVSPMPKPVPRKSDL FQEDLGPTPPRGPDPA LT A EE WLGGRDVG PLFISLKDGYV PP KSRELARVNRLGLD GRRR AAP EASGTPSSDAVSRL EEEMRKLQ ATVQELQKR LDRLEETVQAKL
19659	50027	A	19774	229	475	

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19660	50028	A	19775	225	965	EWAWRSQLRSEHSRADPTRSSCRSCAKMSGEENPASKPTPVQDVQGDGRWMSLHHRFVADSK^DKSGSKKKNPPPEVVFIGDSLVQLMHCEIJWRELFSPLHALNFGIGGDGTQHVWLWRLENGELEHIRPKIVVVVWVG/TPNNHGHATAEQGILLPRGQHPNPLREKNRQVNELGTTGTWLGHPRAHFLDADPGFVHSDGTISHHHDMYDYLHLSRLGYTPVCRALHSLLLRLLAQDQQQGAPLLEPAP
19661	50029	B	19776	691	1077	
19662	50030	A	19777	481	1308	PSVAFL^PSLHRYGHTGTTAGPGWPACAAGS*AA/SSSRGLPVLQASSNSHRCNSTPSGAGQRRVRRAP*MASTTPGGTESGPKARNAFMRSTSAFCRGQ*QRPVPSSSSRSSRACAAGETASGDPRAQRQLRS*DEESSSPSLDFRQA/PWPTAPCVKVSYSSSRMFSGMSPWRSSDNKRNSFLRKTTGSNSAIDLDTPPMPEVCLLPSLGYPLVPPVAEVHMPVPAPILPSAGIRRKIKAASAKQLPLFQMDDDSFSQHRVQGDTKK
19663	50031	C	19778	41	318	
19664	50032	A	19779	970	1193	INNHIRDSCWTCHCSC/QPPPPPPLLPQPPP^LSAPRVIERKE*DRL/CPGEQTSSPTPSRTQSAAAATQLSLPP
19665	50033	A	19780	1	494	MDGRVMAAGGRQAPGQKKAGTSEAPPSQEWPEAWYGLCLQQKLRAVYLVQSQPCGTGPVLAPGAAACPAAAASTPGCAQW/CGPRACSPQTSSQLCAWFAFSSRCPDFCPNPPRPL*DPPSWPTDPADRCSPLELTIRDSCWTCHCSCRRRHRRPCCRSRRPDSPRIG
19666	50034	C	19781	120	392	
19667	50035	A	19782	174	375	

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19668	50036	A	19783	33	1154	QFALCAGWWLCGRGGRTPAT MSGFSTEERAVPFSLEYRVFLK NEKGQY1SPFHDIPIYADKDVFH MIVVEVPRWSNAKMEIAKTDP LNPBKQDVKKGKLRYVA^NLFP^ YKGYIWINYGVAFPQTWEDPG^ HNDKTLGGCGGLTMDP^IDVC^* NWEGKVCARGEIIGVVKVLGIL AMIDGGGTDWKVIAINVDDP GCQPINND^NDVKRLK^PGYL^* KLPVDWFR^RYKVPDGKPENEF AFNAEFKDK^DFAIDIKSTPWT LGKALVT^ENRMKGKISCMNT NFVLRAPFKVCILDAQSPLWD ALPTHPCGICPCHSTQQTVDKG VPITQKNLMRFPIYEQADIAYIR VPSWMVLEVVKVVAFSKAFKFV EPHPNLK
19669	50037	A	19784	I	612	VTQEDDIIEEHKPRTPRSPPLL APSPACQAFGEGHSPGHPAIST GAGPRPSASFSPHLSGLHREPP LNWSVCPGLVWSPKPALDETH PFVQQFPHQATLEWGVFHARDV GRRWGRRLGNLQIGSEVARRR RVGGGLQCRRLVGAGSPGAD W**SG^EEACGGRWAA/GADG WGLGRPRELICRGWRRLA APGPQRPGFVSVSTPRCRPRSG METQTPALRVQQDDLFQS
19670	50038	A	19785	I	951	MEEGISSQIGRRENECQQKKCQ TLIKPSDLVRTHSYHENSMGETI LVQLLPPGTAFDMWELQFKLI TQTFSHHNQLAQKTREREKAR QEAEERREKAERAARLAKEAKS ETSGPQIKELTDEEAERLQLEID QKKDAENHEA^QLKNG^SLDSP GKQDTEEDEEEDEKDKGKLKP NLNGEDLPNRYWTQTLSELD LAVPFCVNFRKGKDMVVDIQ RRHRLRVGLKGQPAI^DGELYNE VKVEESSWLIEDGKVVTVHLE KRGPADAHSRALSVLQASRLL GVHCVPGTVPNAEIQVVDFVIY FWQSVIPQASPISE

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19671	50039	A	19786	87	1191	SAELRDVDRSAARLGGEQEEER FDGMLLAMAQI <sup>Q</sup> HEGGVQELV NTFFSF <sup>L</sup> RRKTDFFIGGEGTAE KLITQT <sup>F</sup> SHHNQL <sup>A</sup> QKTRREK ESPRRRAE <sup>R</sup> RKEAERA <sup>A</sup> RLAK EAKSETSGPQIKEL <sup>T</sup> DEKA <sup>A</sup> ERL QLEIDQKKDAENHEAQLKNGS LDSPGKQDTEEDEEDEDKG KLKP <sup>N</sup> LGNRADLAQ*RLNPDP <sup>C</sup> REL <sup>D</sup> LA <sup>V</sup> PF <sup>C</sup> CVNFR <sup>L</sup> KGKD <sup>M</sup> V VDIQRGTP <sup>R</sup> IV <sup>G</sup> LKGQPSDSL <sup>M</sup> GELVNEVKVEE <sup>S</sup> WLIE <sup>D</sup> GV <sup>K</sup> V VT <sup>V</sup> HLEK <sup>I</sup> NKMEWW <sup>S</sup> RLVS <sup>S</sup> DPEINHPRKINPENSKA <sup>S</sup> DLIDS *DFASMVEKDDG <sup>M</sup> TQRTESPM GLPNFQT <sup>N</sup> RRKQE <sup>I</sup> LK <sup>K</sup> FM <sup>D</sup> Q HP\EMGFP <sup>K</sup> AKF <sup>P</sup> T <sup>N</sup> PC <sup>F</sup> PP
19672	50040	A	19787	3	403	
19673	50041	A	19788	281	1952	DPVPGC <sup>R</sup> RLVAMAP <sup>T</sup> IQTQAQ REDGH <sup>R</sup> PN <sup>S</sup> HRTL <sup>P</sup> ERSG <sup>V</sup> CR VKYCN <sup>S</sup> L <sup>D</sup> IP <sup>F</sup> DP <sup>K</sup> FITY <sup>P</sup> FDQ NRFVQYKATSLEKQH <sup>K</sup> HDL <sup>L</sup> T EPDLG <sup>V</sup> T <sup>I</sup> DL <sup>I</sup> NP <sup>D</sup> TY <sup>R</sup> IDP <sup>N</sup> VL LDPAD <sup>E</sup> KL <sup>L</sup> EE <sup>E</sup> I <sup>Q</sup> APT <sup>S</sup> KS <sup>R</sup> Q QHA <sup>V</sup> V <sup>V</sup> P <sup>W</sup> MRK <sup>T</sup> EY <sup>I</sup> ST <sup>E</sup> N <sup>F</sup> RYC <sup>I</sup> F <sup>H</sup> E <sup>K</sup> \PEV <sup>K</sup> W <sup>G</sup> SV <sup>K</sup> Q <sup>Q</sup> F TEEEIYKDRD <sup>S</sup> Q <sup>I</sup> T <sup>A</sup> E <sup>K</sup> T <sup>F</sup> EDA QKS <sup>V</sup> IE <sup>G</sup> LG <sup>W</sup> GE <sup>A</sup> RISQ <sup>H</sup> YS <sup>K</sup> P RVT <sup>P</sup> VE <sup>V</sup> M <sup>P</sup> V <sup>F</sup> PD <sup>F</sup> KM <sup>W</sup> IN <sup>P</sup> C AQVIFDSDP <sup>A</sup> KD <sup>T</sup> SG <sup>G</sup> AA <sup>A</sup> LEM MSIQAM <sup>I</sup> RGM <sup>M</sup> DE <sup>E</sup> GN <sup>Q</sup> F <sup>V</sup> A YFLP <sup>V</sup> E <sup>E</sup> TLKKRKR <sup>D</sup> Q <sup>E</sup> EMD <sup>M</sup> YAP <sup>D</sup> DY <sup>V</sup> DY <sup>K</sup> IAREY <sup>N</sup> WN <sup>V</sup> K NKASK <sup>G</sup> YE <sup>E</sup> NY <sup>F</sup> F <sup>I</sup> REGD <sup>G</sup> GY <sup>V</sup> YNELE <sup>T</sup> \VRLSKR <sup>R</sup> AK <sup>A</sup> GV <sup>Q</sup> SGTN <sup>A</sup> LL <sup>V</sup> V <sup>K</sup> H <sup>R</sup> D <sup>M</sup> N <sup>E</sup> KE <sup>L</sup> A QETRK <sup>A</sup> Q <sup>L</sup> EN <sup>H</sup> EPE <sup>E</sup> EEEEEE <sup>E</sup> ME TEKE <sup>E</sup> AGGS <sup>D</sup> E <sup>E</sup> Q <sup>E</sup> K <sup>G</sup> S <sup>S</sup> SE <sup>E</sup> KE GSEDEHSG <sup>S</sup> E <sup>S</sup> E <sup>R</sup> E <sup>E</sup> G <sup>D</sup> R <sup>H</sup> EA <sup>S</sup> DKSGSG <sup>G</sup> Q <sup>D</sup> D <sup>S</sup> SDY <sup>*</sup> ARA <sup>A</sup> RD <sup>K</sup> EEIFGSDAD <sup>S</sup> ED <sup>D</sup> AD <sup>S</sup> DD <sup>D</sup> DRG QAQGGS <sup>D</sup> N <sup>D</sup> SD <sup>S</sup> GR <sup>N</sup> GGG <sup>Q</sup> R TRSH <sup>S</sup> R <sup>S</sup> ASP <sup>F</sup> PSG <sup>E</sup> HS <sup>A</sup> Q <sup>E</sup> NG  SEAAASD <sup>S</sup> SEAD <sup>S</sup> D <sup>S</sup> D
19674	50042	A	19789	1	885	
19675	50043	C	19790	164	361	
19676	50044	C	19791	22	156	

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19677	50045	A	19792	1	1344	PGRTTMSMAEDVFLSAPIPRGC ADGRDADPTEEHMAQTERNDE EQFECQELL*CHVQVGAPEEE EEEEDA\VLVAEAEAVAAAGWM LNFLCLSLCRAFREGRS\EDFRR RNSAEAIHGLCSLTACQLRTIYI CQFLTRIAAGKTLDAQFENDER ITPLESALMIWGSIEKHDKLHE EIQNLIKIQAIAVCMENGNFKG AEEVFERIFGDPNS\HMPFKSKL LMIIQSQKDTFHFSF\QHFSYNNH MEKIKSYVNVNVLSEKSSTFLM KAAAKVVESKRTRTITSQDKPS GNDVEMETEANILGYKKKC\LT NSLR*LPNQQRVQYPY*GSHKNL FYLKLQHGTQQQDLNKKRERV GTPQSTKKKESRRATESRIPVS KSQPVTEKHRARKRQAWLWE EDKNLRSGVRKYEGGNWSKIL LHYKFNRNTSVM\KDRWRTM KKLKLISSED
19678	50046	A	19793	1	1444	IPGSTISCLKGQY\PSFPNMAED VSSAAPSRRCADGRDPDPTEE QMAETERNDEEQFEC\QELLEC QVQVGAPEEE\EEEDAGLV AEAEAVAAAGWMLDFLCLSLCR AFRDGRS\EDFRRTRNSAKAIY GLSMLTACPLRTIYICQ\FLTRIA AGKTP*MHRFENDERITPLGISP *MIWGSIEKEHDKLHEEIQNLIK IQAIAVCMENGNFKEAEEVFER IFGDPNSHMPFKSKLLMIIQSKD TFHSFFQHFS\YNHMMG\KIKSY VNYVLSSEKSSTFLM\KAAAKV ESKRTRTITSQDKPSGNDVEME TEANLDTRKRSIHKNLF\LSKLQH GTQQQDLNKKRERVGTPQSTK RRKKEGRATESRIPVSKSQPV TPENDRARK\RQAWLWGRKDK ILRSIGVREFG\EGNWS*ILLHY KFNNR\RTSVM\KARWRTMEG NLKLDFLQDSEDWIVFVKSFDG KGQFKYFDHCILFETCVIDVI
19679	50047	A	19794	1	1020	
19680	50048	A	19795	411	769	SHLGFPGTWTRLWPSRMSPC QQS\RNRRV\QLSTSEL/APALGN WARLPQVTEQ*FRGLRKGSRT MPGSSPPATWTKGCLLA*Q\CL CPQLGWSRVAP*CRLGALFLAC SLLAAPLRCF

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19681	50049	A	19796	171	325	ETVAVSSA GARASSIMRIMVSSRPSETSL ESVFPDSAP/PGL*PPPCLSFGL
19682	50050	A	19797	335	1536	GCSPCPPQ/QSIRNRV1QLSTSEL GEMELTW/QEIMSITEACRVLN APSEPSFEAPKPQLPYL/GPPPTT TY\CPGSIH PDSGFPI\PPPYEL PASTSHV PDPPIYSY\GNMAIPV SK\PLSLSGLLSE\PI\QDPLALLD IGLPAGP\PKPQEDPESDGSGLN YSDAESLE\EGTEA\GRRSELC RRCY\VPVE\YPSLMPNSLAHSN YTL\PAAE\TPLAEPSSGPVRA KPTARGE/AQGSRDER\ALAM KISF\PTDKIVNFPVDDFNELLA RYPLTE\SQLALVRDIRRRGKKN VAAQNCRKRK\LET\U\HLE\RK ERLTNE\ER\U\LR\U\IGEASR\T LKVMRQQLQ\ELY\REH\PSHLR E*NPQ\TAYSP*KK*RACKQAC PN\GDP\PS\PCGPRGT\KMEAHRL
19683	50051	A	19798	1	408	LNLMRWEAVQARGGA\FR\PRV DPGPT\PIPHN\SSSRFDCNSVSTA P\RV\LVSGICAAGSFVLFVAFSHS VGTS\CL/GY\FL\LT\SP\EAQDPGG EEEAE\SAARQ\PLRTE\APESKPG SSSS\SLRERWTVFKGL\WYIV PLV
19684	50052	A	19799	1	759	
19685	50053	A	19800	1	1815	
19686	50054	A	19801	1	942	MGGCAGSRRRFS\DSEGEETVPE PRPLLDHQGAH\WKNAVGFW LLGLC\NNFSYV\VM\LSAAHDILS HKRTSGNQSHVDPGPT\PIPHNS SSRFDCNSVSTA\PRV\LVSGICA AGSFVLFVAFSHS\VGTS\CL/GY\FL LLTSPEAQDPGEE\EA\SAARQ PLRTE\APESKPG\SSSS\SLRER WT\VF\KGL\WYIVPLVVVYFAE Y\FINQGLV\SE\GCL\FR\PP\FSALN VCEVNLVKV\VSQHQ\GG\WVAVV TQGK\KHPISCR\I\NVDGMN\IIS NDGSN\KL\NRSR\KARV\SY\KVQR TINA\SLNA\AT\STR\AV\SS\NP\NFV

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19687	50055	A	19802	82	1620	SLSPVADPHPSRGSPWTLYDP GPSGDLNLMRWIGCAAGSRRRFS DSEG^ETVPEPRPLLDHEGAH WKNAEGFWLLGLCNNSFYVV MLSAAHDLSHKRTSG^NQSHV^ DPGPNQDSPITAYSRFDCCNSVF TGAVLLADILPTLVKLLL^APLG ^LHLLPYRSGRVLLVSGVUCAGG KFRPGFAFSHVSGTSLCGCWSF ASISSGL^GEVTFLSLTAFYPR VISWWSSGTGGAGLLGALSYL GLTQAGLSPQQTLLSMLGIPAL LLASYFLLLTSPEAQ^DPERGEE AKISQAQQP^FIRTEGPE^GKPGSS SSLSLRLERWTVVKGGLWVPLF PWFEVTFPKYF^TQGLFELP/LFF WTTLSLHAQQYR^WYQMLYQA GVFASRSSLRS^CSIGFTW^ALAL LQCL^LNLW^FLLADVVWFGFLPSI YLVF^LNLW^YEGAPWGSASI^REK PVFH^IR^PWRPSDEHREVCKWR PPCHL^*HTGGFILSGASLALPLH DFLLPSSP^DTRDPQDAGHIHLW ARGTGYQ
19688	50056	C	19803	270	542	
19689	50057	A	19804	271	449	CLELRNL^FYGACSWEVSISSDS EKPG^IFN^AS^PASA^VHC^*^G^F^ARP SSWRV^LGA^CTFH^HSV^YAKTA KR^KAST^*RHFHH
19690	50058	A	19805	21	79	
19691	50059	A	19806	1242	1560	WATR^SSCS^MMEMPPWC^PGC AGR^WRRRGASRG^P^REAA^AGH^* K^PRTS^N^QGE^Q^P^T^R^P^S^P^Y^A^C^A R^R^A^F^A^G^P^W^A^S^P^S^P^S^P^S^A^G^G^L A^W^G^A^P^C^V^A^H^P^T^R^P^S^P^Y^L^V
19692	50060	B	19807	148	2949	
19693	50061	A	19808	1335	2173	KQAH^P^R^E^E^K^R^E^E^K^R^K^E^G^P^S V^P^E^T^L^K^K^Q^R^N^F^T^E^L^K^I^K^L^R^K K^F^A^Q^Q^M^L^R^K^A^R^I^R^K^L^I^Y^E^K^A^K H^Y^P^K^E^Y^R^K^M^Y^R^T^*^I^S^N^G^R^G^W^A R^K^A^G^Q^L^Y^L^V^L^K^N^P^K^F^A^V^I^V^R^N Q^K^V^S^M^G^V^S^P^I^L^K^R^V^V^V^S^F^L^R^P S^S^K^S^N^E^T^F^V^K^A^K^L^K^Q^R^P^S^D^*^T^M P^*^G^L^V^R^G^P^I^*^L^P^W^G^Y^P^Q^S^*^S^P^V N^E^P^*^S^Y^K^R^G^Y^A^K^I^Q^*^E^A^L^P^L^T D^N^A^L^I^A^S^W^V^N^S^A^F^C^M^I^D^D^L^I H^E^I^Y^T^V^G^K^R^F^K^I^E^A^N^N^F^W^P^L^Q I^V^L^P^R^G^G^I^M^K^K^T^T^H^F^V^E^G^G^D A^G^T^Q^R^S^D^Q^I^N^R^L^I^R^R^M^N
19694	50062	A	19809	3	186	
19695	50063	A	19810	272	428	

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19696	50064	A	19811	50	2237	RSLKAFICSILSMKQSRDPPVK MQGSITTPGSIALAQAAQAAQV PAKAPLAGQVSTMVTTTSTTTV AKTVTVTRPTGVSFKKDVPPI NTTNIDTLLVATDQTERIVEPPE NIQEKAIFIENNLSQLSNSMTQKEE LVNNTELVQSYRQQIGNVVNQ ANLQLFWNMYSRRLDINRP GTVPNAKTLRCPVMLVVGDNA PAEDGVVECNKSLDPPITITFLK MADSGGLPQVTPQPGKLTLEAFK YFLQGMGYMPMSAMTRLRSR TASLTSASSVDGSRPQACTHSE SSEGLGQLNLKFEIEVLCCKNLA LDINELKPGNLLKDKDRLKNLD EQLSAPKKDKVQPEELPPITTT TSTTPATNSTCTATVPPQPQYS YHDINVYSLAGLVPHTLNPTA HPQLKQCVRQAJERAQELVHP VVDRSIKIAMTTCEQIVRKDFA LDSEESRMRIAHHMMRNLLTA GMAMITC/RE/PLLMSISTNLKN SFASALRTASPLQREMMQAA AQI*AQDNCFLL/CKVGGVDPK QLAVYEEFARNVPGLPTNDLS QPTGFLAQPMKQAWATDDVA QIYDKCITELEQHLHAIPTLAM NPQAQALRSILLEVVVLSRNSRD AIAALGLLQKSMENGLNYMAV AFAMQLVKILLDERSVAHVT EADLFHTIELMRINAHRGNA PEGMDITTRQVNKKREGFND
19697	50065	A	19812	1	3777	KNPEFKMVNLNETYRNIKVLLT SDKAAANFSDRSLLKNLGHWL GMITLAKNPKILHTDLDVKSSL LEAVVKGQQELLYVVPFVAKV ILESSIRS VVFRPPNPWWTMAIMN VLAELHQEHDLLKLNLPKIEVL CKNLALDINELKPGNLLKDKDR LKNLDEQLSAPKKDVQPEELP PITTTTSTTPATNTCTATVPP QPQYSYHDINVYSLAGLAPHIT LNPTIPLFQAHPLQLKQCVRQAI RAVQELVHPVVDR